

AP Bootcamp: Unit 5 – 8 Applications Sunday, April 30th

The following materials have been constructed using a variety of resources including: the <u>2020 CED</u>, the <u>2013 Practice Exam</u>, the <u>2015 CED</u>, & <u>released FRQ questions</u>

This document is designed as a resource to allow you a reference before the session to organize your thoughts and during the session to take notes.

For the multiple choice questions, circle your answer choice and put an arrow next to a second choice (if needed).

For the free response questions, outline/brainstorm your thoughts for the answer. You <u>do not</u> need to write complete sentences for this review.

<u>Unit 5:</u>

The following figures display data collected while studying a family, some members of which have sickle-cell disease a rare genetic disorder caused by a mutation in the hemoglobin beta gene (HBB). There are at least two alleles of the HBB gene: the HbA allele encodes wild-type hemoglobin and the HbS allele encodes the sickle-cell form of hemoglobin. Genetic testing provided insight into the inheritance pattern for sickle-cell disease.

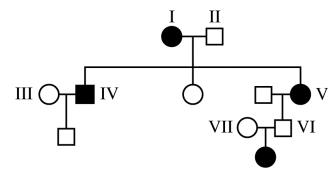


Figure 1. Pedigree of a family with affected individuals. Squares represent males, circles represent females, shaded symbols represent individuals with sickle-cell disease.

5' CTG ACT CCT GAG GAG AAG TCT 3' 3' GAC TGA GGA CTC CTC TTC AGA 5'

Non-template Strand Template Strand

Figure 2. A portion of the DNA sequence from the wild-type hemoglobin allele (HbA) that codes for normal hemoglobin.

Second Base in Codon							
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in Codon	С	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU CAC His CAA CAA Gln	CGU CGC CGA CGG	U C A G	Third Base in Codon
First Base in Codon	А	AUU AUC AUA AUG Met or Start	$ \begin{array}{c} ACU \\ ACC \\ ACA \\ ACG \end{array} \right\} Thr$	AAU AAC AAA AAG	$ \begin{bmatrix} AGU \\ AGC \end{bmatrix} Ser \\ \begin{bmatrix} AGA \\ AGG \end{bmatrix} Arg $	U C A G	Third Base
	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAA GAG Glu	GGU GGC GGA GGG	U C A G	

Figure 3. Codon table showing nucleotide sequences for each amino acid.

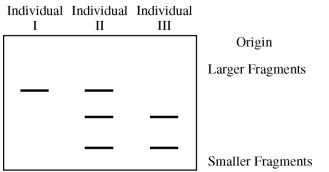


Figure 4. Image of a gel following electrophoretic separation of DNA fragments of the HBB gene from three individuals in the pedigree in Figure 1.

- 1. Based on the data shown in Figure 1, which of the following best describes the genotypes of individual family members in the pedigree?
 - a. All affected individuals possess at least one dominant allele of the hemoglobin beta gene.
 - b. Healthy individuals may possess one mutant allele (HbS) of the hemoglobin beta gene.
 - c. Individuals IV and V must be heterozygous for the HbS (mutant) allele.
 - d. Individuals II and VI possess two copies of the HbA (wild-type) allele.

 A student in a biology class crossed a male Drosophila melanogaster having a gray body and long wings with a female D. melanogaster having a black body and apterous wings. The following distribution of traits was observed in the offspring.

Phenotype	Number of Offspring		
Gray body, long wings	42		
Black body, apterous wings	41		
Gray body, apterous wings	9		
Black body, long wings	8		

Which of the following is supported by the data?

- a. The alleles for gray body and long wings are dominant.
- b. The alleles for gray body and long wings are recessive.
- c. Genes for the two traits are located on two different chromosomes, and independent assortment occurred.
- d. Genes for the two traits are located close together on the same chromosome and crossing over occurred between the two gene loci.

The pyruvate dehydrogenase complex (PDC) catalyzes the conversion of pyruvate to acetyl-CoA, a substrate for the Krebs (citric acid) cycle. The rate of pyruvate conversion is greatly reduced in individuals with PDC deficiency, a rare disorder.

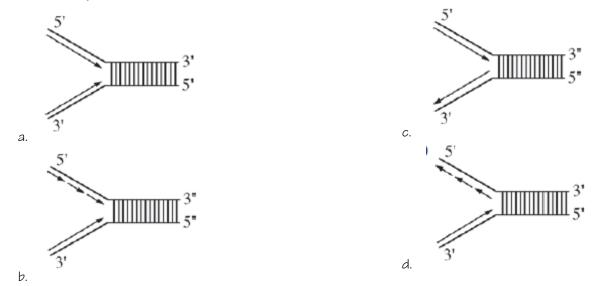
(a) **Identify** the cellular location where PDC is most active.

(b) **Make a claim** about how PDC deficiency affects the amount of NADH produced by glycolysis AND the amount of NADH produced by the Krebs (citric acid) cycle in a cell. **Provide reasoning** to support your claims based on the position of the PDC-catalyzed reaction in the sequence of the cellular respiration pathway.

(c) PDC deficiency is caused by mutations in the *PDHA1* gene, which is located on the X chromosome. A male with PDC deficiency and a homozygous female with no family history of PDC deficiency have a male offspring. **Calculate** the probability that the male offspring will have PDC deficiency.

Unit 6:

1. When DNA replicates, each strand of the original DNA molecule is used as a template for the synthesis of a second, complementary strand. Which of the following figures most accurately illustrates enzyme-mediated synthesis of new DNA at a replication fork?



Use the following information to answer questions 2 & 3:

The following figures display data collected while studying a family, some members of which have sickle-cell disease a rare genetic disorder caused by a mutation in the hemoglobin beta gene (HBB). There are at least two alleles of the HBB gene: the HbA allele encodes wild-type hemoglobin and the HbS allele encodes the sickle-cell form of hemoglobin. Genetic testing provided insight into the inheritance pattern for sickle-cell disease.

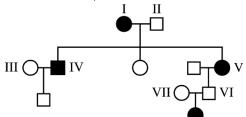


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Second Base in Codon							
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First Base in Codon	С	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU CAC His CAA CAA Gln	CGU CGC CGA CGG	U C A G	e in Codon
First Base	A	AUU AUC AUA AUG Met or Start	$ \begin{array}{c} ACU \\ ACC \\ ACA \\ ACG \end{array} \right\} Thr$	AAU AAC AAA AAG Lys	AGU AGC AGA AGA AGG	U C A G	Third Base in Codon
	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAA GAG Glu	GGU GGC GGA GGG	U C A G	

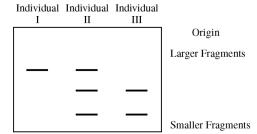


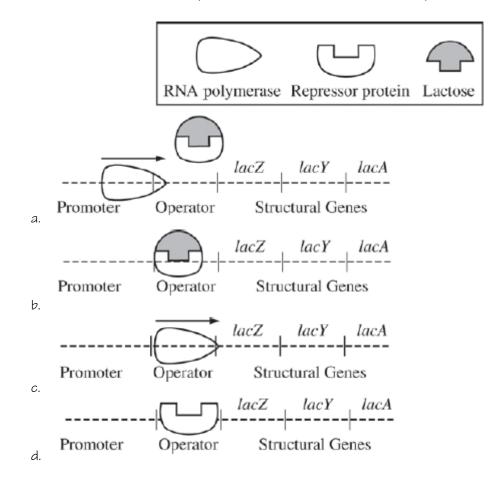
Figure 4. Image of a gel following electrophoretic separation of DNA fragments of the HBB gene from three individuals in the pedigree in Figure 1.

- 2. The HbS allele, which causes sickle-cell disease, results from a mutation in the DNA sequence shown in Figure 2 that produces a valine (val) in the place of a glutamic acid (glu) residue in the hemoglobin protein. Which of the following mRNA sequences is derived from the HbS allele?
 - a. 5' GAC TGA GGA CTC CTC TTC AGA 3'
 - b. 5' UCU GAA GAG GAA UCC UCA GUC 3'
 - c. 5' AGA CTT CTC CTC AGG AGT CAG 3'
 - d. 5' CUG ACU CCU GUG GAG AAG UCU 3'

- 3. The restriction endonuclease Mst II recognizes the sequence 5' CCT(N)AG (where N = any nucleotide) and cuts DNA at that site, producing separate fragments. Which of the following best explains the banding patterns exhibited in Figure 4?
 - a. The HbA DNA contains a recognition site for the Mst II restriction enzyme.
 - b. The HbA/HbS DNA contains three recognition sites for the Mst II restriction endonuclease.
 - c. Individual I has only one copy of the hemoglobin gene; therefore there is only one band on the gel.
 - d. The HbS/HbA DNA contains three different alleles for sickle-cell disease.

4. Lactose digestion in E. coli begins with its hydrolysis by the enzyme b-galactosidase. The gene encoding bgalactosidase, lacZ, is part of a coordinately regulated operon containing other genes required for lactose utilization.

Which of the following figures correctly depicts the interactions at the lac operon when lactose is NOT being utilized? (The legend below defines the shapes of the molecules illustrated in the options.)



			STRAINS	
	MEDIUM	Wild Type	Mutant 1	Mutant 2
Treatment I	All amino acids present	+	+	+
Treatment II	No amino acids present	+	-	-
Treatment III	All amino acids present EXCEPT methionine	+	-	+
Treatment IV	All amino acids present EXCEPT leucine	+	+	-

Table 1. The data show the growth of haploid *Saccharomyces cerevisiae* yeast strains on media that differ in amino acid content. A plus sign (+) indicates that the yeast strains grow, and a minus sign (-) indicates that the strains do not grow.

The yeast *Saccharomyces cerevisiae* is a single-celled organism. Amino acid synthesis in yeast cells occurs through metabolic pathways, and enzymes in the synthesis pathways are encoded by different genes. The synthesis of a particular amino acid can be prevented by mutation of a gene encoding an enzyme in the required pathway.

A researcher conducted an experiment to determine the ability of yeast to grow on media that differ in amino acid content. Yeast can grow as both haploid and diploid cells. The researcher tested two different haploid yeast strains (Mutant 1 and Mutant 2), each of which has a single recessive mutation, and a haploid wild-type strain. The resulting data are shown in Table 1.

(a) **Identify** the role of treatment I in the experiment.

(b) **Provide reasoning** to explain how Mutant 1 can grow on treatment I medium but cannot grow on treatment III medium.

(c) Yeast mate by fusing two haploid cells to make a diploid cell. In a second experiment, the researcher mates the Mutant 1 and Mutant 2 haploid strains to produce diploid cells. Using the table provided, **predict** whether the diploid cells will grow on each of the four media. Use a plus sign (+) to indicate growth and a minus sign (-) to indicate no growth.

		STRAINS			
	MEDIUM	Wild Type (haploid)	Mutant 1 (haploid)	Mutant 2 (haploid)	Diploid Cells Produced by Mating Mutant 1 and Mutant 2
Treatment I	All amino acids present	+	+	+	
Treatment II	No amino acids present	+	-	-	
Treatment III	All amino acids present EXCEPT methionine	+	-	+	
Treatment IV	All amino acids present EXCEPT leucine	+	+	-	

Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydrozylase (GA3H) is the enzyme that catalyzes the reaction that converts a precursor of gibberellin to the active form of gibberellin. A mutation in the GA3H gene results in a short plant phenotype. When a pure-breeding tall plant is crossed with a pure-breeding short plant, all offspring in the F_1 generation are tall. When the F_1 plants are crossed with each other, 75 percent of the plants in the F_2 generation are tall and 25 percent of the plants are short.

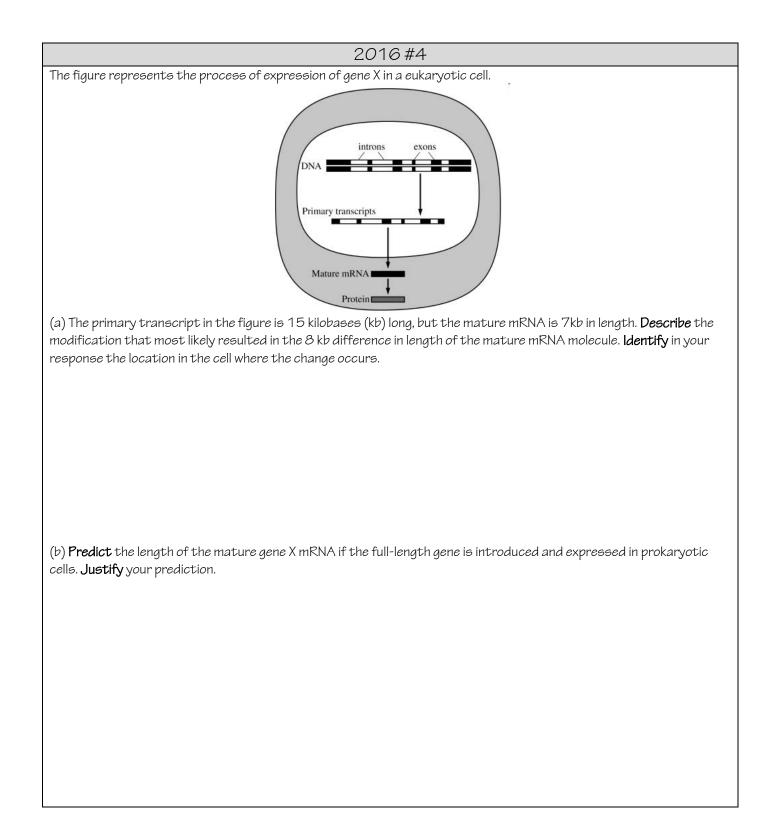
	Second Base in Codon						
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	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAA GAG Glu	GGU GGC GGA GGG	U C A G	

Figure 1. The universal genetic code

(a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants.

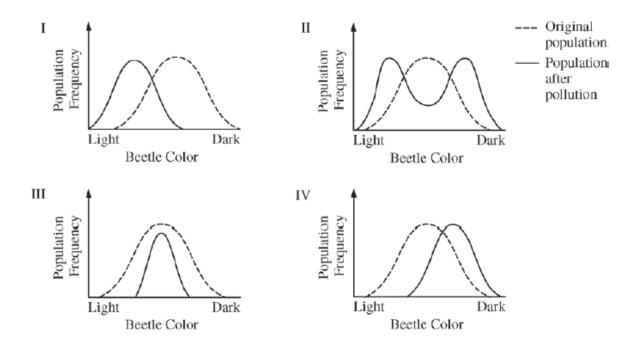
(b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.

(c) **Describe** how individuals with one (heterozygous) or two (homozygous) copies of the wild-type *GA3H* allele can have the same phenotype.



Unit 7:

1. In a hypothetical population of beetles, there is a wide variety of color, matching the range of coloration of the tree trunks on which the beetles hide from predators. The graphs below illustrate four possible changes to the beetle population as a result of a change in the environment due to pollution that darkened the tree trunks.



Which of the following includes the most likely change in the coloration of the beetle population after pollution and a correct rationale for the change?

- a. The coloration range shifted toward more light-colored beetles, as in diagram I. The pollution helped the predators find the darkened tree trunks.
- b. The coloration in the population split into two extremes, as in diagram II. Both the lighter-colored and the darker-colored beetles were able to hide on the darker tree trunks.
- c. The coloration range became narrower, as in diagram III. The predators selected beetles at the color extremes.
- d. The coloration in the population shifted toward more darker-colored beetles, as in diagram IV. The lightercolored beetles were found more easily by the predators than were the darker-colored beetles.

Use the following information to answer question 2:

The following figures display data collected while studying a family, some members of which have sickle-cell disease a rare genetic disorder caused by a mutation in the hemoglobin beta gene (HBB). There are at least two alleles of the HBB gene: the HbA allele encodes wild-type hemoglobin and the HbS allele encodes the sickle-cell form of hemoglobin. Genetic testing provided insight into the inheritance pattern for sickle-cell disease.

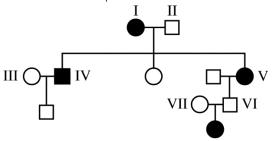


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	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAA GAG Glu	GGU GGC GGA GGG	U C A G	

Figure 3. Codon table showing nucleotide sequences for each amino acid.

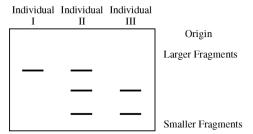


Figure 4. Image of a gel following electrophoretic separation of DNA fragments of the HBB gene from three individuals in the pedigree in Figure 1.

- 2. Possessing a single copy of the HbS allele has been shown to provide some resistance to infection by Plasmodium falciparum, the parasite that causes malaria. Which of the following individuals represented in the pedigree would have the greatest selective advantage in an area where malaria is common?
 - a. I
 - b. II
 - c. III
 - d. V

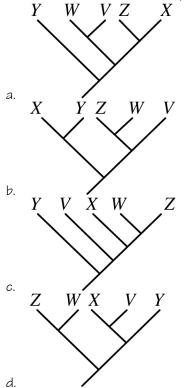
3. The data below demonstrate the frequency of tasters and non-tasters of a certain compound in four isolated populations that are in Hardy-Weinberg equilibrium. The allele for non-tasters is recessive. In which population is the frequency of the recessive allele highest?

Letter Choice	Populations	Tasters	Non-tasters	Size of Population
А	1	110	32	142
В	2	8,235	4,328	12,563
С	3	215	500	715
D	4	11,489	2,596	14,085

4. Data regarding the presence (+) or absence (-) of five derived traits in several different species are shown in the table below.

		Trait			
Species	1	2	3	4	5
V	+	+	+	-	-
W	+	+	-	-	-
Х	+	1	-	-	-
Y	1	1	-	-	-
Z	+	1	-	-	+

Which of the following cladograms provides the simplest and most accurate representation of the data in the table?



In 1981 a single immature male *Geospiza conirostris* finch flew more than 100 kilometers from the Galapagos island of Espanola to the Galapagos island of Daphne Major, where no *G. conirostris* finches were living. The immigrant finch bred with a female *G. fortis*, a species of finch common on Daphne Major. The F1 finches and later generations interbred only within their lineage. By 2012 scientists counted 23 individuals, including eight breeding pairs, within this hybrid lineage on Daphne Major. The hybrid lineage became known as Big Bird.

Bird with different beak shapes and sizes eat different types of food. The dimensions of the Big Bird beaks relative to the beaks of the major competitor finch species on Daphne Major are shown in Figure 1.

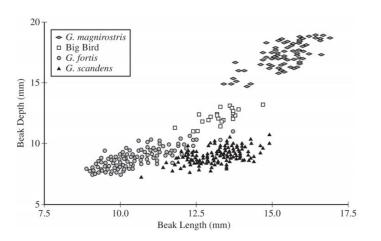


Figure 1. The dimensions of the beaks of the Big Bird lineage and of its major competitor species in 2012 on Daphne Major. Each symbol represents the beak dimensions of a single bird.

(a) The Big Bird lineage became reproductively isolated from *G. fortis*. **Describe** one prezygotic mechanism that likely contributed to the reproductive isolation of the Big Bird lineage from *G. fortis*.

(b) Based on the data in Figure 1, **explain** why the Big Bird population has been able to survive and reproduce on Daphne Major.

(c) A virus infects and kills all *G. magnirostris* on Daphne Major but does not affect the other finch species. Assuming food type and availability stay the same, **predict** the most likely change in the beak phenotype of the Big Bird population after six more generations.

(d) Provide reasoning to **justify** your prediction in part (c).

TABLE 1. DIVERGENCE (IN PERCENT) OF MITOCHONDRIAL DNA SEQUENCES AMONG FIVE PRIMATE SPECIES

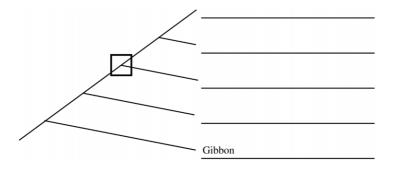
	Human	Gorilla	Orangutan	Gibbon	Chimpanzee
Human	-	10.3	16.1	18.1	8.8
Gorilla		-	16.7	18.9	10.6
Orangutan			-	18.9	17.2
Gibbon				-	18.9
Chimpanzee					-

A researcher studying the evolutionary relationship among five primate species obtained data from a sequence of mitochondrial DNA (mtDNA) from a representative individual of each species. The researcher then calculated the percent divergence in the sequences between each pair of primate species (Table 1).

(a) Based on fossil data, the researcher estimates that humans and their most closely related species in the data set diverged approximately seven million years ago. Using these data, **calculate** the rate of mtDNA percent divergence per million years between humans and their most closely related species in the data set. Round your answer to two decimal places.

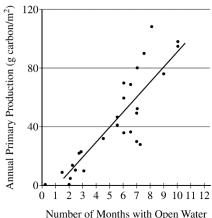
(b) Using the data in the table, **construct** a cladogram on the template provided. **Provide reasoning** for the placement of gibbons as the outgroup on the cladogram.

(c) On the cladogram, **draw** a circle around all of the species that are descended from the species indicated by the node within the square.



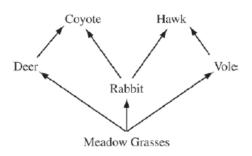
Unit 8:

- 1. In the Arctic Ocean, the predominant primary producers are phytoplankton. Phytoplankton are consumed by zooplankton, which in turn are eaten by codfish. In years when there is more open water (less ice coverage), there are more zooplankton and fish than in years with less open water (more ice coverage). Based on the graph above, the difference is most likely because
 - a. when there is less open water, light is blocked from the zooplankton, so they cannot produce as much food for the fish
 - b. when there is more open water, the temperature is warmer, so the zooplankton and fish populations increase in size
 - c. the ice blocks the light, so in years with more ice coverage, there is less photosynthesis by the phytoplankton
 - d. the ice increases the light available for photosynthesis, so primary production increases and zooplankton populations increase in size



Number of Months with Open Water

2. The following is a food web for a meadow habitat that occupies 25.6 km². The primary producers' biomass is uniformly distributed throughout the habitat and totals 1,500 kg/km².



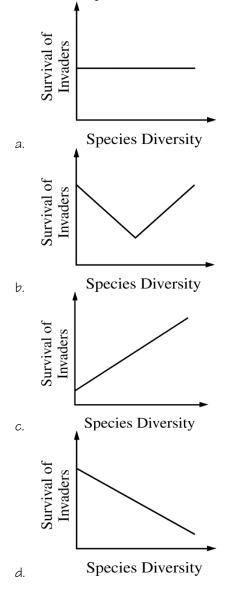
Developers have approved a project that will permanently reduce the primary producers' biomass by 50 percent and remove all rabbits and deer.

Which of the following is the most likely result at the completion of the project?

- a. The biomass of coyotes will be 6 kg, and the biomass of hawks will be 0.5 kg.
- b. The biomass of coyotes will be dramatically reduced.
- The coyotes will switch prey preferences and outcompete the hawks. С.
- d. There will be 50 percent fewer voles and 90 percent fewer hawks.

3. A researcher is investigating the relationship between the existing species diversity in a community and the ability of an introduced nonnative species to destabilize the community.

Which of the following graphs is most consistent with the claim that communities with high diversity are more resistant to change than are communities with low diversity?



In the tongue sole fish (*Cynoglossis semilaevis*), sex is determined by a combination of genetics and environmental temperature. Genetically male fish have two Z chromosomes (ZZ), and genetically female fish have one Z chromosome and one W chromosome (ZW). When fish are raised at 22°C, ZZ fish develop into phenotypic males and ZW fish develop into phenotypic females. However, when fish are raised at 28°C, the Z chromosome is modified (denoted as Z*). Z*W individuals develop as phenotypic males that are fertile and can pass on the Z* chromosome to their offspring even when the offspring are raised at 22°C. A cross between a ZW female and a Z*Z male is shown in the Punnett square below.

	Z	W
Z*	Z* Z	Z* W
Ζ	ZZ	ZW

(a) **Predict** the percent of phenotypic males among the F_1 offspring of the cross shown in the Punnett square if the offspring are raised at 22°C.

(b) At least one Z or Z^* chromosome is necessary for survival of the fish. A researcher crossed two fish and observed a 2:1 ratio of males to females among the offspring. Based on the information, **identify** the genotype of the male parent in the cross. **Describe** ONE fitness cost to the female of mating with this particular male.

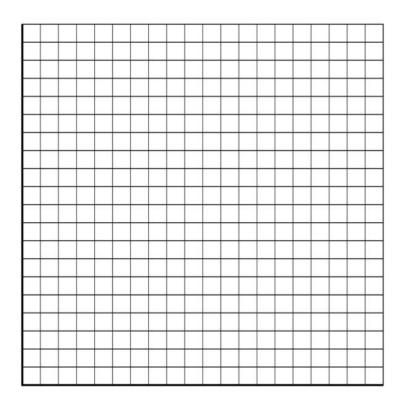
In flowering plants, pollination is a process that leads to the fertilization of an egg and the production of seeds. Some flowers attract pollinators, such as bees, using visual and chemical cues. When a bee visits a flower, in addition to transferring pollen, the bee can take nectar from the flower and use it to make honey for the colony.

Nectar contains sugar, but certain plants also produce caffeine in the nectar. Caffeine is a bitter-tasting compound that can be toxic to insects at high concentrations. To investigate the role of caffeine in nectar, a group of researchers studied the effect of 0.1 mM caffeine on bee behavior. The results of an experiment to test the effect of caffeine on bees' memory of a nectar source are shown in Table 1.

Treatment	$\begin{array}{l} \mbox{Memory} \\ \mbox{(average probability of revisiting a nectar source } \pm 2SE_{\mathcal{R}} \mbox{)} \end{array}$		
	10 Minutes	24 Hours	
Control	0.72 ± 0.09	0.41 ± 0.07	
Caffeine	0.83 ± 0.07	0.78 ± 0.08	

TABLE 1. EFFECT OF 0.1 mM CAFFEINE ON MEMORY IN BEES

(a) On the axes provided, **construct** an appropriately labeled graph to illustrate the effect of caffeine on the probability of bees revisiting a nectar source (memory).



(b) Based on the results, **describe** the effect of caffeine on each of the following:

(i) Short-term (10 minute) memory of a nectar source

(ii) Long-term (24 hour) memory of a nectar source

(c) **Design an experiment** using artificial flowers to investigate potential negative effects of increasing caffeine concentrations in nectar on the number of floral visits by bees. **Identify** the null hypothesis, an appropriate control treatment, and the predicted results that could be used to reject the null hypothesis.

(d) Researchers found that nectar with caffeine tends to have a lower sugar content than nectar without caffeine. Plants use less energy to produce the caffeine in nectar than they do to produce the sugar in nectar. **Propose ONE benefit** to plants that produce nectar with caffeine and a lower sugar content. **Propose ONE cost** to bees that visit the flowers of plants that produce nectar with caffeine and a lower sugar content.