

# Effects of genetic drifts | experiment



**ASSIGN  
BUSTER**

## Introduction

The Hardy Weinberg Theorem is a mathematical formula that allows allele and genotype frequencies in a population of diploid or polyploid individuals to be interrelated, where the frequency of one allele is represented as  $p$ , and the frequency of the other is represented as  $q$  (the sum of which = 1.0). The sum of the different genotype frequencies (homozygotes and heterozygotes) also equates to 1.0. Where  $p$  and  $q$  are the frequencies of the alleles for a particular gene in a population, the genotype frequency can be expressed as:

$$p^2 + 2pq + q^2 = 1$$

Where  $p^2$  = frequency of organisms that are homozygous for the first allele

$q^2$  = frequency of organisms that are homozygous for the second allele

$2pq$  = frequency of heterozygous organisms

The Hardy Weinberg equilibrium stays constant as long as there is random mating, no migration, no natural selection, no mutation and no genetic drift ( $N = \text{infinite}$ ), (Fig. 1).

$N = \text{infinite}$

Therefore the population does not evolve. If an allele or genotype frequency is seen to change from one generation to the next then it is clear that one or more of the micro-evolutionary forces (mutation, migration etc) are acting on those traits in the population. Without mutation there are no new alleles or genes and so no evolution. Mutation must occur in the germ line to be

significant in evolutionary terms. J. B. S. Haldane (1892-1964) stated that the number of germ cell divisions per generation is higher in males; therefore the mutation rate will be higher in males. Gene flow (also called migration) brings new genotypes into populations and is critical for the long term survival of a population, especially if it is a small population. For migration to be effective in respect to evolution there must be successful reproduction among migrating populations. It is the movement of alleles between populations, not individuals.

Wright's Island model of migration (Fig. 2) shows that migration homogenizes populations (where they consist of similar elements uniform throughout).

Genetic drift is another form of micro-evolution and leads to random changes in allele frequencies. It is fundamentally a result of finite population size and has the most rapid and dramatic effect on small populations who show reduced variability. Drift increases divergence between populations so genetic variation must be replenished. Mutation replenishes variation and at equilibrium there is a balance between the rate of mutation and the rate of drift.

Charles Darwin (1859) defined natural selection (another micro-evolutionary force) with his four postulates; 1) individuals within populations are variable, 2) there is heritability (variation among individuals partly passed on from parents), 3) that in every generation there are some individuals that are fitter (survival/reproductive success) than others and 4) fitness is not random. Natural selection is the equivalent of differential reproduction as a

result of an organism's interaction with the environment and the population's inherent variation. It acts on heritable (not acquired) characteristics at an individual level and not for the good of the species. However, the consequences occur in populations. This is demonstrated by melanism in the peppered moth (*Biston betularia*). The causes of melanism in the peppered moth have been well studied since the 1950's and show natural selection at work. Camouflage is key to predator avoidance in the peppered moth and there are two distinct morphs. One being white with black or brown specks (typica) and the other predominantly black (carbonaria). The former is well camouflaged on trees with lichen on their bark and the latter; better suited to dark or blackened bark. During the industrial revolution in the 19th century, an increase of soot and industrial pollution coincided with the appearance of the carbonaria form. Original studies on the relation between *B. betularia*'s crypsis and lichens failed to consider two important details; firstly, that the natural resting place of the moths is high in the canopy during the day and not on the trunk as previously thought, and secondly, human vision was used to simulate a bird's view of the moths originally, but avian species are sensitive to different wavelengths of light and so will have a different view of the moths and their respective camouflage to that of humans. Taking this into consideration, Majerus, Brunton and Stalker (2000) devised a more systematic experiment to examine the UV characteristics of both moth morphs and some of the lichens they rested on.

It was their conclusion that moth colour provides sufficient camouflage both in human-visible and UV- spectra to crustose lichens (as oppose to different

lichen flora originally hypothesised to be rested upon by black and peppered morphs). Ultimately, strong selection pressures gave way to relatively rapid the evolution of the carbonaria form in industrialised areas due to the advantages of its dark colour (predator avoidance etc).

## Methods and Results

### Assignment 1: Testing the Hardy-Weinberg Principle:

#### Method

Using PopGenLab, we are able to set up hypothetical experiments to observe the factors that influence the Hardy Weinberg equilibrium in a population.

We can do this by manipulating different input parameters (genotype frequency, tree type, number of stands (groups of trees), stand size (number of trees within a group), migration rate, mating pattern and disaster frequency). For this assignment the input parameters are as follows:

Number of stands = 1

All other input parameters are left at default values (equal allele frequencies; genotype frequencies of 50% brown, 25% white, 25% black; equal proportions of each tree type; stand size of 4000; no migration; random mating; disaster frequency set at “ Never.”

#### Results

Q 1. 1) When looking at the allele and genotype frequencies, there is a change in both over time. All populations behave differently to one another. This is because the only active evolutionary force is genetic drift.

Q 1. 2) When the initial allele frequencies are changed to  $A = 80\%$  ( $p$ ),  $a = 20\%$  ( $q$ ) ( $p^2 = 0.8 \times 0.8 = 0.64$ );  $AA = 64\%$  (equilibrium reached after one generation) (Fig 6). If all the Hardy Weinberg conditions are all fixed, the equilibrium will always be reduced in the next generation (Fig. 5 and 6). Fig. 5. shows the initial genotype frequency compared with Fig. 6. which shows the genotype frequency after one generation. The actual genotype frequencies (worked out with average stand number) match the Hardy Weinberg predictions as they stay within 1% of the previous generations' genotype frequency, across every generation thereafter. However, the percentage may change by 1% due to genetic drift.

## **Assignment 2: Genetic Drift**

### Method

Q 2. 1) Firstly we ran an experiment with default values for all the Hardy Weinberg conditions and 100 populations.

We then ran a series of experiments with 100 populations and default parameters for all conditions except tree stand size which was systematically reduced for each experiment. We recorded the effects on allele and genotype frequency (below). Fig. 7 shows that stand size 10 produced the largest fluctuations of allele frequencies, and displayed the most cases of allele fixing.

### Results

Stand size = 4000 (carrying capacity)

Allele frequency- the average remains constant for  $A$  and  $a$

Genotype frequency – stays relatively constant throughout.

Stand size = 2000

Allele frequency – the average show slight variation

Genotype frequency – stays relatively constant.

Stand size = 1000

Allele frequency – the average starts to diverge more with each generation from F45 (generation 45) onwards showing a lot more variation than in larger stand sizes

Genotype frequency – the average frequency stays constant although there is some variation compared with larger stand sizes

Stand size = 500

Allele frequency – The average shows variation in the later generations

Genotype frequency – the average stays relatively constant but still with more variation than in any other larger stand thus far

Stand size = 250

Allele frequency – the average shows some variation in the mid-generations, but this returns to a 50: 50 frequency in the later generations

Genotype frequency – on average, the frequency of both white and black variations of moth increases and shows a large variation between stands.

Heterozygosity – the brown variation decreases by 9% over 100 generations

Stand size = 100

Allele frequency – the average shows more variation, but to the point where in some stands alleles within individual populations become fixed

Genotype frequency – the frequency of homozygotes increases. In some stands the homozygosity (black) becomes fixed, phasing out the other two variations (white and brown)

Heterozygosity – drops by 22%

Stand size = 50

Allele frequency – frequencies become fixed for a single allele quickly (by F23)

Genotype frequency – Many stands become fixed for one variation within a few generations

Heterozygosity – drops by 33% after 100 generations

Stand size = 10

Allele frequency – becomes fixed within a population after two generations, and continues to become fixed in other populations. By F77, all are fixed

Genotype frequency – every single genotype becomes homozygous or extinct



Heterozygosity – by F77 all heterozygosity is lost and by F100 there are only homozygous populations, with the other (70%) becoming extinct

There are many variations in allele and genotype frequency between different stands because as the stand number decreases, the chance of genetic drift increases. Figure 7 shows that at stand size 10, heterozygosity was lost completely by F77.

Q 2. 2) As the stand size decreased, so did the heterozygosity. Populations began fixation in stand size 100 to stand size 50. As the stand size decreased, the number of fixed alleles increased. When the carrying capacity became too small, there was not enough variation to prevent fixation. Random mating account for the variation between fixed and non-fixed alleles in stand size 100 and stand size 50. Fig. 8. shows that with a stand size of 10, heterozygosity diminished completely by F77. Therefore, the smaller the population, the quicker heterozygosity is lost.

Q 2. 3) Yes – populations from stand size 10 became extinct (70% of them) therefore, as the carrying capacity decreases, the risk of extinction increases. There is variation within generations due to factors like predation or whether the offspring are male biased for example. There may be a lower population size in the next generation depending on mating strategies (random mating) and occasionally, the parameters reach a point of no return and the population can not recover and so becomes extinct. Others avoid extinction because the experiment is random. Fig. 9. (where stand size = 10) shows population of stand number 15 and how it fluctuates around the average value, it also shows that when the population dwindled to a certain

point, it wasn't able to re-establish the numbers enough to prevent extinction.

### **Assignment 3: The Influence of Mating Patterns on Population Genetics**

#### **Method**

In this experiment we set all default parameters except for the number of tree stands which was set to 100. The first experiment was carried out with random mating, and the subsequent experiments with non-random mating. We then varied the population size as before, this time to compare the effects of assortative mating with genetic drift.

#### **Results**

##### **Q 3. 1)**

The effects of 25% assortative mating:

Genotype frequency – 25% assortative mating causes an increase in homozygotes, and heterozygosity is lost by F80

Allele frequency – (produces a sigmoidal shaped graph). All become fixed for a single allele.

Heterozygosity – the average heterozygosity is lost at F80

50% assortative mating:

Genotype frequency – all homozygotes with an almost 1: 1 ratio – 'aa' being slightly more dominant

Allele frequency – (sigmoidal graph) all fixed by F50

Heterozygosity – lost by F33 (average heterozygosity)

100% assortative mating

Genotype frequency – quickly becomes homozygote dominated

Allele frequency – All fixed for a single allele by F15

Heterozygosity – Average lost by F4

Heterozygosity is lost under assortative mating. This is because heterozygotes are at a reproductive disadvantage as homozygotes will mate with like genotypes. Heterozygotes will not be produced by these matings either.

### **Q 3. 2) Results**

Population size 2000 (stand size), 100% assortative mating:

Genotype frequency – all homozygous by F4

Allele f – fixed by F14

Heterozygosity – average lost by F4

Population size 2000, 50% assortative mating

Genotype f – all homozygous by F25

Allele f – all fixed by F29

Heterozygosity – average lost by F25

Population size 250, 100% assortative mating

Genotype f – all homozygous by F4

Allele f – all fixed by F12

Heterozygosity – lost at F4

Population size – 250, 50% assortative mating

Genotype f – all homozygous by F25

Allele f – all fixed by F28

Heterozygosity – lost at F25

Assortative mating dominates control of allele frequencies and the speed that alleles become fixed within a population compared with the effects of genetic drift (because the homozygotes are all mating with the same genotype and not with heterozygotes). Assortative mating is not dependant on carrying capacity. The size of the population is irrelevant when assortative mating is occurring. The results are similar for a high or a low population size.

### **Q 3. 3) Method**

We conducted a series of experiments using disassortative mating and selected different levels of mating between 0% (random mating) and 100% (only unlike phenotypes mate). We then changed the population size from 2000 to 250 to see the effects of disassortative mating on genetic drift.

Results

Dissortative mating shows that AA and aa will mate which increases heterozygosity and stabilises the population as shown in the results below:

Population size 2000, 100% disassortative mating

Geno (genotype frequency) – heterozygote is predominant

Allele (allele frequency) – none become fixed. There is variation but it stays within 31% – 68% variation

Hetero (heterozygosity) – increases in the first generation then remains constant

Pop size 2000, 50% disassortative mating

Geno – predominantly heterozygote

Allele – none become fixed. There is less variation than with 100% disassortative mating. Variation is between 43% and 57%

Hetero – Increases in 1st generation and remains constant

Pop size 250, 100% disassortative mating

Geno -slight heterozygote increase

Allele – No fixed alleles. There is much greater variation than seen previously with a larger population size, between 21% and 79%

Hetero – increases in 1st generation then remains steady and begins to decrease. Remains above the initial percentage

Pop size 250, 50% disassortative mating

Geno – heterozygosity increases steadily

Allele – No fixed alleles. Variation is less than with 100% disassortative mating and population size of 250. Variation levels out between 33% and 67%

Hetero – increases in the 1st generation and remains constant with a few small fluctuations which level back out

Q 3. 4) There would be more heterozygosity in the next generation when disassortative mating occurs and if this kind of mating is maintained, the effects of genetic drift occur much slower because the populations are prevented from diverging. Fig. 10 shows the comparison between disassortative mating and random mating where random mating allows genetic drift. Drift can still occur during disassortative mating when the carrying capacity is very low.

Q 3. 5) Method

For this experiment we varied the initial genotype frequency for assortative and disassortative mating. We tried experiments where the initial allele frequency

favoured one or the other allele. Fig. 11 show starting frequencies of 50/50% assortative mating. A small deviation in starting frequencies affects the final fixation percentages (Fig. 11). We did not include the brown allele in this experiment as the extra variable is not needed.

## Results

Under disassortative mating the time taken for equilibrium to establish is negatively correlated with the degree of deviation from a 1: 1 starting allele ratio. Under assortative mating, fixation or loss of alleles is negatively correlated with the degree of deviation from a 1: 1 starting allele ratio.

### **Assignment 4: Modes of Natural Selection**

#### Q 4. 1) Method

In this experiment we investigated how fitness affects changes in allele frequency in the population. We began with default parameters except tree stand number (set at 100) and genotype frequencies. We changed the tree frequency to set up several experiments under conditions of directional selection for dark moths, directional selection for light moths, balancing selection favouring the brown moth, and diversifying selection favouring the dark and light moths.

We tried experiments with the different conditions of selection and initial allele frequencies near zero and one.

## Results

Directional selection for black moths where the tree frequencies are 50% black, 25% white and 25% brown trees gave the following results:

Allele frequency – becomes fixed rapidly by F10 (on average by F9)

Genotype frequencies – at F10 genotype becomes fixed for black allele

In a small population, alleles become fixed more quickly but in larger populations allele frequencies are not affected as much. We kept the population size high so we would not see genetic drift in the experiment (4000 carrying capacity) with tree frequencies of 35%, 32% and 33%. Even the small amount of selection (35% black trees) shows fixation of alleles for the black morph of moth (Fig. 12). Selection for light moths gives the same results as selection for black moths.

Q 4. 2) Starting figures are as follows:

- Black tree – 25%
- Allele black – 25%
- Brown tree – 50%
- Allele brown – 50%
- White tree – 25%
- Allele white – 25%

After one generation, allele frequency remains stable (between 48% and 52%) and the genotype frequency becomes predominantly brown. This is because there is always the presence of black and white genotypes which cause slight variation. If you change the selection of trees to black – 10%, white – 10%, brown – 80%, almost identical results occur (between 49% and 51% variation in allele frequency = stabilized).

Q 4. 3) To show diversifying selection we set the tree types to 45% black, 45% white and 10% brown.

Genotype frequency – by the 1st generation, there was a large decrease in brown morphs of moth and the equivalent increase in black and white



morphs. This continues till F5 when the black morph became slightly more dominant (on average) due to random mating. The brown morph was phased out by F18 (on average) on most of the 100 tree stands. All alleles become fixed for either black or white by F23 (49% white, 51% black) (Fig 13).

Q 4. 4) Small differences in fitness are effective in changing allele frequencies. Small differences in fitness have proportionally slower rates of allele frequency change compared with large differences in fitness.

We conducted additional experiments with varying proportions of tree types. The results are as follows:

(Where stand size = 4000, number of stands = 100, allele frequencies = white 20%, brown 60%, black 20%, tree frequencies = white 32%, brown 32%, black 36%). Even though there are a lower proportion of black alleles (A) to begin with, those alleles will have a higher fitness than white or brown as there is a higher percentage of black tree types. Over time this will equate to an increase in black morphs. There is, however, a point where even if the black allele is fittest but there isn't a high enough population in the first place, it will crash and not recover.

Q 4. 5) Genetic variation is maintained under balancing selection because the allele frequencies remain stable. There is no fixation (presuming the all mating is random). The heterozygote allele is favoured and thus balances the homozygous allele.

### **Assignment 5: Migration**

Q 5. 1) Migration counteracts the effects of genetic drift. (Fig 14 and 15)

**Assignment 6: Population Bottlenecks**

Q 6. 1) Disaster led to the loss of alleles and reduced heterozygosity. The more disasters there were, the more decreased the diversity became. (Fig 16, 17, 18)

Q 6. 2) Disaster increased the rate of extinction. The more regular the disaster, the more extinctions.

Q 6. 3) Migration moderated the effect that disasters had on the population.

**Discussion**

The results of our experiments clearly show that genetic drift affects smaller populations where heterozygosity is lost rapidly and as the carrying capacity decreases, the risk of extinction increases. This is because the proportion of individuals with a certain phenotype within a small population are largely influenced by random variation in survival, and over time, the change in proportion of genotypes in subsequent generations leads to genetic drift. If one was to aim to conserve a hypothetical species, one would expect that because it is endangered, it would be a small population. To maintain genetic diversity among this species, one would need a large enough breeding population to begin with. Unfortunately, as is the case with most endangered species, populations become geographically isolated, mainly due to human disruption of habitat. Migration between breeding populations decreases and they become fragmented. Conservation efforts may be due to natural disasters such as tsunamis, fires etc, but are mainly to prevent the constant onslaught of human activities such as illegal logging in conservation areas. Figure 17 illustrates the effects of a bottleneck following a disaster,

showing reduced variability (and a small population) leading to loss and/or fixation of alleles. As with genetic drift, the way to prevent population crashes, or rather soften the effects of bottlenecks, is to encourage migration among populations. This can be achieved by implementing the protection of 'corridors' between known endangered populations. In theory, the populations can migrate between areas, maintaining a high enough level of breeding and genetic variation, to counter the effects of inbreeding depression or genetic drift (Fig 14 and 15). An example of how corridors may re-connect fragmented populations can be seen in Bhutan's Jigme Singye Wangchuck National Park ([www. panthera. org](http://www.panthera.org)).

The proposed Eastern Himalayan corridor may help towards connecting isolated populations of tigers, and thus increasing genetic diversity (if these populations successfully reproduce with one another) (Fig 19).

Random mating, as apposed to assortative mating, will increase heterozygosity and stabilise a population (Fig 10). This acts against genetic drift and stops the population from diverging as quickly. In a hypothetical situation then, you would preferably allow mating to occur naturally and at random. However, some conservation efforts include that of translocation of individuals or cross breeding certain individuals from separate populations. For this to be advantageous to the species, one must consider maintaining genetic diversity by genotyping the individuals before translocation. It would be senseless to swap or breed an AA individual with another AA individual from a separate population as this would lead to loss or fixation and not increase diversity. Our studies with *B. betularia* in question 4 to 4. 5 show that intermediates are favoured over extreme phenotypes and that genetic

variation is maintained under balancing (stabilizing) selection because the allele frequencies remain stable. There is no fixation (presuming the all mating is random). The heterozygote allele is favoured and thus balances the homozygous allele.

As well as considering the genetic diversity of a species and its genealogy, one must understand the species by means of observations in the field including its behaviour. Later studies of *B. betularia* reinforced the need for such observations as it was found to rest high in the branches rather than on the trunks of trees as previously calculated. Also, modern science allowed for the study of its UV qualities which had otherwise been unaccounted for when considering levels of predation by birds. A close study of mating patterns should ideally be assessed to ensure the outcome of migration; corridors, translocation etc will be advantageous in terms of fitness.