

King's College London (KQC) University of London

SCIENCE SIMULATIONS LABORATORY

EVOLUTION AND NATURAL SELECTION

STUDENTS' MANUALS (Version 1.02.2003)

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STUDENTS' MANUAL A – EVOLUTION BY NATURAL SELECTION

On 1st July 1858 the Darwin-Wallace lecture was delivered before the Linnean Society of London. It marked the beginning of all modern biological thought. The theory of evolution was announced. Charles Darwin and A.R. Wallace independently put forward the view that species are not individually created and unchanging, but that each could give rise gradually to new species during the course of time. The essential directing and controlling agent in this change or evolution is natural selection.

Charles Darwin began to formulate the theory of evolution on his famous voyage on HMS Beagle which began in 1831. Several observations started Darwin's revolt against the view, current at that time, that species are a result of special creation and cannot change. In the Galapagos Islands he found that the species of finches differed slightly from island to island, while showing resemblances not only to each other but also to finches on the adjacent mainland of South America. If all had been created separately, he could not explain the reason for either such an excessive amount of creation or why geographical closeness should cause all of these birds to resemble one another. Darwin also noticed as he travelled through South America that other species, although different in many ways, had many similarities if they lived in the same type of environment.

These observations were not explicable if the species had not changed since they were created. However, if the species had been subject to modification during descent and had diverged into different lines, he could explain it all. The finches of the Galapagos Islands are similar because they are all descended from a common ancestor, but they differ because they are all adapted to different ways of life on their own particular island. Examples of Darwin's finches, are shown in Figure A1.

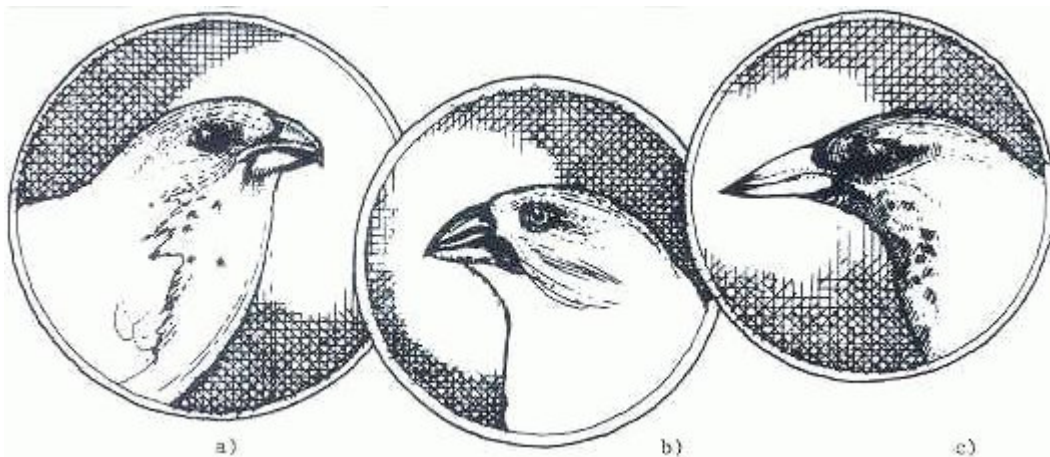


Figure A1 Three species of Darwin's finches: (a) a tree finch, *Camarhynchus psittacula*, (b) a ground finch, *Geospiza fortis*, (c) a cactus finch, *Geospiza scandens*.

A1 How are the finches in Figure A1 adapted to different food supplies?

A2 What other adaptations would these finches need for their different ways of life?

Darwin searched through biological knowledge to find evidence to support the hypothesis that species have undergone successive changes through many generations, resulting in modifications of the ancestral species.

Apart from his general comparison of organisms around the world, his studies of chronologically ordered fossils demonstrated gradual change and adaptation of organisms through geological time. He found similarities between the embryos of quite different organisms as shown in Figure A2, suggesting a common ancestor in the past.



Figure A2 Vertebrate embryos at an early stage of development.

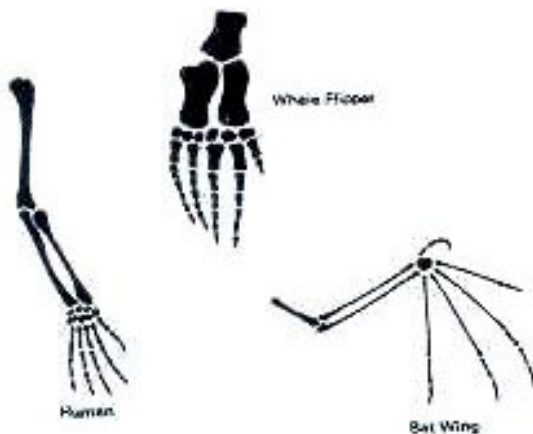


Figure A3 Skeleton of the forelimbs of a whale and a bat compared to that of a human.

Comparing the anatomy of similar organisms, adapted for quite different ways of life, revealed that common structures had been used and modified for different functions, such as the whale and bat forelimbs shown in Figure A3. Even Darwin's knowledge of breeding pigeons demonstrated the effect of selective breeding in producing and maintaining specific characteristics.

Darwin had to explain how this change had come about and his line of reasoning was as follows. Members of any one species are not identical but differ in size, strength, fertility, habits and so on. These characteristics are passed from parents to offspring and although they are similar, offspring are not identical to each other or their parents.

A3 If characteristics are inherited from one generation to the next, how does so much variation occur amongst offspring?

Even relatively slow breeding organisms can produce a large number of offspring. If four offspring were produced for every two parents, the population would double. Most organisms produce far more offspring than this. Rabbits, by no means the fastest breeders, produce about six offspring every litter, usually four times a year.

A4 If a lone breeding pair of rabbits colonised a remote area, try to work out how many rabbits you might expect to find after five years?

A5 What environmental conditions would be necessary for all these offspring to survive?

Most organisms produce more offspring than the environment can support. There is competition for survival. Any variation that increases an organism's ability to survive, increases its chance of success in the struggle for existence. These organisms produce more offspring, so passing on their favourable characteristics to future generations. Any variation reducing an organism's chance of survival or the number of offspring being produced will be eventually eliminated. Darwin called this natural selection. By this process organisms gradually become better adapted to their environment. Different environments will require different adaptations for survival and as environments change so the adaptations of organisms must change.

STUDENTS' MANUAL B – A BEAD MODEL TO INVESTIGATE THE POWER OF SELECTION

The characteristics of organisms on which natural selection operates are controlled by a complex genetic make-up. Not all characteristics are controlled by a single gene (or set of alleles) and not all genes control a single characteristic. To study the effect of natural selection on the frequency of alleles and so on the occurrence of different characteristics, we can set up a simplified model of a population. One such model uses coloured beads. Different colours represent different alleles of a single gene which controls the variations of one characteristic of the organism. This model can be used to investigate different degrees of selection on different sizes of population under various conditions.

1. Start with 50 red and 50 yellow beads. These represent 100 gametes, 50% carrying the red allele and 50% carrying the yellow allele. At fertilization gametes come together in pairs and we will assume this pairing is random. Mix the red and yellow beads together in a beaker. However, not all gametes are successful at fertilization and not all offspring produced will reproduce. Take out 80 beads at random to represent 40 individuals which are potentially capable of producing offspring.
2. To represent random fertilization put the 80 beads onto a tray and shake until they come to lie along one side. Count them off in pairs. Two beads the same colour represent a homozygote and two beads of different colours represent a heterozygote. Assume the red beads are dominant and that the 'red' characteristic has an advantage over the 'yellow' characteristic within the particular environment.
3. Show the effects of natural selection against the 'yellow' characteristic by removing half of the yellow pairs of beads. If there is an odd number leave the extra pair. This represents a selection of 50% against the yellow homozygotes.
4. Count the numbers of red and yellow beads remaining.

For example, suppose the first sample contained:

8 pairs of yellow beads	=	8 yellow homozygotes
20 pairs of yellow and red beads	=	20 heterozygotes
12 pairs of red beads	=	12 red homozygotes

Total before selection:	36 yellow beads
	44 red beads

8 yellow beads will be removed to represent a 50% selection against yellow homozygotes.

Total after selection:	28 yellow beads
	44 red beads

5. If we assume that there is sufficient food to maintain a population of constant size, the numbers of beads must be corrected in the right proportions to produce the next

generation. In the example given 72 beads remain in the proportion 28 yellow to 44 red beads.

The population is reduced to about three quarters of its original size. To adjust it to about 100, you would add about one quarter of the number of yellow beads and about one quarter of the number of red beads.

If you add 10 yellow and 15 red beads the population is made up to 97. It does not have to be exactly 100 for every generation.

6. Repeat the process nine times to represent ten generations.
7. Record your results in a table as shown below:

Generation Number	Number of gametes		Number of offspring genotypes						% red alleles
	Red	Yellow	Before selection			After selection			
			RR	RY	YY	RR	RY	YY	
1	50	50	12	20	8	12	20	4	
2									
3									
4									
5									
6									
7									
8									
9									
10									

Table B1 Record of results with bead model.

8. When you have completed ten generations draw a graph to show the changes in the percentage of red alleles over the ten generations. Then answer the following questions.

- B1 What changes in the frequency of the yellow allele have occurred in the population over ten generations?*
- B2 What changes would have occurred in the allele frequencies if the experiment had been continued for more generations?*
- B3 In what ways would the results have differed if the selection had been against the red phenotypes?*

STUDENTS' MANUAL C – A COMPUTER SIMULATION OF NATURAL SELECTION

A bead model can be used to study the frequencies of alleles in a population, but can become rather tedious. A far quicker means of obtaining the results through the same process is by using the computer program *Evolution and Natural Selection*. The computer will count numbers, randomly produce pairs, apply selection and adjust the proportions for the next generation. You can choose the direction and amount of selection, the size of the population and the initial percentage of each allele. As in the bead model we will assume that external conditions allow the population to remain at a constant size. It is assumed that 80% of the individuals are potentially capable of producing offspring.

When first using the program *Evolution and Natural Selection* select *Part 1* and then use the same values that you used in the bead model of Manual B. Figure C1 is an example of the initial computer dialogue where you enter your values.

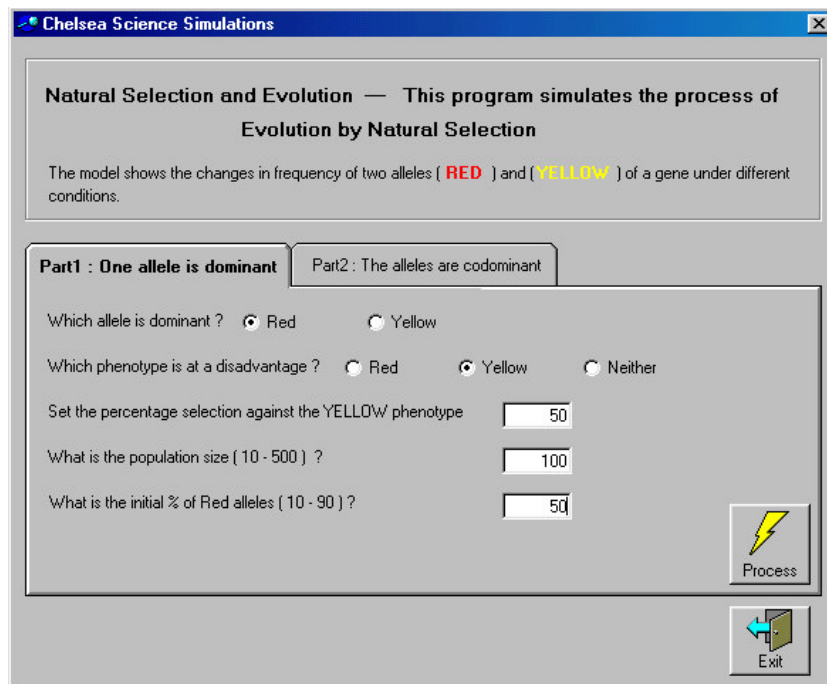


Figure C1 Screen printout from *Evolution and Natural Selection* showing the use of *Part 1*.

After you have entered the values required, the results will be tabulated as shown in Figure C2.

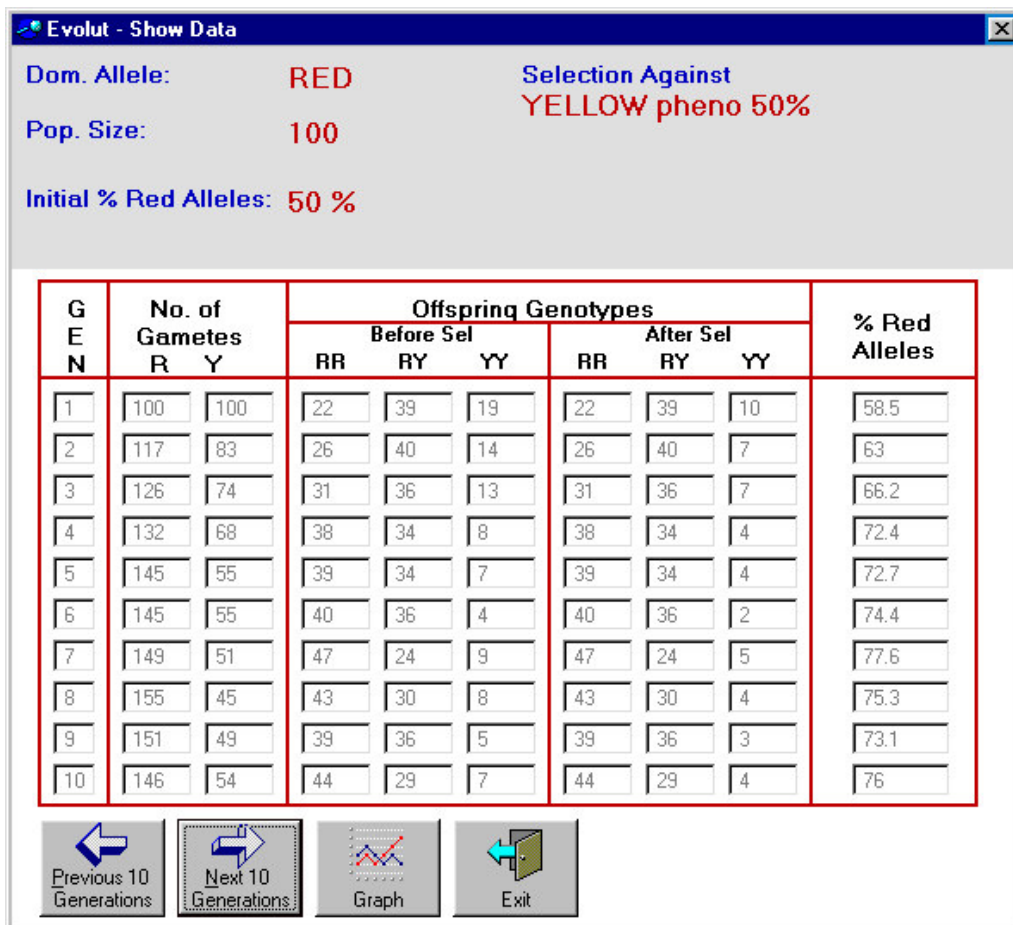


Figure C2 Screen printout from *Evolution and Natural Selection* showing a table of results obtained with the values in Figure C1.

Record the results displayed on the screen in the table in Manual H and draw a graph of the percentage of red alleles against the generation number.

- C1 Are your results exactly the same as those you obtained from your bead model?
- C2 Would you expect the same results again if you re-ran the program using the same initial values?

You now have a model in which you can easily change all the possible variables and simulate the fluctuations in allele frequencies as a result of natural selection.

After ten generations have been tabulated you have a choice of what to do next. For example if you want to continue for another ten generations, you click the *Next 10 Generations* button and the program will calculate and tabulate the next ten generations.

Try to answer the following questions by changing the appropriate values. Only change one value at a time and re-run the program to see how it affects your results.

- C3 Selection need not always act to the same degree. How does increasing or decreasing the percentage of selection affect your results?*
- C4 How do results differ if selection acts against the red phenotype?*
- C5 Does the starting percentage of red alleles affect the final results or just the speed of change of the allele frequency?*

STUDENTS' MANUAL D NATURAL SELECTION IN ACTION – INDUSTRIAL MELANISM IN THE PEPPERED MOTH

Industrial melanism in the peppered moth, *Biston betularia*, illustrates how natural selection can be seen at work in directing change and adaptation to the environment.

The peppered moth is a common British species. It exists in a grey, speckled form, remarkably well adapted to resemble lichen on the bark of trees. These moths fly at night but rest motionless on the surface of the trees during the day. Their appearance offers them a good protection against their predators, mainly birds such as thrushes which hunt the moths during the day, by sight. About 1850 a black pigmented variety of moth, the melanic form, was first recorded in the Manchester area. The two forms of the moth are shown in Figure D1.



Figure D1 Two forms of the peppered moth - the grey form on the left and the melanic form on the right.

D1 Which form of moth appears to have been at a disadvantage in 1850 and why?

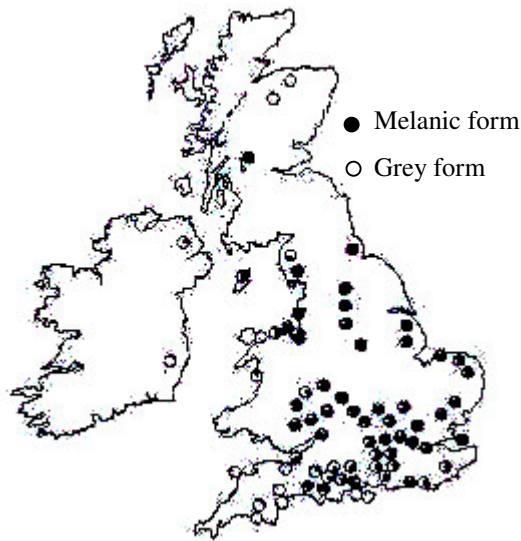
The melanic form was not eliminated by selection. In fact, by 1900 the proportion of the melanic form to the grey form was 99:1 in the Manchester area. By this time the Industrial Revolution had greatly changed the character of much of the countryside. From industrial centres such as Manchester and Birmingham, a vast amount of soot and other waste products poured from factory chimneys, polluting the surrounding areas. The white, lichen covered trees had become black. Away from these industrial areas however the countryside remained relatively unchanged.

D2 How was the selection in 1900 different from the two forms of peppered moth to the selection operating in 1850?

The two forms of the peppered moth are controlled by a single gene which has two alleles. The dominant allele controls the production of the dark pigment of the melanic form and the recessive allele does not produce pigment.

D3 How do you account for the sudden appearance of the melanic form in about 1850?

Study Figure D2 and compare the distribution of the two forms of the moth with your knowledge of the main industrial areas in Britain.



D4 Why are the two forms of moths unequally distributed throughout the country?

Figure D2 Map showing the distribution of grey and melanic forms of the peppered moth in 1952-56.

We can use the computer program *Evolution and Natural Selection* to simulate the changes in frequency of the two alleles under different environmental conditions. Select *Part 1*. Use a population of at least 200 and assume red represents the dominant allele producing the melanic form and yellow represents the recessive allele.

Consider two environments:

- a A rural area such as Dorset.
- b An industrial area such as Birmingham.

D5 Which phenotypes and genotypes are at a disadvantage in each environment?

D6 Would you expect there to be 100% selection against either of the forms in the two areas?

By using the programme attempt to show the changes in frequency of the red and yellow alleles in the two areas. You will need to decide the initial proportion of alleles and the direction and percentage of selection.

D7 Why does the frequency of the yellow alleles decrease more slowly in an industrial area than the frequency of the red alleles in a rural area?

D8 Would you expect the grey form of the moth to disappear completely from industrial areas?

Consider two other environments:

- a A rural area with new industrial developments.
- b An industrial area becoming a smokeless zone.

D9 In which case is the frequency of the alleles most affected by the changing conditions?

STUDENTS' MANUAL E - NATURAL SELECTION AND THE MAINTENANCE OF A STABLE POLYMORPHISM

The land snail, *Cepaea nemoralis*, is commonly found in a variety of habitats in this country. It has one main predator, the song thrush, which hunts by sight. The shell of the snail ranges in colour from light yellow, which appears quite green with the animal inside, to dark brown and varies in the extent to which the colour is broken up by banding as shown in Figure E1.

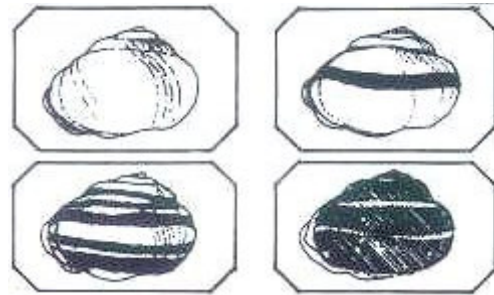


Figure E1 Variation in banding on the shell of the snail, *Cepaea nemoralis*.

Study Figure E2 and compare the percentages of yellow and unbanded shells in the different habitats.

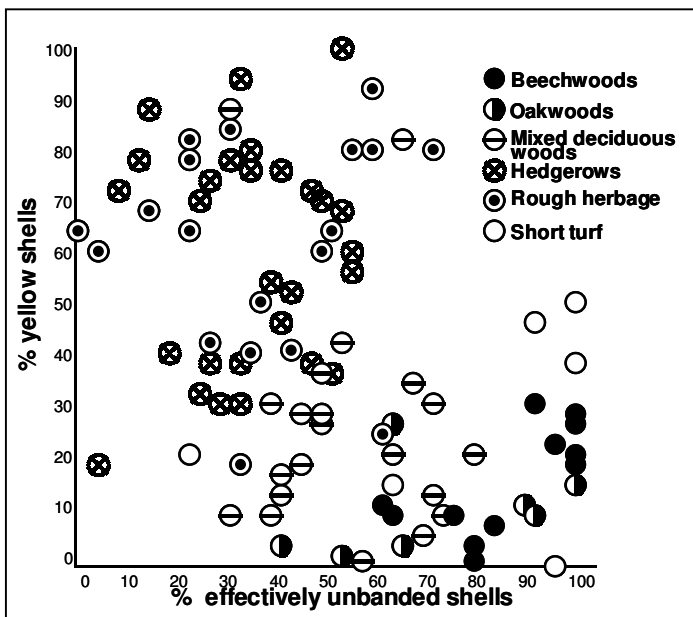


Figure E2 Frequencies of yellow and of unbanded forms of the snail, *Cepaea nemoralis*, in various habitats.

E1 What is the predominant shell colour in those habitats where the background is mainly green?

E2 How does the degree of banding vary according to the environment?

E3 What explanation can you give for the different frequencies of yellow and unbanded snails in the various habitats?

If all the selection was due to visual predation, one would expect to find only one variety of shell in any one environment, as these would be the only ones surviving. This is not the case. More than one variety of snail is often found together in any one habitat. The reason for this is that the heterozygotes have an advantage over the homozygotes because of some other effect of the gene on viability or fertility. The alleles only have an advantage in the heterozygous state.

Use the program *Evolution and Natural Selection* to investigate how these extra selective

forces can affect the frequencies of different forms. For this investigation select *Part 2*. This part of the program assumes that the alleles are codominant. Use an initial population of about 100 with 80% of one allele. This represents a situation where one allele has been at a disadvantage as it produces a conspicuous colour. Apply a 50% selection against both homozygotes. Run for ten generations. From your results draw a graph of percentages of red and yellow alleles against the number of generations.

E4 *What happens to the frequencies of the red and yellow alleles?*

E5 *Predict what you would expect to happen in further generations if the same level of selection continued.*

You have just illustrated the production of a stable polymorphism. A polymorphism literally translated means 'many forms', and is defined as the occurrence together in the same habitat, at the same time, of two or more forms of the same species in such proportions that the rarest cannot be maintained by mutation alone. They are maintained by a balance of selective factors. Each type of selection acts against each form or morph in a different way, with the net result that none are completely eliminated. In the model you have set up, both alleles are maintained in equal proportions. This is because in the homozygotes both the red and yellow alleles are at a disadvantage, whereas in the heterozygote both the red and yellow alleles are at an advantage.

Another example of polymorphism is found in man in a condition known as sickle-cell anaemia' .

In certain parts of the world, as shown in Figure E3, there is a mutant form of haemoglobin, the red blood pigment that transports oxygen around the body, known as sickle-cell haemoglobin. This different type of haemoglobin is produced by a mutant allele, HbS, which differs from the normal allele HbA, in that it affects the red blood cells of the homozygote HbS/HbS. These cells easily become distorted and soon die. This produces a fatal condition called sickle-cell anaemia. Individual homozygotes for this condition rarely survive past childhood. However, the red blood cells of the heterozygote HbS/HbA, carriers of the mutant allele, function normally.

E6 *Would you expect the allele which produces sickle-cell haemoglobin to disappear from the human population?*

The sickle-cell allele occurs in areas where malaria is endemic.

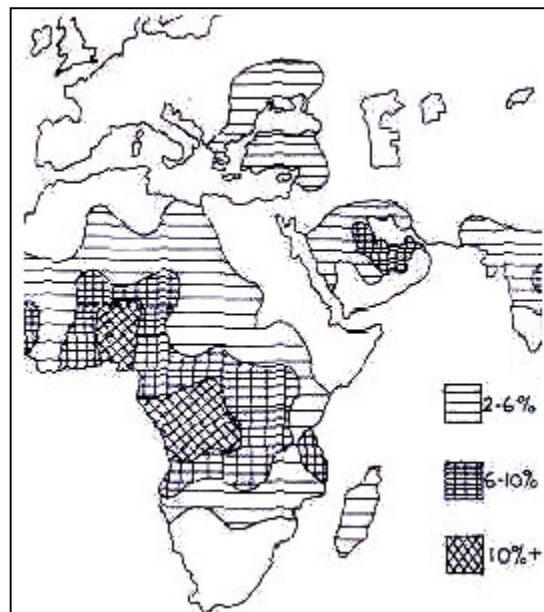


Figure E3 A map showing the parts of the world where the sickle-cell allele is common.

E7 What selective advantage does the heterozygote appear to have and why?

Use *Part 2* in the program *Evolution and Natural Selection* to illustrate this polymorphism. Remember that the percentage selection against the two homozygotes will be different.

E8 What effect will malaria eradication have on the frequencies of these alleles?

STUDENTS' MANUAL F - CHANCE VERSUS SELECTION

The degree and direction of selection cannot be the only factor controlling the allele frequencies. If it were, then if no selection or mutation occurs, the allele frequencies should remain constant. In large populations this is usually the case. However, in small populations small random changes may produce significant fluctuations in allele frequencies. Ten alleles lost by chance from a gene pool of 500 represents only 2% of the total but the same number lost from a gene pool of 50 represents 20% of the total. The effect of these random fluctuations is known as genetic drift.

Demonstrate genetic drift using *Part 1*, starting with 50% yellow alleles and no selection. Re-run with the same values but with different sized populations. Assume small populations are under 100 and large populations over 300.

Fluctuations in allele frequencies produce fluctuations in the range of forms within the population and hence provide the potential for a faster rate of change.

F1 Do you find the greatest fluctuations in allele frequencies in large or small populations?

Consider the organisms living on islands such as the Galapagos Islands shown in Figure F1.

F2 In what way did the geography of the Galapagos Islands affect the evolution of organisms such as Darwin's finches?

In nature populations may become geographically isolated, for example as a result of floods or land movements.

F3 How will the rate of change be affected if a large population becomes permanently subdivided?

F4 Will the direction of change be the same in the subdivided groups?

F5 How will this affect the long term evolution of the population?



Figure F1 A map of the Galapagos Islands

Genetic drift can be demonstrated to occur in small populations with no selection and so it must also occur when selection is present, perhaps modifying or counteracting the effects of selection.

Use the computer program to compare the effect of different amounts of selection in a population of 50 and one of 300. Start with 50% of red alleles and maintain the same direction of selection throughout.

F6 In what size of population and under what conditions do you find the fastest fluctuation in allele frequencies?

STUDENTS' MANUAL G - STUDYING POPULATION GENETICS

When biologists are studying the characteristics and adaptations of organisms in nature they may want to know the frequencies of certain alleles within a population and investigate how these frequencies fluctuate over a period of time. The study of population genetics investigates the 'gene pool' of a population, the genes possessed by the individuals of that population. Such a study can only be carried out on most living organisms by observing their outward appearance. As it is rarely possible to examine every individual, samples must be taken. However the phenotype of an organism does not always provide sufficient information about the alleles it carries. It is not possible to distinguish the heterozygotes from the dominant homozygotes because individuals with both these genotypes have the same phenotype. However it is possible to calculate the frequencies of both alleles of any gene, if the numbers of recessive homozygotes, easily distinguished by their different phenotype, and the population size are known. This can be done by applying the Hardy Weinberg equation:



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

where 1 is the frequency of the total population
 p is the frequency of red alleles
 q is the frequency of yellow alleles

Since in our sample there are only either red or yellow alleles $p + q = 1$

The probability of a gamete from this population carrying a red allele is p and the probability of a gamete carrying a yellow allele is q. At random fertilization the probability of both gametes carrying a red allele and producing a red homozygote is

$$p \times p \text{ or } p^2$$

and the probability of both carrying a yellow allele and producing a yellow homozygote is

$$q \times q \text{ or } q^2$$

The probability of one gamete carrying a red allele and the other a yellow allele and producing a heterozygote is

$$p \times q \text{ or } pq$$

However a heterozygote may be produced from an egg carrying a red allele and a sperm a yellow allele or from an egg carrying a yellow allele and a sperm a red allele. Therefore since there are two ways of producing a heterozygote, the probability of drawing randomly both a red and yellow allele is $2pq$.

There are no other possible combinations so $p^2 + 2q + q^2 = 1$ (the frequency of all possible genotypes). If the value of either p^2 or q^2 is known then the values of both p and q can be calculated and hence the frequency of all the genotypes. For example, if the frequency of the recessive homozygotes was found to be 0.81.

$$\begin{aligned} \text{Then } q^2 &= 0.81 \\ q &= 0.9 \\ \text{Since } p + q &= 1 \\ p &= 0.1 \end{aligned}$$

The frequencies of all genotypes can then be calculated.

$$\begin{aligned} P^2 &= 0.01 \text{ (frequency of dominant homozygotes)} \\ 2pq &= 0.18 \text{ (frequency of heterozygotes)} \end{aligned}$$

Imagine that you are studying a population over five-generations in which the red allele is dominant and there is no selection against either phenotypes. Every generation you take a sample of the population to find out the frequencies of the two phenotypes and you obtain the results shown in Table G1, which have actually been obtained from the program *Evolution and Natural Selection*.

Generation number	Number of phenotypes		Frequency of genotypes			% red alleles
	Red	Yellow	RR	RY	YY	
1	306	94				
2	307	93				
3	301	99				
4	314	86				
5	316	84				

Table G1

Calculate the frequencies of the three genotypes and the percentages of red alleles for generations 1 to 5. When you have filled in the table compare your calculated figures with those actually obtained from the program *Evolution and Natural Selection*. Your teacher will be able to provide you with these.

- G1 *Why is there a difference between the calculated and observed results?*
- G2 *How would selection alter your observed results compared to those you calculated?*
- G3 *Explain why the Hardy Weinberg equation is more applicable to large rather than small populations.*

A simple population genetics study that you could carry out for yourself is to find out the

frequency of the tongue-rolling allele within your class, school or local community. Tongue-rolling is controlled by the dominant allele.

G4 What are the genotypes of (a) tongue-rollers and (b) non tongue-rollers?

When planning the investigation you must consider the size of the population you want to study and your method of sampling.

G5 How would you set about finding out the number of recessive homozygotes in your population?

G6 How can you calculate the frequency of recessive and then dominant alleles in your population?

G7 What factors in your study might produce errors in your results?

