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#### Exercise 1

$$f(SS) = 0/100 = 0$$
  
 $f(ww) = 58/100 = 0.58$   
 $f(Sw) = 42/100 = 0.42$   
 $f(S) = 42/200 = 0.21 = p$   
 $f(w) = 158/200 = 0.79 = q$   
 $f(SS) = 0.21^2 = 0.0441$   
 $f(ww) = 0.79^2 = 0.6241$   
 $f(Sw) = 2*0.21*0.79 = 0.3318$   
Relative fitness

Relative fitness  $W_{SS}:\ 0 \ W_{Sw}:\ 1$ 

 $W_{ww}$ : 1

Zygotes frequencies:

$$f(SS)$$
:  $p^2 = 0.21^2 = 0.0441$   
 $f(Sw)$ :  $2pq = 2*0.21*0.79 = 0.3318$   
 $f(ww)$ :  $q^2 = 0.79^2 = 0.6241$ 

Average fitness

$$W = p^2 * W_{SS} + 2pq * W_{Sw} + q^2 * W_{ww} \rightarrow W = 0.0441*0 + 0.3318*1 + 0.6241*1$$
 
$$W = 0.9559$$

Adults after selection frequencies:

$$f(SS): p^2*W_{SS} = 0.0441*0 = 0$$
  
 $f(Sw): 2pq*W_{Sw} = 0.3318*1 = 0.3318$   
 $f(ww): q^2*W_{ww} = 0.6241*1 = 0.6241$ 

Normalized frequencies:

$$P: \frac{p^2 * W_{SS}}{W} = \frac{0}{0.9559} = 0$$

$$H: \frac{2pq * W_{Sw}}{W} = \frac{0.3318}{0.9559} = 0.3471$$

$$Q: \frac{q^2 * W_{ww}}{W} = \frac{0.6241}{0.9559} = 0.6529$$

Allele frequencies: 
$$q' = Q + \frac{H}{2} = 0.6529 + \frac{0.3471}{2} = 0.8265$$
 
$$p' = 1 - q' = 1 - 0.8265 = 0.1735$$

Over time, the "S" gene variant will become less common in the population. Even though it won't disappear completely, it will show up less of ten.

#### Exercise 2

$$p(A) = q(a) = 0.5$$

7 / 10 individuals die due to the disease

Relative fitness 
$$W_{AA}: 1$$
  $W_{Aa}: 1$   $W_{Aa}: 1$ 

Generation 0 before the disease:

$$f(AA)$$
:  $p^2 = 0.5^2 = 0.25$   
 $f(Aa)$ :  $2pq = 2*0.5*0.5 = 0.5$   
 $f(aa)$ :  $q^2 = 0.5^2 = 0.25$ 

Average fitness 
$$W = p^2*W_{AA} + 2pq*W_{Aa} + q^2*W_{aa} \rightarrow W = 0.25*1 + 0.5*1 + 0.25*0.3$$
 
$$W = 0.825$$

Generation 0 after the disease with normalized frequencies:

$$P: \frac{p^2 * W_{AA}}{W} = \frac{0.25}{0.825} = 0.3030$$

$$H: \frac{2pq * W_{Aa}}{W} = \frac{0.5}{0.825} = 0.6060$$

$$Q: \frac{q^2 * W_{aa}}{W} = \frac{0.075}{0.825} = 0.0909$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.3030 + \frac{0.6060}{2} = 0.606$$

$$q' = 1 - p' = 1 - 0.606 = 0.394$$

1st Generation before the disease:

$$f(AA)$$
:  $p^2 = 0.606^2 = 0.3672$   
 $f(Aa)$ :  $2pq = 2*0.606*0.394 = 0.4775$   
 $f(aa)$ :  $q^2 = 0.394^2 = 0.1552$ 

Average fitness

$$W = p^2 * W_{AA} + 2pq * W_{Aa} + q^2 * W_{aa} \rightarrow W = 0.3672 * 1 + 0.4775 * 1 + 0.1552 * 0.3$$
  
$$W = 0.8913$$

1st Generation after the disease with normalized frequencies:

$$P: \frac{p^2 * W_{AA}}{W} = \frac{0.3672}{0.8913} = 0.4120$$

$$H: \frac{2pq * W_{Aa}}{W} = \frac{0.4775}{0.8913} = 0.5357$$

$$Q: \frac{q^2 * W_{aa}}{W} = \frac{0.0466}{0.8913} = 0.0522$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.4120 + \frac{0.5357}{2} = 0.6799$$

$$q' = 1 - p' = 1 - 0.6799 = 0.3201$$

$$f(AA)$$
:  $p^2 = 0.6799^2 = 0.4623$   
 $f(Aa)$ :  $2pq = 2*0.6799*0.3201 = 0.4353$   
 $f(aa)$ :  $q^2 = 0.3201^2 = 0.1024$ 

Average fitness 
$$W = p^2*W_{AA} + 2pq*W_{Aa} + q^2*W_{aa} \rightarrow W = 0.4623*1 + 0.4353*1 + 0.1024*0.3$$
 
$$W = 0.9283$$

2nd Generation after the disease with normalized frequencies:

$$P: \frac{p^2 * W_{AA}}{W} = \frac{0.4623}{0.9283} = 0.4980$$

$$H: \frac{2pq * W_{Aa}}{W} = \frac{0.4353}{0.9283} = 0.4689$$

$$Q: \frac{q^2 * W_{aa}}{W} = \frac{0.0307}{0.9283} = 0.0331$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.4980 + \frac{0.4689}{2} = 0.7325$$
$$q' = 1 - p' = 1 - 0.7325 = 0.2675$$

The population will settle into balance when p equals 1 because the p frequency keeps going up while the q frequency keeps going down.

3 / 10 individuals die due to the disease

Relative fitness 
$$W_{AA}$$
: 1  $W_{Aa}$ : 1  $W_{Aa}$ : 1  $W_{Aa}$ : 1 - 0.3 = 0.7

*Generation* 0 *be fore the disease* :

$$f(AA)$$
:  $p^2 = 0.5^2 = 0.25$   
 $f(Aa)$ :  $2pq = 2*0.5*0.5 = 0.5$   
 $f(aa)$ :  $q^2 = 0.5^2 = 0.25$ 

Average fitness 
$$W = p^2*W_{AA} + 2pq*W_{Aa} + q^2*W_{aa} \rightarrow W = 0.25*1 + 0.5*1 + 0.25*0.7$$
 
$$W = 0.925$$

Generation 0 after the disease with normalized frequencies:

$$P: \frac{p^2 * W_{AA}}{W} = \frac{0.25}{0.925} = 0.27$$

$$H: \frac{2pq * W_{Aa}}{W} = \frac{0.5}{0.925} = 0.54$$

$$Q: \frac{q^2 * W_{aa}}{W} = \frac{0.175}{0.925} = 0.19$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.27 + \frac{0.54}{2} = 0.54$$

$$q' = 1 - p' = 1 - 0.54 = 0.46$$

1st Generation before the disease:

$$f(AA): p^2 = 0.54^2 = 0.2916$$
  
 $f(Aa): 2pq = 2*0.54*0.46 = 0.4968$   
 $f(aa): q^2 = 0.46^2 = 0.2116$ 

Average fitness

$$W = p^2 * W_{AA} + 2pq * W_{Aa} + q^2 * W_{aa} \rightarrow W = 0.2916 * 1 + 0.4968 * 1 + 0.2116 * 0.7$$

$$W = 0.9365$$

1st Generation after the disease with normalized frequencies:

$$P: \frac{p^2 * W_{AA}}{W} = \frac{0.2916}{0.9365} = 0.3114$$

$$H: \frac{2pq * W_{Aa}}{W} = \frac{0.4968}{0.9365} = 0.5304$$

$$Q: \frac{q^2 * W_{aa}}{W} = \frac{0.1481}{0.9365} = 0.1581$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.3114 + \frac{0.5304}{2} = 0.5766$$
$$q' = 1 - p' = 1 - 0.5766 = 0.4234$$

2nd Generation before the disease:

$$f(AA)$$
:  $p^2 = 0.5766^2 = 0.3324$   
 $f(Aa)$ :  $2pq = 2*0.5766*0.4234 = 0.4883$   
 $f(aa)$ :  $q^2 = 0.4234^2 = 0.1793$ 

$$W = p^2*W_{AA} + 2pq*W_{Aa} + q^2*W_{aa} \rightarrow W = 0.3324*1 + 0.4883*1 + 0.1793*0.7$$
 
$$W = 0.9462$$

2nd Generation after the disease with normalized frequencies:

$$P: \frac{p^2 * W_{AA}}{W} = \frac{0.3324}{0.9462} = 0.3513$$

$$H: \frac{2pq * W_{Aa}}{W} = \frac{0.4883}{0.9462} = 0.5161$$

$$Q: \frac{q^2 * W_{aa}}{W} = \frac{0.1255}{0.9462} = 0.1326$$

Allele frequencies:  

$$p' = P + \frac{H}{2} = 0.3513 + \frac{0.5161}{2} = 0.6094$$

$$q' = 1 - p' = 1 - 0.6094 = 0.3906$$

The population to reach equilibrium faster will be the 70% as individuals killed population (p will reach 1 faster than in the 30% as individuals killed population)

### Exercise 3

$$f(S): 0.12 = q$$
  
 $f(A): 1-0.12 = 0.88 = p$   
 $f(AA): p^2 = 0.88^2 = 0.7744$ 

$$f(AS)$$
:  $2pq = 2*0.88*0.12 = 0.2112$   
 $f(SS)$ :  $q^2 = 0.12^2 = 0.0144$ 

Relative fitness  $W_{AA}$ : 0.88  $W_{AS}$ : 1  $W_{SS}$ : 0.14

Selection coefficient  $W_{AA} = 1 - s_1$   $s_1 = 1 - W_{AA} = 1 - 0.88 = 0.12$ 

$$W_{SS} = 1 - s_2$$
  
 $s_2 = 1 - W_{SS} = 1 - 0.14 = 0.86$ 

Equilibrium frequency  $^{p} = \frac{s_2}{s_1 + s_2} = \frac{0.86}{0.12 + 0.86} = 0.8775$   $^{q} = 1 - ^{p} = 1 - 0.8775 = 0.1225$ 

$$Average \ fitness$$
 
$$W = p^2*W_{AA} + 2pq*W_{AS} + q^2*W_{SS} \rightarrow W = 0.7744*0.88 + 0.2112*1 + 0.0144*0.14$$
 
$$W = 0.8946$$

We can say that the population is indeed in equilibrium

Exercise 4

Case A

Relative fitness

 $W_{AA}$ : 1

 $W_{Aa}$ : 1

 $W_{aa}:0.75$ 

Selection coefficient

$$W_{aa} = 1 - s$$
  
 $s = 1 - W_{aa} = 1 - 0.75 = 0.25$ 

$$W_{Aa} = 1 - hs$$

$$h = \frac{1 - W_{Aa}}{s} = \frac{1 - 1}{1} = 0$$

Case B

Relative fitness

 $W_{AA}$ : 1

 $W_{Aa}: 0.6$ 

 $W_{aa} : 0.6$ 

Selection coefficient

$$W_{aa} = 1 - s$$

$$s = 1 - W_{aa} = 1 - 0.6 = 0.4$$

$$W_{Aa} = 1 - hs$$

$$h = \frac{1 - W_{Aa}}{s} = \frac{1 - 0.6}{0.4} = 1$$

Case C

Relative fitness

 $W_{AA}: 0.4$ 

 $W_{Aa}: 0.8$ 

 $W_{aa}:1$ 

Selection coefficient

$$W_{AA} = 1 - s_1$$

$$s_1 = 1 - W_{AA} = 1 - 0.4 = 0.6$$

$$W_{Aa} = 1 - s_2$$

$$s_2 = 1 - W_{Aa} = 1 - 0.8 = 0.2$$

$$W_{Aa} = 1 - hs_2$$

$$h = \frac{1 - W_{Aa}}{s_2} = \frac{1 - 0.8}{0.2} = 1$$

Case D

Relative fitness

 $W_{AA}: 0.8$ 

 $W_{Aa}: 1$ 

 $W_{aa} : 0.55$ 

Selection coefficient

$$W_{AA} = 1 - s_1$$

$$s_1 = 1 - W_{AA} = 1 - 0.8 = 0.2$$

$$W_{aa} = 1 - s_2$$
  
 $s_2 = 1 - W_{aa} = 1 - 0.55 = 0.45$ 

$$M_{Aa} = 1 - hs_2$$

$$h = \frac{1 - W_{Aa}}{s_2} = \frac{1 - 1}{0.2} = 0$$

Favoured allele in each case:

Case A: Dominant dominance (h = 0), selection against recessive phenotype

Case B: Intermediate dominance  $(0 \le h \le 1)$ 

Case C: Recessive dominance (h = 1), selection against dominant phenotype

Case D: Heterozygote advantage

## Exercise 5

		Genotype	
	TT	Tt	tt
Newborns (240)	142	84	14
Adults (196)	128	66	2
Absolute fitness	128 / 142 = 0.9	66 / 84 = 0.78	2/14 = 0.14
Relative fitness to TI	0.9/0.9 = 1	0.78 / 0.9 = 0.86	0.14 / 0.9 = 0.15
Relative fitness to Tt	0.9 / 0.78 = 1.15	0.78 / 0.78 = 1	0.14 / 0.78 = 0.18
Relative fitness to tt	0.9 / 0.14 = 6.43	0.14 / 0.78 = 0.9	0.14 / 0.14 = 1

Newborn allele frequencies:

$$p = \frac{2*142 + 84}{2*240} = 0.76$$

$$q = 1 - p = 1 - 0.76 = 0.24$$

Adult allele frequencies:

$$p = \frac{2*128 + 66}{2*196} = 0.82$$

$$q = 1 - p = 1 - 0.82 = 0.18$$

$$p:\ 0.76\ \neq 0.82\ /\!/\ q:\ 0.24\neq 0.18$$

The allele frequencies are different between adult and newborn turtles

Genotype frequencies of newborns 
$$p = 0.82$$
  
 $q = 0.18$ 

Relative fitness 
$$W_{TT}$$
: 1  $W_{Tt}$ : 0.86  $W_{tt}$ : 0.15

$$f(TT): p^2 = 0.82^2 = 0.6724$$
  
 $f(Tt): 2pq = 2*0.82*0.18 = 0.2952$   
 $f(tt): q^2 = 0.18^2 = 0.0324$ 

Average fitness 
$$W = p^2 * W_{TT} + 2pq * W_{Tt} + q^2 * W_{tt} \rightarrow W = 0.6724 * 1 + 0.2952 * 0.86 + 0.0324 * 0.15$$
 
$$W = 0.9311$$

Adults after selection with normalized frequencies:

$$P: \frac{p^2 * W_{TT}}{W} = \frac{0.6724}{0.9311} = 0.7221$$

$$H: \frac{2pq * W_{Tt}}{W} = \frac{0.2539}{0.9311} = 0.2726$$

$$Q: \frac{q^2 * W_{tt}}{W} = \frac{0.0049}{0.9311} = 0.0053$$

Allele frequencies:  

$$p' = P + \frac{H}{2} = 0.7221 + \frac{0.2726}{2} = 0.8584$$

$$q' = 1 - p' = 1 - 0.8584 = 0.1416$$

Genotype frequencies of newborns of the next generation

$$f(TT): p^2 = 0.8584^2 = 0.7369$$
  
 $f(Tt): 2pq = 2*0.8584*0.1416 = 0.2431$   
 $f(tt): q^2 = 0.1416^2 = 0.02$ 

$$W = p^2*W_{TT} + 2pq*W_{Tt} + q^2*W_{tt} \rightarrow W = 0.7369*1 + 0.2431*0.86 + 0.02*0.15$$
 
$$W = 0.9489$$

Adults after selection with normalized frequencies

$$P: \frac{p^2 * W_{TT}}{W} = \frac{0.7369}{0.9489} = 0.7765$$

$$H: \frac{2pq * W_{Tt}}{W} = \frac{0.2091}{0.9489} = 0.2203$$

$$Q: \frac{q^2 * W_{tt}}{W} = \frac{0.003}{0.9489} = 0.0032$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.7765 + \frac{0.2203}{2} = 0.8867$$

$$q' = 1 - p' = 1 - 0.8867 = 0.1133$$

Exercise 6

#### Case A

We see from the table that both populations have the same level of fitness. However, in population 1, where p=0.8 is greater than p=0.1 in population 2, where the allele A is more common. Because allele A is favored, we would expect its frequency to increase until it becomes the only allele present (p=1) in both populations. Additionally, in population 1, we will reach this equilibrium faster compared to population 2 because the favored allele already has a higher frequency there.

#### Case B

In the table, we see that both populations have the same mix of alleles. This means the time it takes for one allele to completely take over (when p equals 1) depends only on how fit each type of gene is in the population.

We notice that in population 1, the aa genotype is a bit stronger compared to population 2. So, we think the A gene will take over faster in population 2

## Case C

In Case A, we noticed that both populations had equal fitness. From this, we predict that the favored allele (the recessive allele aa) will take over faster in population 2 compared to population 1. This means population 2 will likely reach equilibrium quicker than population 1 since it has a higher frequency of the recessive allele (shown as p which represents the dominant allele AA)

#### Case D

In Case B, we observed that the allele frequencies were identical in both populations. Since we're favoring the recessive allele aa, this suggests that at equilibrium,

the frequencies will be 1 and 0, which indicates fixation. Looking closer, we notice that in population 1, the fitness for the dominant homozygous genotype is higher than in population 2. This leads us to believe that in population 2, the recessive allele aa will reach fixation faster.

#### Exercise 7

 $A_1$  and  $A_2$  are codominant between each other

$$f(A_1) = 0.4$$
  
$$f(A_2) = 1 - 0.4 = 0.6$$

80% death, s = 0.8 for  $A_2$  allele

Relative fitness 
$$W_{A_1A_1}: 1$$
  $W_{A_1A_2}: 1 - \frac{s}{2} = 1 - \frac{0.8}{2} = 0.6$   $W_{A_2A_2}: 1 - s = 1 - 0.8 = 0.2$ 

Zygote frequencies  

$$f(A_1A_1): p^2 = 0.4^2 = 0.16$$
  
 $f(A_1A_2): 2pq = 2*0.4*0.6 = 0.48$   
 $f(A_2A_2): q^2 = 0.6^2 = 0.36$ 

$$W = p^2*W_{A_1A_1} + 2pq*W_{A_1A_2} + q^2*W_{A_2A_2} \rightarrow W = 0.16*1 + 0.48*0.6 + 0.36*0.2$$
 
$$W = 0.52$$

After selection (normalized frequencies):

$$P: \frac{p^2 * W_{A_1 A_1}}{W} = \frac{0.16}{0.52} = 0.3077$$

$$H: \frac{2pq * W_{A_1 A_2}}{W} = \frac{0.288}{0.52} = 0.5538$$

$$Q: \frac{q^2 * W_{A_2 A_2}}{W} = \frac{0.072}{0.52} = 0.1385$$

Allele frequencies:

$$p' = P + \frac{H}{2} = 0.3077 + \frac{0.5538}{2} = 0.5846$$
$$q' = 1 - p' = 1 - 0.5846 = 0.4154$$

#### Exercise 8

Environment	SS	SR	RR
Without warfarin	1	0.77	0.46
With war farin	0.68	1	0.37

Without war farin, the selection favors the allele S over the allele R which indicates directional and purifying selection.

With war farin, the selection is balanced because it favors the SR genotype.

Allele frequencies 
$$f(S) = 0.8$$
,  $f(R) = 0.2$ 

Environment without warfarin:

Relative fitness

 $W_{SS}$ : 1

 $W_{SR}: 0.77$ 

 $W_{RR}: 0.46$ 

$$f(SS)$$
:  $p^2 = 0.8^2 = 0.64$   
 $f(SR)$ :  $2pq = 2*0.8*0.2 = 0.32$ 

f(RR):  $q^2 = 0.2^2 = 0.04$ 

Average fitness

$$W = p^2 * W_{SS} + 2pq * W_{SR} + q^2 * W_{RR} \rightarrow W = 0.64 * 1 + 0.32 * 0.77 + 0.04 * 0.46$$
  
$$W = 0.9048$$

Adults after selection with normalized frequencies

$$P: \frac{p^2 * W_{SS}}{W} = \frac{0.64}{0.9048} = 0.7073$$

$$H: \frac{2pq * W_{SR}}{W} = \frac{0.2464}{0.9048} = 0.2723$$

$$Q: \frac{q^2 * W_{RR}}{W} = \frac{0.0184}{0.9048} = 0.0203$$

Allele frequencies:  

$$p' = P + \frac{H}{2} = 0.7073 + \frac{0.2723}{2} = 0.8435$$

$$q' = 1 - p' = 1 - 0.8435 = 0.1565$$

Environment with war farin:

Relative fitness  $W_{SS}$ : 0.68  $W_{SR}$ : 1  $W_{RR}$ : 0.37

$$f(SS): p^2 = 0.8^2 = 0.64$$
  
 $f(SR): 2pq = 2*0.8*0.2 = 0.32$   
 $f(RR): q^2 = 0.2^2 = 0.04$ 

Average fitness 
$$W = p^2*W_{SS} + 2pq*W_{SR} + q^2*W_{RR} \rightarrow W = 0.64*0.68 + 0.32*1 + 0.04*0.37$$
 
$$W = 0.77$$

Adults after selection with normalized frequencies

$$P: \frac{p^2 * W_{SS}}{W} = \frac{0.4352}{0.77} = 0.5652$$

$$H: \frac{2pq * W_{SR}}{W} = \frac{0.32}{0.77} = 0.4156$$

$$Q: \frac{q^2 * W_{RR}}{W} = \frac{0.0148}{0.77} = 0.0192$$

Allele frequencies:  

$$p' = P + \frac{H}{2} = 0.5652 + \frac{0.4156}{2} = 0.773$$

$$q' = 1 - p' = 1 - 0.773 = 0.227$$

Allele frequencies at equilibrium without war farin

$$W_{SS}: 1$$

$$W_{SR}: 1 - s_1$$

$$s_1 = 1 - W_{SR} = 1 - 0.77 = 0.23$$

$$W_{RR}: 1 - s_2$$

$$s_2 = 1 - W_{RR} = 1 - 0.46 = 0.54$$

$$^p = \frac{s_2}{s_1 + s_2} = \frac{0.54}{0.23 + 0.54} = 0.7013$$

$$^q = 1 - ^p = 1 - 0.7013 = 0.2987$$

Allele frequencies at equilibrium with war farin

$$W_{SS}: 1-s_1$$
 $s_1 = 1 - W_{SS} = 1 - 0.68 = 0.32$ 
 $W_{SR}: 1$ 

$$W_{RR}: 1-s_2$$
 $s_2 = 1 - W_{RR} = 1 - 0.37 = 0.63$ 

$$^p = \frac{s_2}{s_1 + s_2} = \frac{0.63}{0.32 + 0.63} = 0.6632$$
 $^q = 1 - ^p = 1 - 0.6632 = 0.3368$ 

$$\mu = 1x10^{-5}$$

 $\mu = Mutation rate$ 

Fitness for PKU individuals is half of healthy individuals

Relative fitness 
$$W_{Aa}:1$$
  $W_{aa}:1-s$   $s=1-W_{aa}=1-0.5=0.5$ 

Frequency of PKU in equilibrium

Frequency of affected individuals by PKU

$$q^2 = 0.00447^2 = 2x10^{-5}$$

$$PKU \ fitness = 0.8$$

$$W_{aa}: 1-s$$
  
 $s = 1 - W_{aa} = 1 - 0.8 = 0.2$ 

Frequency of PKU in the new equilibrium

Frequency of affected individuals by PKU

$$q^2 = 0.00707^2 = 5x10^{-5}$$

The frequency of individuals with PKU has changed due to increasing their fitness from 0.5 to 0.8. As a result, the frequency of a fected individuals has also increased.

# By augmenting fitness, we decreased the selective pressure against the allele, allowing it to become more common in the population

Exercise 10

Blindness in mice: 3 in 10.000

Mutation rate  $\mu$  of the recessive allele for blind mice:

$$q^{2} = \frac{3}{10000} = 3x10^{-4}$$

$$q = \sqrt{3x10^{-4}} = 0.0173$$

$$\mu = \frac{q}{1 - q} = \frac{0.0173}{1 - 0.0173} = 0.0176$$

80% heterozygotes in population (we reduce 20%)

$$p = 1 - q = 1 - 0.0173 = 0.9827$$

*New mutation rate*  $\mu$  *of the recessive allele for blind mice* :

$$p^{2} + 2pq*0.8 + q^{2} = 1$$

$$q^{2} = 1 - p^{2} - 2pq$$

$$q^{2} = 1 - 0.9827^{2} - 2*0.9827*0.0173*0.8$$

$$q^{2} = 0.00709$$

$$q = \sqrt{0.00709}$$

$$q = 0.0842$$

$$\mu = \frac{q}{1 - q} = \frac{0.0842}{1 - 0.0842} = 0.0919$$

The variation in mutation rates arises from the impact of selection on the frequency of

heterozygotes, resulting in a 20% reduction within the population. We incorporate this reduction when calculating the second mutation rate, leading to a decrease in heterozygosity and an increase in the frequency of the recessive allele (blind mice). These adjustments contribute to an increase in the estimated mutation rate.