Sickle cell anemia is caused by the sickle cell allele (Hb^S) of a gene that contributes to hemoglobin (*Hb*) production. The abnormal hemoglobin (hemoglobin-S) produced causes red blood cells to become deformed and block capillaries. Tissue damage results. Affected individuals homozygous for the sickle cell gene rarely survive to reproductive age. Heterozygous individuals produce both normal hemoglobin and a small percentage of hemoglobin-S. These individuals are more resistant to malaria than individuals who are homozygous for the allele for normal hemoglobin (Hb^A). Their red blood cells are prone to sickling when there is a deficiency of oxygen.

The malaria-causing microorganism *Plasmodium falciparum* is injected by mosquitoes into the bloodstream of humans. Historically, the frequency of the Hb^S allele in Africa relates directly to the presence of malaria-causing organisms. In western Africa, the frequency of the Hb^S allele in the gene pool is 0.15. In central Africa, the frequency is 0.10, and in southern Africa the frequency is 0.05.

a. What is the frequency of the Hb^A allele in central Africa?

$p + q = 1.0$ $p + 0.1 = 1.0$ $p = 0.90$

b. What percentage of people in central Africa would have higher resistance to malaria?

$2pq = 2(0.1)(0.9) = 0.18 = 18\%$

c. In which part of Africa is the Hb^S allele most frequent?

western

Which of the following conclusions can be drawn from all the information provided on sickle cell anemia?

A. The sickle cell gene will eventually disappear because of its interaction with malaria.

B. Malaria causes heterozygous individuals to be less fertile than homozygous individuals.

C. In Africa, sickle cell anemia will disappear since it is lethal in the homozygous condition.

D. In Africa, carriers for sickle cell anemia have an advantage over homozygous individuals.

Topic 1 – Hardy-Weinberg Equilibrium
Review Sheet

Use the following information to answer the next question.

> A program to detect carriers of β-thalassemia (a mild blood disorder) found the incidence of the disease to be 4% in a particular population. A recessive allele found on an autosomal chromosome causes β-thalassemia.

Numerical Response

$4\% = aa = q^2 = 0.04$

7. What is the frequency of the recessive β-thalassemia allele in the gene pool of this population?

(Record your **answer as a value from 0 to 1 rounded to one decimal place** in the numerical-response section on the answer sheet.)

Answer: 0.2

A population of 200 includes 32 individuals that are homozygous recessive (*bb*) for a given trait. Assuming the population meets the conditions for Hardy–Weinberg equilibrium, how many of the 200 individuals would you expect to be homozygous dominant (*BB*)?

$\frac{32}{200} = 0.16 = q^2$

$q = 0.40$

$p = 0.60$

$p^2 = 0.36$

$0.36 \times 200 = 72$

Cystic fibrosis is a recessive condition that affects about 1 in 2500 people in the Caucasian population of Canada. Calculate the following:

(a) the population frequencies for the dominant (*C*) and recessive (*c*) alleles

$\frac{1}{2500} = 0.0004 = q^2$

$q = 0.02$ $p = 0.98$

(b) the percentage of the population that is a carrier of the recessive allele

$2pq = 2(0.02)(0.98) = 0.0392$

3.92%

(c) the number of students in your school that are likely to be carriers of the cystic fibrosis allele

$0.0392 \times 600 = 23.5$

$= 24$

A recessive allele (*h*) codes for complete hair loss in chimpanzees. Homozygous recessive individuals lose all their hair by about six months of age. Chimpanzees with one or two dominant alleles (*H*) show no signs of this disorder. In a population of captive chimpanzees, 16 % of the chimpanzees lose all their hair.

(a) Calculate the allele frequencies of *H* and *h*.

$q = 0.4$

$p = 0.6$

(b) What percentage of the chimpanzees could *not* be the parents of chimpanzees with this condition.

36 %

(c) Hairless chimpanzees have reduced survival rates and lower reproductive success. Predict how the allele frequencies will change over tim
Explain your reasoning as it relates to the Hardy–Weinberg equilibrium assumptions.

A large population consists of 400 individuals, of which 289 are homozygous dominant (*MM*), 102 are heterozygous (*Mm*), and 9 are homozygous recessive (*mm*). Determine the allele frequencies of *M* and *m*.

The gene pool of a certain large population of fruit flies contains only two eye-colour alleles: the dominant red allele, *R,* and the recessive white allele, *r.* Only 1 % of the population has red eyes. Determine the allele and genotype frequencies of this population

Manx cats have no tails (or have very short tails) and have large hind legs. The no-tail trait results from a heterozygous genotype, *Tt*. Interestingly, *TT* genotypes are normal cats, while the *tt* genotype is lethal and cat embryos that possess it do not survive. In a population of 1000 cats, only 1 % are Manx and 99 % are normal.
(a) What are the allele frequencies in this population?

$T = p = 0.9949$ $t = q = 0.005$

(b) Determine the expected frequency of each genotype in the next generation.

F_1
$p^2 = 0.99$
$2pq = 0.009974$
$q^2 = 0.000025125$

(c) Determine the allele frequencies of the population of cats from (b).

$p^2 + 2pq = 1.0$

(d) Predict the long-term result of a lethal homozygous recessive trait in a wild population.

	T ($p = 0.995$)	*t* ($q = 0.005$)
T ($p = 0.995$)	*TT* $p^2 = 0.99$ (normal)	*Tt* $pq = 0.005$ (no tail)
t ($q = 0.005$)	*Tt* $pq = 0.005$ (no tail)	*tt* $q^2 = 0.000025$ (lethal)

$TT = 0.99$

$Tt = 0.005 + 0.005 = 0.01$

$tt = 0.000025$, but these individuals do not survive.

The expected frequency of normal cats (*TT*) is 0.99 and of Manx cats (*Tt*) is 0.01. Embryos with genotype *tt* will not survive and so will not contribute.

(c) The genotype frequencies of this next generation is the same as that of the first generation, so calculation will be the same as part (a). Therefore, the frequency of allele *T* is 0.995 and the frequency of allele *t* is 0.005.

(d) They have no effect on allele frequencies since the genotype frequencies in this population have reached a level where they remain stable from one generation to the next. The allele frequencies are therefore also maintained.

(e) From the analysis in the rest of the population, the lethal homozygous trait would initially cause a reduction in the frequency of the recessive allele in the population until a stable, low frequency was obtained.