Unit 6 PRACTICE 2021

1. Read each question carefully. Write your response in the space provided for each part of each question. Answers must be written out in paragraph form. Outlines, bulleted lists, or diagrams alone are not acceptable and will not be scored.

Certain pathogens have what is known as a mutator phenotype associated with a high frequency of DNA mutations that enable them to change rapidly. *Cryptococcus neoformans* is a fungus that causes severe infections that are often difficult to treat. Scientists assessed whether strains of *C. neoformans* possess a mutator phenotype.

The scientists analyzed eleven wild, environmental strains (E1 through E11) and eleven clinical isolate strains (from patients, C1 through C11) of *C. neoformans*. The scientists inoculated an equal number of cells from each strain into 20 replicate liquid cultures in test tubes. After a period of growth, they removed cells from each culture and plated the cells on petri dishes containing a solid growth medium with a chemical that is typically toxic to the fungi. After an incubation period, the scientists counted the number of colonies (each colony is derived from division of a single cell) that grew in each dish and combined the data from the 20 dishes for each strain. Representative data are shown in Figure 1. The data for all environmental strains resembled the data shown for strains E1, E4, and E10. The data for all clinical strains except strains C3 and C6 resembled the data shown for strain C8.

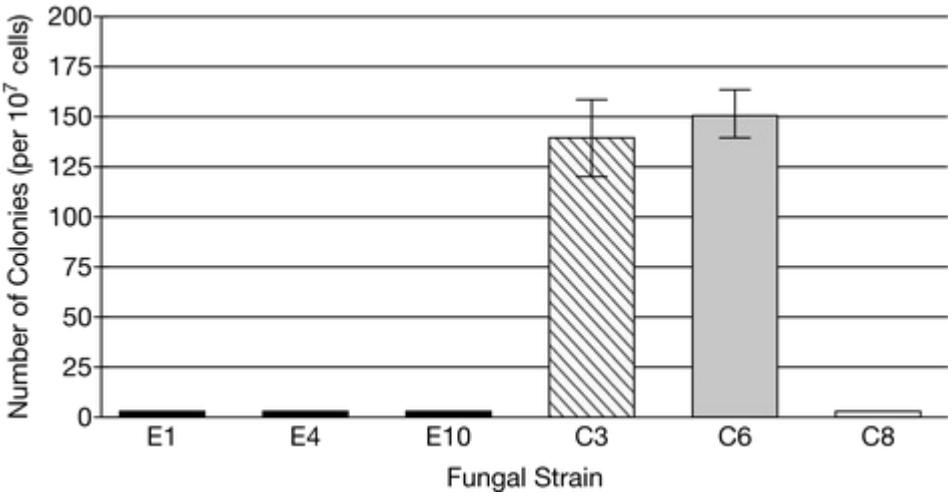

Figure 1. Number of colonies produced from *C. neoformans* cells grown on a medium containing a toxic chemical. Representative data from 11 environmental (E) strains and 11 clinical isolate strains (C). The error bars represent $\pm 2SE_{\bar{x}}$.

In a further experiment, the scientists investigated the mechanism responsible for the greater number of colonies produced by strains C3 and C6 than by the other strains. Based on DNA sequence analyses of the strains, the scientists introduced a wild-type copy of the fungal *MSH2* gene, a gene encoding a repair enzyme involved in identifying nucleotides in DNA that contain incorrect bases, into cells of strains C3 and C6 and again analyzed the number of colonies that grew in the presence of the toxic chemical (Figure 2).

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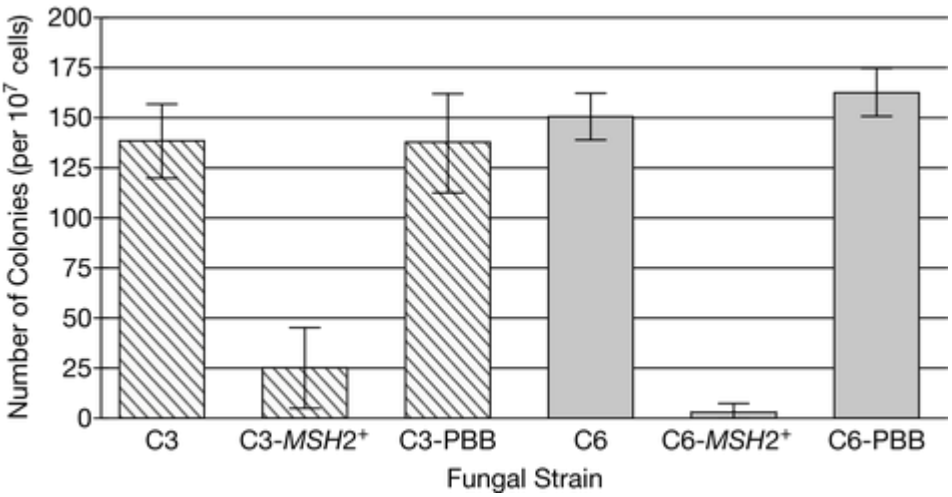

Figure 2. Number of colonies produced from *C. neoformans* strains **C3** and **C6** cells grown on a medium containing a toxic chemical. A wild-type copy of the fungal ***MSH2*** gene was introduced into strains **C3-*MSH2*$^+$** and **C6-*MSH2*$^+$**. The plasmid into which the ***MSH2*** gene was cloned for introduction into the fungi is present in strains **C3-PBB** and **C6-PBB**. The error bars represent $\pm 2SE_{\bar{x}}$.

(a) **Describe** why **DNA** replication is said to be a semiconservative process. **Explain** how random mutations such as those in pathogens with a mutator phenotype may arise in the **DNA** of an organism.

Please respond on separate paper, following directions from your teacher.

(b) **Identify** a dependent variable in the experiments. **Identify** the reasoning of the scientists when they tested the number of colonies produced by strains **C3-PBB** and **C6-PBB**. The scientists also analyzed the number of colonies produced from each of the environmental and clinical isolate strains when the strains were plated on a growth medium lacking the toxic chemical. **Justify** this analysis.

Please respond on separate paper, following directions from your teacher.

(c) Based on the data in Figure 1, for each strain **describe** the relationship between the number of colonies observed and the likely mutation rate of the strain.

Please respond on separate paper, following directions from your teacher.

(d) **State** the null hypothesis for the experiment whose data are graphed in Figure 2. **Provide evidence**

to support or refute the scientists' claim that more colonies grew in strains C3 and C6 than in the other strains because the genes for proteins that are normally targeted by the toxic chemical contain nucleotides with incorrect bases in the C3 and C6 cells. The scientists additionally determined that the C3 and C6 strains had no decrease in virulence (disease-causing ability) in comparison with the virulence of the other clinical isolate strains and concluded that these two strains have mutator phenotypes. **Explain** why mutator phenotypes were found only among clinical isolate strains and not among environmental strains.

Please respond on separate paper, following directions from your teacher.

Part A (i)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

The response indicates that one strand of DNA serves as the template for the synthesis of a new strand of complementary DNA .

Part A (ii)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

The response indicates that errors in DNA replication or in DNA repair mechanisms or changes induced by external factors (such as radiation or certain chemicals) can introduce or not correct errors in nucleotide sequence.

Part B (i)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

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0	✓ 1

The response indicates that the dependent variable is the number of colonies produced per 10^7 cells for each of the *C. neoformans* strains analyzed.

Part B (ii)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	✓ 1

The response indicates that strains **C3-PBB** and **C6-PBB** are controls for the number of colonies produced when only the plasmid backbone is introduced into the **C3** and **C6** strains, respectively.

Part B (iii)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	✓ 1

The response indicates that analyzing the number of colonies produced from each of the environmental and clinical isolate strains when the strains were plated on a growth medium lacking the toxic chemical was a positive control to demonstrate that all of the strains can grow and produce colonies.

Part C

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

	✓
0	1

The response indicates that those strains that produced a relatively large number of colonies were those with cells that contained DNA mutations making them less susceptible to damage by the toxic chemical.

Part D (i)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

	✓
0	1

The response indicates that the null hypothesis is "Mutations to the *MSH2* gene are not responsible for the high mutation rate or large number of colonies produced by the C3 and C6 strains in the presence of the toxic chemical" or "Introduction of a wild-type *MSH2* gene will not decrease the mutation rate or reduce the large number of colonies produced by the C3 and C6 strains in the presence of the toxic chemical."

Part D (ii)

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

	✓
0	1

The response indicates that the evidence is that when the *MSH2* gene was introduced into C3 and C6 cells (Figure 2), the number of colonies that grew from the C3 and C6 cells was much reduced. It also indicates that the gene encodes a DNA repair enzyme, suggesting that the cells were now able to repair the mutation to a gene encoding a protein targeted by the chemical.

Part D (iii)

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Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

The response indicates that the mutator phenotypes confer a selective advantage to *C. neoformans* strains that are isolated from infected individuals. It also indicates that strains such as **C3** and **C6** are less likely to be killed by antifungal drugs than are clinical strains without a mutator phenotype or environmental strains that are not subject to selection by antifungal drugs.

2. Read each question carefully. Write your response in the space provided for each part of each question. Answers must be written out in paragraph form. Outlines, bulleted lists, or diagrams alone are not acceptable and will not be scored.

A processed eukaryotic **mRNA** (lacking introns) is introduced into bacteria so that the bacteria can produce a large quantity of the encoded polypeptide. Translation of the **mRNA** to produce a polypeptide involves the binding of large and small ribosomal subunits to an **mRNA**. Each complete ribosome has three **tRNA** binding sites that align with three sequential codons in the **mRNA**. Three steps in the process of translation elongation, the addition of amino acids to a growing polypeptide chain, are illustrated in Figure 1.

Figure 1. A schematic drawing of three steps in translation elongation. Sequential codons are numbered, and **AA** represents amino acid.

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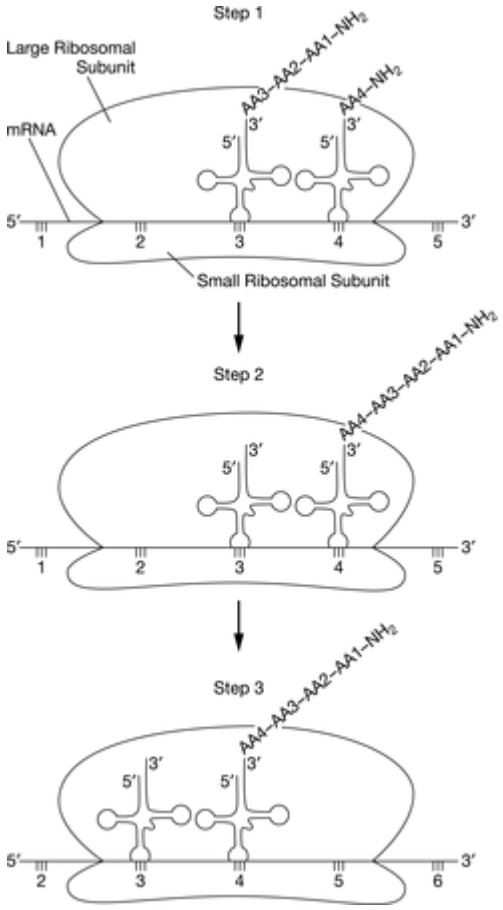

(a) **Describe** why translation of an **mRNA** can start before transcription of the **mRNA** is complete in prokaryotes but not in eukaryotes.

Please respond on separate paper, following directions from your teacher.

(b) Referring to Figure 1, **explain** the process illustrated between Step 1 and Step 2.

Please respond on separate paper, following directions from your teacher.

(c) Fill in the boxes in the template to **identify** the nucleotide sequence, from **3′** to **5′**, of the **tRNA** anticodon that will recognize codon 5 and the **tRNA** anticodon that will recognize codon 510 of the **mRNA** template and to **identify** the amino acids that will be added at these two positions. A codon table is provided for reference.

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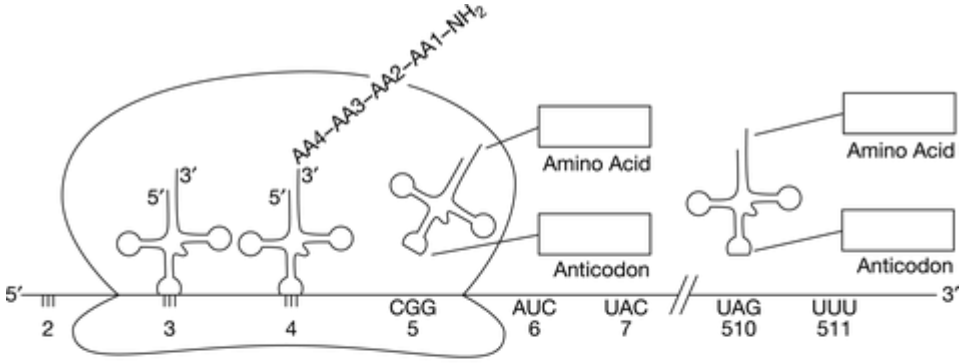

Second Base in Codon

First Base in Codon	U	C	A	G	Third Base in Codon
U	UUU Phe, UUC Phe, UUA Leu, UUG Leu	UCU Ser, UCC Ser, UCA Ser, UCG Ser	UAU Tyr, UAC Tyr, UAA Stop, UAG Stop	UGU Cys, UGC Cys, UGA Stop, UGG Trp	U C A G
C	CUU Leu, CUC Leu, CUA Leu, CUG Leu	CCU Pro, CCC Pro, CCA Pro, CCG Pro	CAU His, CAC His, CAA Gln, CAG Gln	CGU Arg, CGC Arg, CGA Arg, CGG Arg	U C A G
A	AUU Ile, AUC Ile, AUA Ile, AUG Met or Start	ACU Thr, ACC Thr, ACA Thr, ACG Thr	AAU Asn, AAC Asn, AAA Lys, AAG Lys	AGU Ser, AGC Ser, AGA Arg, AGG Arg	U C A G
G	GUU Val, GUC Val, GUA Val, GUG Val	GCU Ala, GCC Ala, GCA Ala, GCG Ala	GAU Asp, GAC Asp, GAA Glu, GAG Glu	GGU Gly, GGC Gly, GGA Gly, GGG Gly	U C A G

Please respond on separate paper, following directions from your teacher.

(d) Referring to the figures provided, **explain** why the polypeptide produced when the transformed bacteria translate the introduced eukaryotic mRNA provides evidence for the common ancestry of all living organisms.

Please respond on separate paper, following directions from your teacher.

Part A

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

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The response indicates that prokaryotes do not have a nuclear envelope that separates the genome from ribosomes in the cytoplasm of the cell, whereas eukaryotes do.

Part B

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

The response indicates that the growing polypeptide chain attached to the tRNA aligned with codon 3 of the mRNA is transferred to the amino (NH_2) terminus of amino acid 4 (AA4) attached to the tRNA aligned with codon 4 of the mRNA.

Part C

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

The response indicates that for codon 5, the anticodon sequence is GCC and the amino acid added is arginine (Arg). The response also indicates that for codon 510, there will be no tRNA with a complementary anticodon because UAG in the mRNA is a translation stop sequence, and no amino acid will be added/translation terminates.

Part D

Select a point value to view scoring criteria, solutions, and/or examples and to score the response.

0	1 ✓

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The response indicates that the polypeptide produced by translation of a processed eukaryotic mRNA by a eukaryotic cell or a prokaryotic cell into which it has been introduced should have the same amino acid sequence because the genetic code is almost universal and the same codon chart can be used for both prokaryotic and eukaryotic organisms.