101-NYA Class 16: Mechanisms of Evolution

Marks

Total Score: 0 /17

Part A: 40 Minutes

Group:

In rock pocket mice, the Mc1r allele for dark-coloured fur (called D here for simplicity) is dominant to the wild-type Mc1r allele for light fur (d). Therefore, individual pocket mice can have one of three genotypes and one of two phenotypes, as summarized in the table below.

	Genotype	Phenotype
Homozygous Dominant	DD	Dark
Heterozygous	Dd	Dark
Homozygous Recessive	dd	Light

Dr. Nachman and colleagues collected pocket mice across 35-kilometers of the Arizona Sonoran Desert that included both dark, rocky lava outcrops and light rocky granite areas. Substrate colour and coat colour frequencies were recorded for each location. Each site was separated from any of the others by at least 8 kilometers. A total of 207 mice were trapped and their genomes sequenced. The data are summarized below:

Collecting	Substrate	Number of	Phenotype and Genotype			
Site	Colour	Mice	Light (dd)	Dark (Dd)	Dark (DD)	
1	Light	85	80	5	0	
2	Dark	45	3	26	16	
3	Dark	77	2	41	34	

Source of data: Hoekstra, H, K. Drumm, and M. Nachman. Source: Ecological Genetics of Adaptive Color Polymorphism in Pocket Mice: Geographic Variation in Selected And Neutral Genes. 2004. Evolution, 58(6), pp. 1329-1344.

Assuming that 8 Km is enough distance to establish each collecting site as an isolated population, calculate p and q for each population, where p is the frequency of D and q is the frequency of d:

1)	p =	0.029	q =	0.971
2)	p =	0.644	q =	0.356
3)	p =	0.708	q =	0.292

Grading Explanation

0.5 marks per correct answer. Auto-graded.

0.5 marks per correct answer. No part marks, but be easy regarding potential rounding.

Using your answers for the question above, calculate the expected Hardy-Weinberg genotype frequencies for each of the populations:

1)	DD =	0.001	Dd =	0.057	dd =	0.942
2)	DD =	0.415	Dd =	0.458	dd =	0.126
3)	DD =	0.501	Dd =	0.414	dd =	0.085

Now, using the original data, calculate the actual frequency of each genotype within each of the populations:

1)	DD =	0.000	Dd =	0.059	dd =	0.941
2)	DD =	0.356	Dd =	0.578	dd =	0.067
3)	DD =	0.442	Dd =	0.532	dd =	0.026

/4.5

/4.5

/3

Are the populations in Hardy-Weinberg equilibrium for the Mc1r gene? Write 'Y' or 'N' for each in the space below

1)	Y
2)	Ν
3)	N

/1

/1

/2

/2

Even though these are judgement calls, the answers here are the correct calls to make. 1 mark per correct answer, no part marks.

1 mark for reasonable

description. Many versions are possible; as long as

what's written makes some

sense, full marks awarded.

Describe the rationale you employed to answer the previous question The expected HW genotype frequencies were visually compared against the observed genotype frequencies, and a judgement call was made about whether the numbers were close enough to each other. A chi square test could provide some statistical insight to help make the decision, but that was not used here (we'll save that for the lab). Instead, you might consider that if the difference between all of the frequencies does not add up to more than 0.1 (or 10%), your population is probably in HW equilibirum. However, if all of the differences add up to more than 0.2, the population probably isn't in HW equilibrium. Between a difference of 0.1 and 0.2 is a grey area, requiring a bit of a judgement decision.

For the populations above which you determined were not in Hardy-Weinberg equilibrium with respect to the Mc1r gene, why do you believe they are not in equilibrium? In other words, what evolutionary mechanism is working to move these populations away from Hardy-Weinberg equilibrium? Explain your answer.

As identified in the activity on natural selection from class 16, there is selection for a coat colour which matches the background in pocket mice. Population 1 is on light substrate, so there will be selection for light coloured mice, as they are more camouflaged against the background and can more easily escape detection from predators. In populations 2 and 3 the substrate is dark, and so there will be selection for dark coloured mice. Natural selection is the most important evolutionary mechanism, and it is working here to move the populations away from equilibrium, with constant selection against the non-matching coat colour allele.

If all the mouse predators were somehow removed from the Sonoran Desert environment, what do you predict would happen with regard to evolution of mouse coat colour, specifically with regard to the allele and genotype frequencies for the Mc1r gene in the population? Explain your answer.

If the predators were removed, there would no longer be selection for coat colour, because this is primarily a mechanism of camouflage against predators. Without this selective force, it's possible the populations could enter into a HW equilibrium with regard to the 'D' gene, so long as no other evolutionary mechanisms were having an effect (i.e., a smaller effect that was washed out by the strong selective force; this seems unlikely). This implies that the MC1R allele frequencies (p and q) would remain the same as they were at the point when the predators were removed, and that the genotype frequencies would stabilize as p^2, 2pq, and q^2.

1 mark for mention of natural selection. 1 mark for description of how selection is working. Part marks possible for the description.

1 mark for alluding to no selection for coat colour. 1 mark for mention of entering HW equilibrium. Alternatively, 1 mark for mentioning other types of selection for coat colour (e.g., sexual) or other traits being selected for, or other evolutionary mechanisms becoming more important and keeping the population from enterring HW equilibrium. Part marks possible.

Part B: Extra

The numbers from the table above only represent small samples from each of the collecting sites. In reality, the mouse population numbers from each of these collecting sites are likely in the thousands, or even the tens of thousands.

Imagine now that a particular mouse pathogen (for example some kind of bacterium) begins infecting and killing mice in one of these populations, and reduces the numbers to less than 100. What would this kind of event be called?

A population bottleneck

In the scenario described for the previous question, what would be the effect on genetic variation within the population? Would the allele frequencies for the 'D' gene in the population remain the same after passage of the pathogen as they were before?

This bottleneck would likely decrease the overall genetic variation in the population, as it's unlikely that every allele from the original gene pool would still be represented in the surviving small population. It's also possible, and in fact very likely, that the overall allele frequencies would change, and that the frequencies for the 'D' gene would change as well. The only way this wouldn't happen would be if the exact same proportions of dd, Dd, and DD mice died from the pathogen. As it's unlikely that this would occur, the 'D' gene allele frequencies would probably change.

In the scenario from above, what evolutionary mechanism(s) would be most likely to lead to changes in the 'D' gene allele frequency within the new small population? Is there any way that the genetic variation in the population could conceivably increase?

Natural selection would still be important for the 'D' gene, as it's unlikely that the bottleneck would remove predation pressure from the surviving mice. However, in a small population, genetic drift becomes an important factor, and it's possible that allele frequencies could change simply through the random nature of sexual reproduction. Even though the bottleneck would most likely have reduced genetic variation, this could increase again over time through mutation, but also potentially through migration if mice from neighbouring populations, with different mutations and alleles, immigrated into the new small population (where competition for space and resources would be minimal). Finally, there's no indication that non-random mating would be a factor here, as coat colour does not appear to have a direct effect on mating success.

1 mark for correct answer. No part marks.

0.5 marks for indicating a decrease in genetic variation, 0.5 marks for mentioning that allele frequencies would probably change. Explanation not necessary.

1 mark for mention of any evolutionary mechanism, as long as it makes sense (no explanation necessary for genetic drift). 1 mark for adequate description of how mutation and/or migration could lead to an increase in genetic variation over time. Part marks for second element if description is not included or flawed; only mutation or gene flow are appropriate answers here.

/2

/1

/2