Microevolution, the Hardy-Weinberg Theorem and Natural Selection in Simulated Populations

1601 ENV: Biological Systems

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Abstract

Population genetics involves the study of allelic and genotypic frequencies in populations of species over time. It can be affected by various factors. For example, mutations and sexual recombination create new alleles and shuffle alleles with a population. Genetic drift and inbreeding in small populations decrease genetic diversity and natural selection results in populations adapting to their environments. The Hardy-Weinberg theory states that, in large theoretical populations not affected by these factors and in which random breeding occurs, allelic and genotypic frequencies will remain constant in subsequent generations. This was observed in 33 simulated populations of 50 moths where allelic and genotypic frequencies remained relatively constant. Slight changes (average fluctuations in allelic and genotypic frequencies of 0.01 and 0.02, respectively) represented what can occur due to non-random mating in a population not in Hardy-Weinberg equilibrium. Natural selection is the mechanism by which microevolutions (changes in genetic information between generations) occur and involves adaptive change within a population to better suit environmental factors. Within a small, simulated population of 50 moths, drastic changes in allelic and genotypic frequencies due to natural selection were observed over seven generations. The frequency of the recessive allele for a particular trait decreased from 0.80 0.39, which resulted in an increase in the frequency of homozygous dominant and heterozygous genotypes and a decrease in the frequency of homozygous recessive genotypes within the population (0.64 in the parent generation to 0.06). This demonstrated how genetic drift may result in decreased genetic diversity in small populations due to the potential loss of alleles. This can be detrimental to a population and can result in extinction as it decreases the population's ability to adapt to changing environmental conditions.

1.0 Introduction

Population genetics involves a change in the allelic frequencies of populations and can be defined as "the study of how populations change genetically over time" (Campbell et al. 2006:455). It can be affected by mutation, sexual recombination, natural selection, genetic drift and gene flow and is fundamental to the modern synthesis, an integrated and widely accepted notion of evolution (Campbell et al. 2006). A population of any species is a local group, whose members are anatomically similar, interbreeding individuals, capable of creating fertile young (Campbell at al. 2006). Evolution is defined as the "change over time in the genetic composition of a population" (Campbell at al. 2006:438). Allelic frequency is the proportions of alleles in the gene pool of a population and relates to genotypic frequency; the proportion of genotypes in the population. For example, the trait of colour in a population of moths has a recessive (b) and a dominant (B) allele, which may be found in the proportions of 0.8 (b) to 0.2 (B). A homozygous recessive individual (two recessive alleles) is light coloured and heterozygous (one recessive and one dominant allele) or homozygous dominant individual (two dominant alleles) is dark coloured. Allelic frequencies determine the likelihood of a trait being expressed anatomically as a phenotype. In this example, more light moths would be expected than dark due to the allelic frequency, despite this being the genotype of two recessive alleles.

Within a population, microevolution is the change in genetic information between generations and affects allelic frequencies predominantly via natural selection. For example, if light moths were at a reproductive disadvantage to dark moths, the allelic

frequency of recessive alleles (b) would decrease in future generations. Mutations (the way in which alleles are created) and sexual recombination (the shuffling of alleles between generations) are responsible for the genetic variation required for evolution to occur (Campbell et al. 2006). Natural selection is the mechanism by which populations evolve to better suit their environments and genetic drift refers to unpredictable fluctuations in allelic frequencies between generations of a population due to its restricted size (Campbell et al. 2006). Genetic drift can result in a decrease in genetic variation (the range of phenotypic differences in the population) within a population due to the loss of alleles from the gene pool (Frankham 2005).

The Hardy-Weinberg Theorem states that; in a large population of randomly mating individuals who are unaffected by factors that change the proportion of genes, genotypic frequencies remain constant in following generations (Cambell et al. 2006). Such a population is said to be in Hardy-Weinberg equilibrium and must must be large, have no gene flow, have no mutations, be able to undergo random mating and must not be subject to natural selection (Cambell et al. 2006). This means that the same allelic frequencies would theoretically continue to occur in subsequent generations and gene frequencies would be predictable (Campbell et al. 2006). Assuming random mating is occurring in a population in Hardy-Weinberg equilibrium, the equation $p^2 + 2pq + q^2 = 1$ can be used to predict the genotypic frequencies from allelic frequencies (for a trait with two alleles) (Campbell et al. 2006). However, such conditions are hypothetical and, in nature, allele and gene frequencies do change over time (Campbell et al. 2006).

Genetic drift can result in allelic frequencies not being accurately represented in subsequent generations of a population and the chance of this occurring in small populations is far greater than in large populations (Campbell et al. 2006). This also means that there is a greater chance that genetic variation will be decreased due to individual alleles becoming lost completely from the population (Frankham 2005). If the remaining alleles in the gene pool represent traits that are disadvantageous under future environmental conditions, the lost allele is no longer available to create individuals with traits that might be better suited to the new conditions (Campbell et al. 2006). In cases such as these, which are common in small populations, extinction can occur (Frankham 2005). Additionally, inbreeding and non-random, selective mating tends to occur in most real, small populations (Campbell et al. 2006). This generally results in particular alleles not being appropriately represented in subsequent generations and tends to cause lower genetic diversity within a population (Campbell et al. 2006). Frankham (2005) stresses that these conditions can often lead to the extinction of a population.

Natural selection is the "differential success in reproduction among individuals that vary in their heritable traits" (Campbell et al. 2006:445). The concept of natural selection was first proposed by Darwin in 1859 and it is the mechanism by which populations evolve and adapt to their environments (Campbell et al. 2006). Natural selection occurs due to particular variations between individuals being more compatible with local environmental factors than others (Campbell et al. 2006). Over time, natural selection will theoretically result in a population with higher proportions of favourable traits (Campbell et al. 2006). Consequently, the frequencies of the alleles responsible for those traits will also increase within the population over time (Campbell et al. 2006).

To simulate and examine population genetics, two experiments were conducted testing: (1) the preservation of allelic and genotypic frequencies due to the Hardy-Weinberg Equilibrium Theorem; and (2) the effect on allelic and genotypic frequencies due to natural selection over time.

2.0 Methods

Within the laboratory, allelic and genotypic frequencies were compared between generations of a simulated population of moths. Red and blue coloured beads were used to represent the two alleles for the trait of colour in the simulated population. For this trait, 'B' represents the dominant allele (blue bead) and 'b' represents the recessive (red bead).

In order to simulate the production of new generations of moths, 100 beads (in set proportions) were placed into a paper bag that represented the gene pool for a population of 50 moths. The bag was shaken to ensure random selection and two beads were unsystematically chosen from the bag 50 times, to represent the genotypes of 50 moths in a new generation. Three possible genotypes occurred (represented by three combinations of bead pairs), which were apparent as two phenotypes (either dark or light colouring). Two blue beads represented the genotype for a dark, homozygous recessive moth (BB), a blue and a red bead represented the genotype for a dark, heterozygous moth (Bb) and two red beads represented the genotype for a light, homozygous recessive moth (bb).

Table 2.1: Expected genotypic and allelic frequencies in new generations of the population.

Parent Population		New Populations				
Allelic frequency		*Genotypic frequency*			*Allelic Frequency*	
B	*b*	*BB*	*Bb*	*bb*	*B*	*b*
0.80	0.20	0.64	0.32	0.04	0.80	0.20

The aim of the first experiment was to confirm that allelic and genotypic frequencies remain the same in a new generation of a population in Hardy-Weinberg equilibrium. In order to do this, predicted genotypic frequencies were compared to actual frequencies observed in 33 replicate experiments (from lab class two), each simulating a population of 50 moths using the 'gene pool' bag of 100 'allele' beads. The frequencies of the dominant alleles (blue beads) and the recessive alleles (red beads) within the population are denoted by p and q, respectively, where p+q=1 (Campbell et al. 2006). The frequency of the genotype BB is p^2, the frequency of the genotype bb is q^2 and the frequency of the genotype Bb is 2pq, so the equation $p^2+2pq+q^2=1$ can be utilised to calculate expected genotypic frequencies from known allelic frequencies (Table 2.1) (Campbell et al. 2006). The expected numbers of each genotype can be calculated by multiplying the number of individuals in the population by the calculated genotypic frequency (Campbell et al. 2006). For example, 32 homozygous dominant moths, 16 heterozygous moths and 2 homozygous recessive moths were expected in the subsequent generation (Table 2.2).

The initial proportion of alleles (beads) in the gene pool in the moth populations simulated in the 33 experiments was 0.80 dominant alleles (represented by 80 blue beads) to 0.20 recessive alleles (represented by 20 red beads).The results of the 33 experiments were averaged so as to represent a larger population of moths

(33 x 50 = 1,650 moths), as the Hardy-Weinberg Theorem is more apparent in larger populations (Campbell et al. 2006). The mean frequencies were then compared to the results predicted using the equation $p^2+2pq+q^2 = 1$ (where p=0.80 and q=0.20) in order to assess whether the allelic and genotypic frequencies remained the same in a population in Hardy-Weinberg equilibrium. As there were theoretically no factors affecting the allelic frequency of the gene pool and the population was in Hardy-Weinberg equilibrium, it was expected that the genotypic and allelic frequencies would remain the same in the new generation of simulated moths.

Table 2.2: Expected number of each genotype in a new generation of the population of 50 moths.

Expected number of BB	Expected number of Bb	Expected number of bb
32	16	2

In order to examine changes in allelic and genotypic frequencies due to natural selection, seven generations within a small population of 50 original moths were simulated. Between generations, random number tables were used to determine the survival rates of moths with different phenotypes and several moths were 'culled' each time, simulating natural selection in a real population. The gene pool for the initial population of 50 moths had allelic frequencies of 0.80 recessive alleles (for light colouring) and 0.20 dominant alleles (for dark colouring). However, the simulation involved dark moths being at a significant advantage as they were able to camouflage to the dark bark of trees in their habitat. Dark moths, with homozygous dominant (BB) or heterozygous (Bb) genotypes, were considered to be at a reproductive advantage, as their colour did not allow them to be preyed upon easily. Moths with these genotypes were randomly 'culled' at an average rate of 10% each generation using the random number tables. On the other hand, white moths, with the homozygous recessive genotype (bb), were at a reproductive disadvantage as their colour allowed them to be more easily preyed upon. These moths were 'culled' at an average rate of 50% each generation.

To simulate the changes in the gene pool between subsequent generations the proportions of blue beads (B alleles) and red beads (b alleles) in the bag were altered to represent the new allelic frequencies in the population's gene pool. In order to effectively simulate the effects of natural selection on small population genetics, only one population of 50 moths were simulated and no replicate experiments were conducted. Due to the simulated environmental conditions favouring the dominant allele (B), it was expected that an increase in the frequency for that allele would increase, resulting in a noted increase in dark moths within the population after six subsequent generations.

3.0 Results

Genotypic and allelic frequencies remained relatively constant in a simulated population of moths from one generation to the next, as is expected in a population in Hardy-Weinberg equilibrium. However, the average frequency of dominant (B) alleles observed in the populations was slightly larger (by 0.011) than that predicted and, consequently, the average frequency of recessive (b) alleles was slightly smaller (Figure 3.1).

	Genotypic frequency			Allelic frequency	
	BB	*Bb*	*bb*	*B*	*b*
Predicted frequencies	0.64	0.32	0.04	0.80	0.20
Mean actual frequencies	0.66	0.30	0.04	0.81	0.19
Difference	**+0.02**	**-0.02**	**0.00**	**+0.01**	**-0.01**

Additionally, the genotypic frequencies were slightly different to those predicted (Table 3.1). Slightly larger frequencies of homozygous dominant genotypes (BB) occurred (0.66 rather than 0.64ation) and slightly lower frequencies of heterozygous genotypes (Bb) occurred (0.30 rather than 0.32) than were expected (Figure 3.2). The genotypic frequency of homozygous recessive individuals (bb), however, was the same as was predicted (0.04) (Figure 3.2). The mean allelic frequency of the dominant allele (B) was 0.81, slightly greater than the expected 0.80, and the allelic frequency for the recessive allele (b) was 0.19, slightly less than the 0.20 expected (Table 3.1).
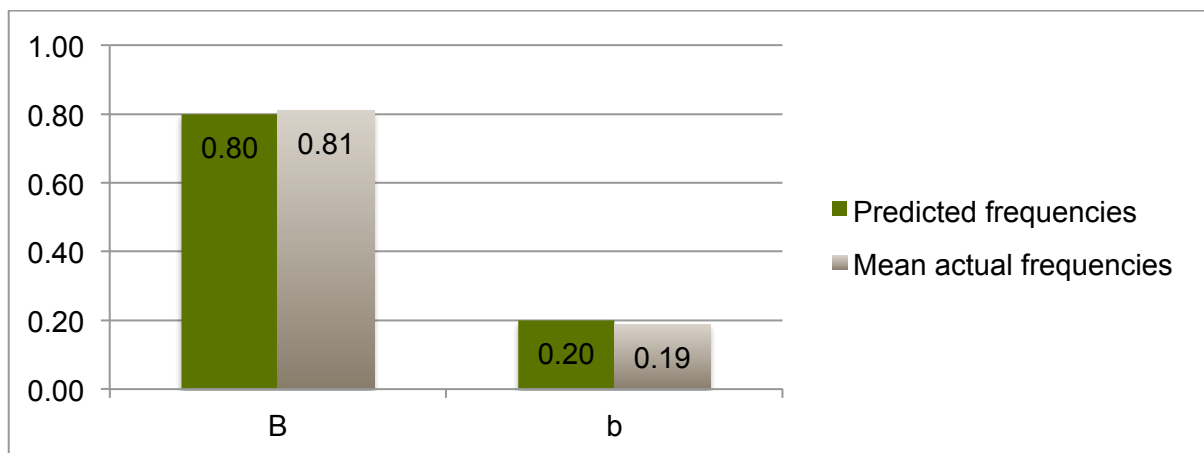

Figure 3.1: Comparison between predicted allelic frequencies and mean actual allelic frequencies in the new generation.

The ranges of values for the genotypic and allelic frequencies from the 33 replicate experiments are shown in table 3.2. It can be seen that the range of values was relatively significant (up to 0.30). The ranges for the genotypic frequencies of a homozygous dominant individual (BB), a heterozygous individual (Bb) and a homozygous recessive individual (bb), respectively, were 0.30, 0.28 and 0.10 (Table 3.2). Furthermore, the ranges for the allelic frequencies for the dominant allele (B) and the recessive allele (b), respectively, were 0.19 and 0.09 (Table 3.2).

Table 3.2: Ranges and mean values for genotypic and allelic frequencies found in the 33 replicate experiments.

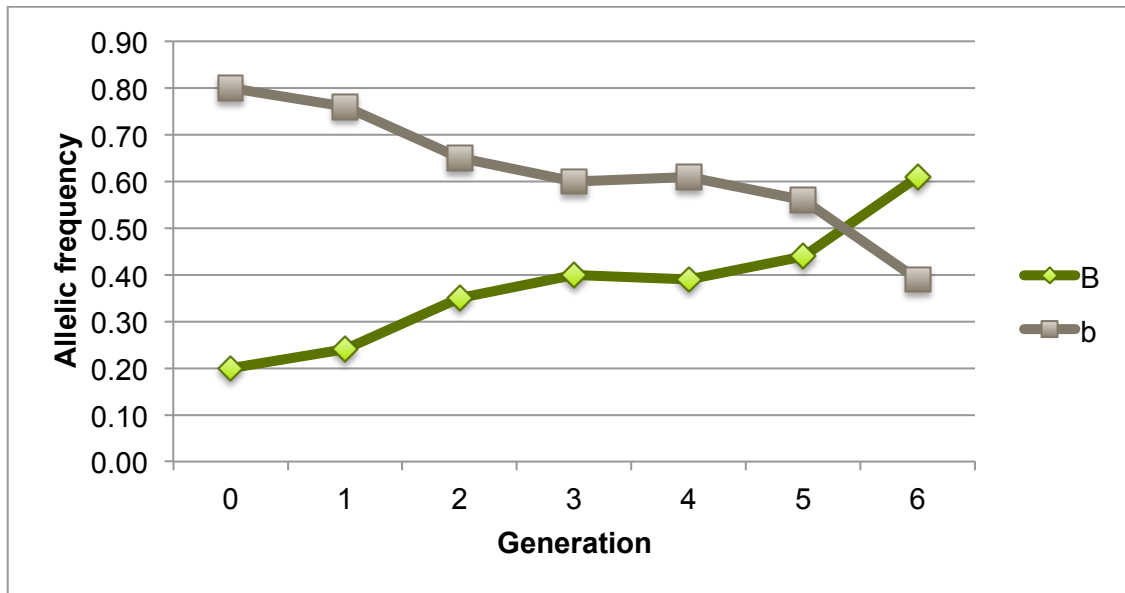|	Genotypic frequency			Allelic frequency	
	BB	*Bb*	*bb*	*B*	*b*
Lowest value	0.52	0.18	0.00	0.72	0.19
Highest value	**0.82**	**0.46**	**0.10**	**0.91**	**0.28**
Range	0.30	0.28	0.10	0.19	0.09
Mean Value	0.66	0.30	0.04	0.81	0.19
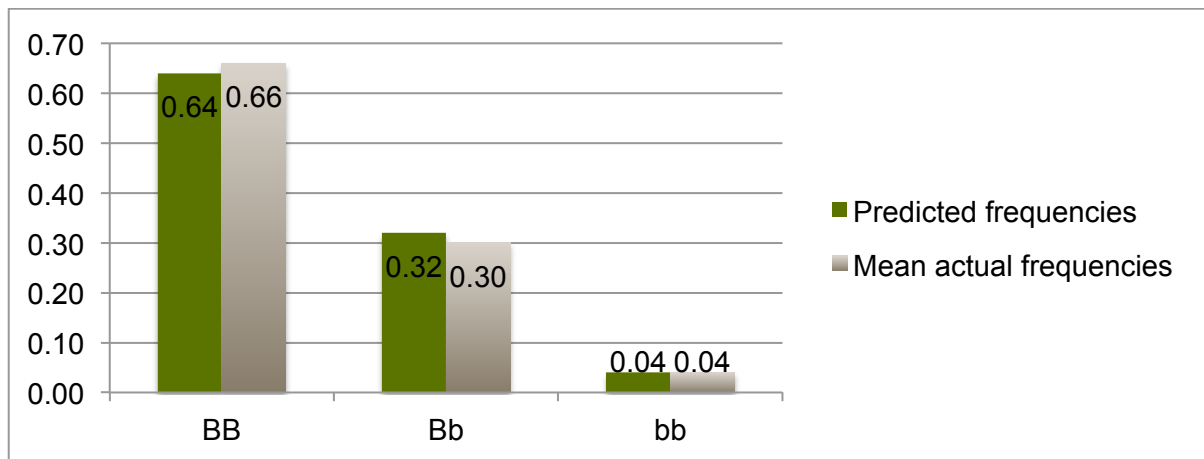
Figure 3.2: Predicted genotypic frequencies and mean actual genotypic frequencies in the new generation.

Allelic and genotypic frequencies in a small, simulated population of 50 moths changed over six generations due to natural selection. The initial frequencies of the dominant and recessive alleles increased and decreased, respectively, by 0.41 after six generations of new moths (Table 3.3). This resulted in higher frequencies of the homozygous dominant (BB) and heterozygous (Bb) genotypes and, consequently, a lower frequency of the homozygous recessive (bb) genotype. The frequency of the dominant allele increased from 0.20 in the parent population to 0.61 in the sixth generation and the frequency of the recessive allele decreased from 0.80 in the parent population to 0.39 in the sixth generation (Figure 3.3). The changes in each generation were relatively consistent, and an average shift of 0.068 was observed in the frequency each generation. However, this pattern was interrupted in the production of the fourth generation, which saw a slight decrease in the frequency of the dominant allele and a slight increase in the frequency of the recessive allele (Figure 3.3).

Table 3.3: Changes in allelic and genotypic frequencies over six generations due to natural selection.

	Allelic frequency		Genotypic frequency		
Generation	*B*	*b*	*BB*	*Bb*	*bb*
0	0.20	0.80	0.04	0.32	0.64
1	0.24	0.76	0.00	0.49	0.51
2	0.35	0.65	0.12	0.46	0.42
3	0.40	0.60	0.14	0.53	0.33
4	0.39	0.61	0.16	0.47	0.38
5	0.44	0.56	0.20	0.49	0.32
6	0.61	0.39	0.27	0.67	0.06

Genotypic frequency also changed relatively consistently over the six generations. The frequency of homozygous dominant genotypes (BB) increased from 0.04 in the parent population to 0.27 in the sixth generation, the frequency of heterozygous genotypes (Bb) increased from 0.32 to 0.67 and the frequency of homozygous recessive genotypes (bb) decreased from 0.64 in the parent population to 0.06 in the sixth generation (Table 3.3).

Figure 3.3: Changes in allelic frequency over six generations due to natural selection.
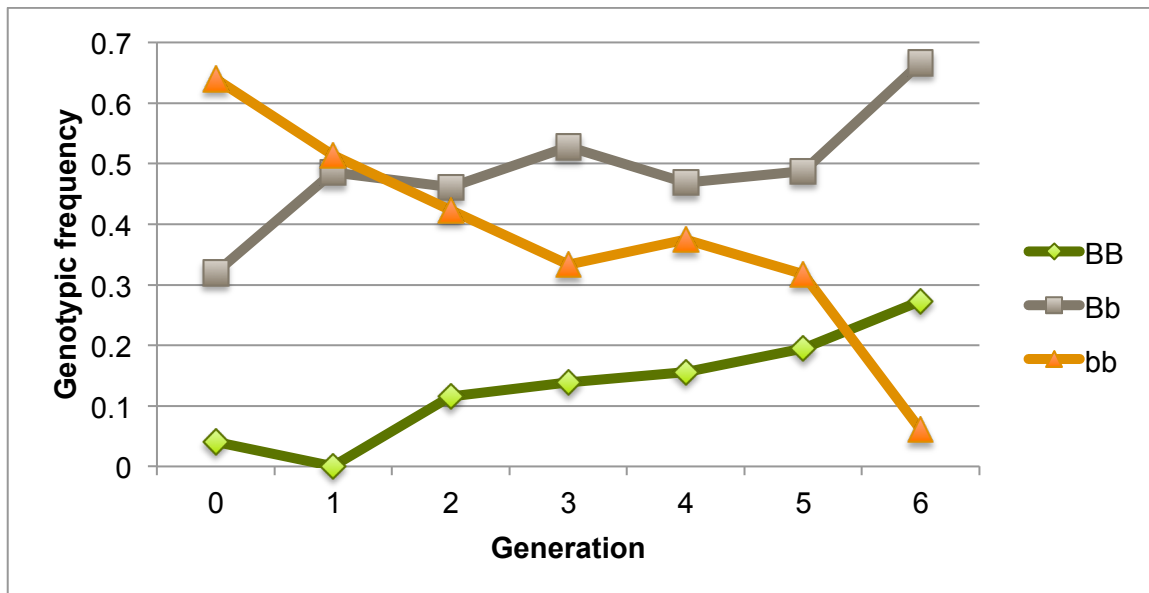
Figure 3.4: Changes in genotypic frequency over six generations due to natural selection.

The changes in the frequencies of each genotype were mostly consistent apart from a few occasions. The gradual increase in the frequency of the homozygous dominant genotype (BB) occurred in all but the first generation of offspring and the gradual decrease in the frequency of the homozygous recessive genotype (bb) occurred in all but the fourth generation of offspring (Figure 3.4). The frequency of the heterozygous genotype (Bb) did not increase consistently over the six generations but rather increased dramatically from 0.32 to 0.49 and 0.49 to 0.67 in the first and sixth generations, respectively (Figure 3.4). In generations two to five, the frequency of the heterozygous genotype (Bb) increased and decreased slightly, varying up to 0.07 between generations (Figure 3.4).

4.0 Discussion

Allelic and genotypic frequencies remained relatively consistent in the new generation of a simulated population of 50 moths that was in Hardy-Weinberg equilibrium. The average allelic and genotypic frequencies within the new generation of moths simulated in 33 replicate experiments only changed by 0.01 and 0.02, respectively. Although these frequency changes may seem trivial in one generation, they would eventually account for a large shift in the genetic makeup of future generations. This observed change in allelic and genotypic frequencies is representative of non-random mating, which occurs in real populations who are not in Hardy-Weinberg equilibrium (Campbell et al. 2006).

Real populations are subject to many variables that can alter their allelic and genotypic frequencies and result in microevolutions between generations (Campbell et al. 2006). Genetic diversity can be increased in two ways; mutations can create new alleles within a population and sexual recombination ensures alleles are shuffled between generations (Campbell et al. 2006). Small populations can be subject to inbreeding and genetic drift, which can result in allelic frequencies not being accurately represented in new generations of a population (Campbell et al. 2006). This tends to decrease genetic diversity through the chance loss of alleles over time (Campbell et al. 2006).

Allelic and genotypic frequencies changed within a small, simulated population of 50 moths over seven generations as a result of natural selection. The frequency of the dominant allele increased by 0.41 after six subsequent generations within the population, which resulted in higher homozygous dominant (BB) and heterozygous (Bb) genotype frequencies and a lower homozygous recessive (bb) genotype frequency. This simulated how rapidly the genetic makeup of a population can be altered by adaptive microevolution due to natural selection.

The rapid decrease in recessive alleles demonstrated how, within small populations, natural selection may result in decreased genetic diversity (Campbell et al. 2006). Genetic diversity is important within populations as it provides the variations that must be present for natural selection to occur (Campbell et al. 2006). A decrease in genetic diversity occurs through the loss of alleles from the gene pool of a population (Campbell et al. 2006). For example, at the rate of change of allelic frequencies observed in the second experiment (0.068 each generation), the recessive allele for the trait of colour cold be lost from the gene pool within the next six generations, resulting in decreased genetic diversity.

Frankham (2005:135) states that the "loss of genetic diversity in small populations is expected to increase extinction risk by adversely affecting the ability of populations to evolve to cope with environmental change". This is the case for the small, simulated population examined in the second experiment, as future loss of alleles from the gene pool could result in extinction. This is because, under future environmental conditions, the habitat might have light-barked trees and light moths (produced by two recessive alleles) would have a greater surviveability rate due to their ability to camouflage. A population lacking the recessive allele might become extinct due to the fact that only the readily-preyed upon dark moths would exist and this population would be unable to evolve to adapt to the new conditions. The detrimental effects of small population sizes on the likelihood of species survival have been outlined in this report and there is much support for the preservation of viable populations of individuals in the wild, in order to promote their continued existence over time (Eisworth & Cornelis van Kooten 2009).

5.0 References

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