

Past-paper walk-through

Population Genetics ■ 7.4

eXercise

Questions in this set

- 2022 Q4
- 2016 Q1
- 2015 Q6
- 2014 Q4
- 2014 Q8

Reading the mark scheme

- **B1** a mark that stands on its own – the point is either made or not.
- **M1** a *method* mark: the right approach, even if the number is wrong.
- **A1** an *answer* mark, and it usually needs its M mark first.
- **C1** a working mark on the way to the answer.
- **//** separates answers the examiner accepts equally.
- **ecf** = error carried forward: a later part is marked on your own earlier answer.
- **owtte** = “or words to that effect” – the wording need not match.

Question 4

2022 ■ Q4

Existing isolated brook trout populations in Newfoundland, Canada, were once part of a larger population that was fragmented at the end of the most recent glaciation period about 10,000 to 12,000 years ago. Researchers investigated 14 naturally separated stream populations of brook trout. They found that the populations are all genetically distinct and show differences in morphology.

- (a)** Describe the prezygotic barrier that results in these genetically distinct populations.
- (b)** Brook trout with longer fins are able to swim faster than brook trout with shorter fins. In one of the Newfoundland streams, the main prey of the brook trout evolved to move faster. For brook trout living in this stream, explain the difference in fitness between longer-finned individuals and shorter-finned individuals.
- (c)** If two morphologically and behaviorally distinct populations of brook trout remain isolated for many generations, predict the likely impact on both populations.

Question 4

(d) Researchers claim that there are more genetic differences between any two current brook trout populations than there are between any single current population and the ancestral brook trout population from which all the trout are descended. Provide reasoning to justify their claim.

Solution 4

(a)

Mark scheme

- The prezygotic barrier is geographic isolation, which prevents gene flow between the separated brook trout stream populations.

Solution 4

(b)

Mark scheme

- Longer-finned individuals swim faster and are therefore more likely to capture the (now faster-evolved) prey and survive to reproduce, giving them higher fitness than shorter-finned individuals, which are less able to catch the faster prey and thus have lower fitness (fewer offspring).

Solution 4

(c)

Mark scheme

- If the two populations remain isolated for many generations, they will likely become separate species; alternatively, the two populations will continue diverging behaviorally, morphologically, and/or genetically (increasing reproductive isolation over time, i.e. potential speciation).

Solution 4

(d)

Mark scheme

- Justification: each isolated population accumulates its own mutations and experiences its own genetic drift (distinguishing it from the ancestral population), and the mutations each population accumulates are likely to differ as a result of different selective pressures; so, allele production via random mutation plus genetic drift and selection by local environmental conditions produces a collection of alleles unique to each population - making any two current populations differ more from each other than either does from the shared ancestral population.

Question 1

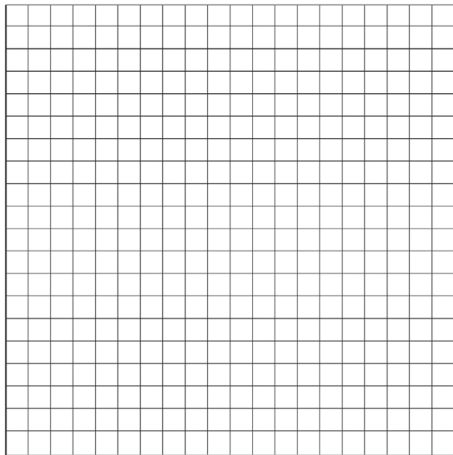
2016 ■ Q1

Leucine aminopeptidases (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*⁹⁴, in mussels from each sample site (table 1).

[Blank graphing grid provided below part (a): a rectangular grid of small squares, no axis labels or scale printed, for the student to construct their own bar graph.]

(a) On the axes provided, **construct** an appropriately labeled bar graph to illustrate the observed frequencies of the *lap*⁹⁴ allele in the study populations.

Question 1



Question 1

2016 ■ Q1

Leucine aminopeptidases (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*⁹⁴, in mussels from each sample site (table 1). [Blank graphing grid provided below part (a): a rectangular grid of small squares, no axis labels or scale printed, for the student to construct their own bar graph.]

(b) Based on the data, **describe** the most likely effect of salinity on the frequency of the *lap*⁹⁴ allele in the marine mussel populations in Long Island Sound. **Predict** the

Question 1

likely *lap*⁹⁴ allele frequency at a sampling site between site 1 and site 2 in Long Island Sound.

Question 1

2016 ■ Q1

Leucine aminopeptidases (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*⁹⁴, in mussels from each sample site (table 1).

[Blank graphing grid provided below part (a): a rectangular grid of small squares, no axis labels or scale printed, for the student to construct their own bar graph.]

(c) Describe the most likely effect of *LAP*⁹⁴ activity on the osmolarity of the cytosol. **Describe** the function of *LAP*⁹⁴ in maintaining water balance in the mussels living in the Atlantic Ocean.

Question 1

2016 ■ Q1

Leucine aminopeptidases (LAPs) are found in all living organisms and have been associated with the response of the marine mussel, *Mytilus edulis*, to changes in salinity. LAPs are enzymes that remove N-terminal amino acids from proteins and release the free amino acids into the cytosol. To investigate the evolution of LAPs in wild populations of *M. edulis*, researchers sampled adult mussels from several different locations along a part of the northeast coast of the United States, as shown in Figure 1. The researchers then determined the percent of individuals possessing a particular *lap* allele, *lap*⁹⁴, in mussels from each sample site (table 1). [Blank graphing grid provided below part (a): a rectangular grid of small squares, no axis labels or scale printed, for the student to construct their own bar graph.]

(d) Marine mussel larvae are evenly dispersed throughout the study area by water movement. As larvae mature, they attach to the rocks in the water. **Explain** the differences in *lap*⁹⁴ allele frequency among adult mussel populations at the sample sites

Question 1

despite the dispersal of larvae throughout the entire study area. **Predict** the likely effect on distribution of mussels in Long Island Sound if the *lap*⁹⁴ allele was found in all of the mussels in the population. **Justify** your prediction.

Solution 1

(a)

Mark scheme

- Construct a correctly plotted bar graph of lap^{94} allele frequency (%) vs. sample site (1-8) using Table 1: Site 1: 13%, Site 2: 16%, Site 3: 25%, Site 4: 37%, Site 5: 55% (Long Island Sound, increasing salinity); Site 6: 59%, Site 7: 59%, Site 8: 59% (Atlantic Ocean, high salinity). Points awarded for: (1) a correctly plotted bar graph that accurately represents the increasing trend from site 1 to 8; (1) correct axis labeling (x-axis = site, y-axis = lap^{94} frequency); (1) correct scale and units (% on y-axis, evenly spaced 0-60% or similar).

Solution 1

(b)

Mark scheme

- Description (1 point): As salinity increases, lap^{94} frequency increases (equivalently, as salinity decreases, lap^{94} frequency decreases). Prediction (1 point): The lap^{94} allele frequency at a site between site 1 (13%) and site 2 (16%) should fall between 13 and 16 percent (any value in that range is acceptable), since frequency increases roughly monotonically with salinity along the sound.

Solution 1

(c)

Mark scheme

- Effect of LAP^{94} activity on cytosol osmolarity (1 point): LAP^{94} increases the osmolarity/solute concentration of the cytosol (equivalently, it decreases the water potential of the cytosol) by releasing free amino acids from proteins. Function in maintaining water balance in Atlantic Ocean (high-salinity) mussels (1 point): It prevents water loss to the environment - by raising internal solute concentration, the mussel reduces the osmotic gradient that would otherwise draw water out of its cells into the high-salinity seawater.

Solution 1

(d) Mark scheme

- Explanation (1 point): Mussels carrying the lap^{94} allele are more likely to survive (and less likely to survive in low salinity), while mussels without the allele are less likely to survive in high salinity/more likely to survive in low salinity - i.e., natural selection acting on the salinity gradient (not the larval dispersal pattern) produces the site-to-site allele frequency differences despite even larval dispersal. Prediction (1 point): If the lap^{94} allele were found in all mussels, the mussel population would increase in high-salinity areas and decline in low-salinity areas. Justification (1 point): Mussels in high salinity carrying lap^{94} can osmoregulate (maintain water balance) and thrive, whereas mussels in low salinity carrying lap^{94} cannot

Solution 1

osmoregulate properly (excess internal osmolarity in a low-salinity environment is disadvantageous), so they fare poorly there.

Question 6

2015 ■ Q6

In an attempt to rescue a small isolated population of snakes from decline, a few male snakes from several larger populations of the same species were introduced into the population in 1992. The snakes reproduce sexually, and there are abundant resources in the environment.

The figure below shows the results of a study of the snake population both before and after the introduction of the outside males. In the study, the numbers of captured snakes indicate the overall population size.

Question 6

[Bar graph; y-axis “Number of Snakes Captured” from 0 to 35; x-axis “Year” from 1989 to 1999 (odd years labeled: 1989, 1991, 1993, 1995, 1997, 1999). Two bars per year: light gray “Total Snakes Captured” and dark gray “Juvenile Snakes Captured”. An arrow labeled “Males from Outside Populations Introduced” points up to the 1992 position on the x-axis. Approximate bar values by year:

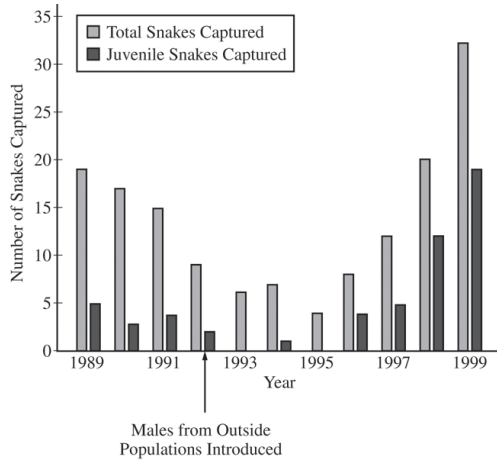
Year	Total Snakes Captured	Juvenile Snakes Captured
1989	19	5
1990	17	3
1991	15	4
1992	9	2
1993	6	0
1994	7	1
1995	4	0
1996	8	4
1997	12	5
1998	20	12
1999	32	19

Question 6

]

- (a) **Describe** ONE characteristic of the original population that may have led to the population's decline in size between 1989 and 1993.
- (b) **Propose** ONE reason that the introduction of the outside males rescued the snake population from decline.
- (c) **Describe** how the data support the statement that there are abundant resources in the environment.

Question 6



Solution 6

(a)

Mark scheme

- 1 point for any ONE plausible characteristic of the original (declining) population, e.g.: it lacked genetic diversity/variation; it was an aged/post-reproductive population with not enough young snakes; it had an unfavorable sex ratio/too few males; or it possessed a harmful mutation/disease.

Solution 6

(b)

Mark scheme

- 1 point for any ONE reason the introduction of outside males rescued the population from decline, e.g.: increased genetic diversity in the population; increased reproductive success; established a beneficial sex ratio/sufficient proportion of males for reproduction; or introduced resistance to a disease that was affecting the original population.

Solution 6

(c)

Mark scheme

- 1 point. The data show the (total and juvenile) snake population size increasing/growing after the introduction of outside males (visible in the bar graph from the early-to-late 1990s); a population can only grow this way if resources are abundant — if resources were limited, the population would not be able to grow.

Question 4

2014 ■ Q4

Adult male guppies (*Poecilia reticulata*) exhibit genetically determined spots, while juvenile and adult female guppies lack spots. In a study of selection, male and female guppies from genetically diverse populations were collected from different mountain streams and placed together in an isolated environment containing no predators. The study population was maintained for several generations in the isolated area before being separated into two groups. One group was moved to an artificial pond containing a fish predator, while a second group was moved to an artificial pond containing no predators. The two groups went through several generations in their new environments. At different times during the experiment, the mean number of spots per adult male guppy was determined as shown in the figure below. Vertical bars in the figure represent two standard errors of the mean (SEM).

Question 4

[Line graph titled “Mean Number of Spots per Adult Male Guppy” vs. “Time (months)”; y-axis from ~8 (with a break symbol) to 14 in increments of 1; x-axis from 0 to 20, tick marks at 0, 10, 20. A vertical dotted arrow labeled “Population Separated into Groups” points to approximately month 6. Two data series with error bars (± 2 SEM): “Predator present” (dashed line) starting at (0,10) with a very large error bar (from about 8.2 to 11.9), rising to a peak at (6,11.8), then declining to (10,10.5) and (20,9.3). “Predator absent” (solid line) starting at (0,10) with the same large error bar, rising to (6,11.8), continuing to rise to (10,12.5) and (20,13.2). Both lines coincide from month 0 to month 6, then diverge after separation into groups.]

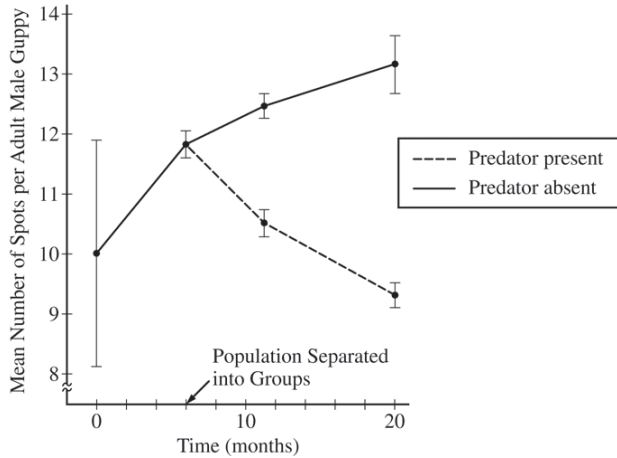
(a) Describe the change in genetic variation in the population between 0 and 6 months and **provide** reasoning for your description based on the means and SEM.

Question 4

(b) Propose ONE type of mating behavior that could have resulted in the observed change in the number of spots per adult male guppy between 6 and 20 months in the absence of the predator.

(c) Propose an evolutionary mechanism that explains the change in average number of spots between 6 and 20 months in the presence of the predator.

Question 4



Solution 4

(a)

Mark scheme

- Describe change (1 point): genetic variation is decreasing between 0 and 6 months. Provide reasoning (1 point): the SEM (standard error of the mean) gets smaller over this interval.

Solution 4

(b)

Mark scheme

- 1 point for proposing a plausible mating behavior, e.g.: sexual selection for individuals with more spots, OR random mating behavior resulted in an increased number of spots by chance.

Solution 4

(c)

Mark scheme

- 1 point for proposing a plausible evolutionary mechanism, e.g.: directional selection against individuals with large numbers of spots / directional selection for individuals with fewer spots (natural selection used in context), OR genetic drift resulting in several generations of decreased numbers of spots.

Question 8

2014 ■ Q8

A research team has genetically engineered a strain of fruit flies to eliminate errors during DNA replication. The team claims that this will eliminate genetic variation in the engineered flies. A second research team claims that eliminating errors during DNA replication will not entirely eliminate genetic variation in the engineered flies.

(a) Provide ONE piece of evidence that would indicate new genetic variation has occurred in the engineered flies.

(b) Describe ONE mechanism that could lead to genetic variation in the engineered strain of flies.

(c) Describe how genetic variation in a population contributes to the process of evolution in the population.

Solution 8

(a)

Mark scheme

- 1 point for ONE piece of evidence of new genetic variation, e.g.: new phenotypes; different DNA sequence; new genotypes; chromosomal differences; different mRNA sequence; or a protein with a different amino acid sequence.

Solution 8

(b) Mark scheme

- 1 point for ONE mechanism that could produce genetic variation, e.g.: sexual reproduction/meiosis/crossing over/independent assortment/random fertilization producing new combinations of alleles or traits; immigration/gene flow introducing new alleles or gene sequences; viral infection inserting DNA into the genome; nondisjunction causing a chromosome-number anomaly; chromosomal rearrangements (large deletions, duplications, translocations, inversions, transposons, etc.) inactivating genes or producing multiple gene copies; or radiation/chemicals/mutagens inducing mutations/changes in DNA.

Solution 8

(c)

Mark scheme

- 1 point for describing that genetic variation is the basis of phenotypic variation on which natural selection can act — i.e. without genetic variation there is no phenotypic variation for natural selection to act upon, so evolution (change in allele frequency) could not occur.