AP® BIOLOGY
2010 SCORING GUIDELINES (Form B)

Question 2

Certain human genetic conditions, such as sickle cell anemia, result from single base-pair mutations in DNA.

(a) **Explain** how a single base-pair mutation in DNA can alter the structure and, in some cases, the function of a protein. **(4 points maximum)**

DNA (3 points maximum)

- Define mutation; change in bases: A, C, G or T.
- Describe type of mutation: duplication, frameshift, nonsense, deletion, substitution (point mutation).
- Describe central dogma: DNA → RNA → protein.
- Describe process of central dogma: transcription → translation.
- Translation of codons: 3 nucleotides → 1 amino acid.
- Redundancy in genetic code: 64 combinations: 20 amino acids (or can result in "stop" codon).

Protein (3 points maximum)

- Describe altered protein structure: primary, secondary, tertiary, quaternary.
- Describe protein function change: active site conformation, oxygen binding.
- Describe structural change: hydrophobic/hydrophilic interactions, disulfide bonds, R-group interactions, hydrogen bonds.

(b) **Explain**, using a specific example, the potential consequences of the production of a mutant protein to the structure and function of the cells of an organism. **(4 points maximum)**

- Type of change: dominant, recessive.
- Changed protein → changed trait/character/function (gain or loss of function).
- Description of example (any trait).
- Description of protein structure or example after change.
- Description of function after change.
- Elaboration with sickle: mutation/effect in organism, Glu → Val, etc.
- Heterozygotic advantage (resistance to malaria).

(c) **Describe** how the frequency of an allele coding for a mutant protein may increase in a population over time. **(4 points maximum)**

- Hardy-Weinberg equation, with description ($p^2 + 2pq + q^2 = 1$; $p + q = 1$).
- Natural selection/adaptation, with description or example.
- Additional point for elaboration of natural selection.
    - More born than will survive, variations in individuals, variations in gene pool, sexual selection, adaptations to environment → differential reproductive success.
- Small population, with description or example (genetic drift).
- Sexual selection or inbreeding, with description or example.
- Immigration/emigration/migration, with description or example.
- Effects of germ line vs. somatic change.

2A,

2. Certain human genetic conditions, such as sickle cell anemia, result from single base-pair mutations in DNA.

   (a) **Explain** how a single base-pair mutant in DNA can alter the structure and, in some cases, the function of a protein.

   (b) **Explain**, using a specific example, the potential consequences of the production of a mutant protein to the structure and function of the cells of an organism.

   (c) **Describe** how the frequency of an allele coding for a mutant protein may increase in a population over time.

a) A single base-pair mutation (of the insertion or deletion type) results in a frameshift mutation which means that none of the codons transcripted after that mutation will be correct. For example, a ACTGCTACTT sequence will become ACTGTACTT after a mutation deletes the second C and the two last codons will now be GTA CTT instead of GCT ACT. These new codons code for entirely different amino acids. They match with different tRNA anticodons and so for the whole polypeptide chain translated after the mutation, the amino acid sequence (primary structure) will be completely different. Substitution mutations are less harmful because only that codon is affected and no others. There is no frameshift. In all kinds of mutations, however, different amino acids have different properties so by changing them their interactions with each other (secondary, tertiary, quadrenary structures) will change, and this can change where the active sites are on the polypeptide, as well as allosteric sites, utterly changing its function.

However, in a substitution, if the new amino acid has similar properties to the correct one the protein won't change much and may still be functional. A frameshift mutation is guaranteed to mess the polypeptide up though.

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2A2

ADDITIONAL PAGE FOR ANSWERING QUESTION 2

b) In sickle-cell anemia, the genetic mutation alters one of the proteins in red blood cells so that they become sickle shaped and don't transport O_2 and CO_2 as well as normal donut shaped cells do. This results in weakness, decreased fitness, and sickliness in sickle-cell patients, but also grants them resistance to the malaria virus because it usually latches on to the groove in the donut shaped red blood cells. Most mutations have ~~harmful consequences~~ neutral consequences, ~~only a few are beneficial~~. some are harmful, and rarest of all are beneficial mutations.

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ADDITIONAL PAGE FOR ANSWERING QUESTION 2

c) There are many mechanisms by which a harmful mutant allele can increase in frequency in a population. Firstly, by genetic drift. If a natural disaster or similar factor separates a population and one of the new smaller populations has a member with the mutation, then the frequency of the allele out of the whole population is more. This is the bottleneck effect. Similarly, if a smaller group migrates away from an original population and settles elsewhere, and some members carry the mutation, there is a higher frequency of the allele and more offspring will have it passed on to them. This is the founder effect.

The example of sickle-cell anemia illustates the heterozygote advantage well. Malaria resistance is very useful in Africa so people with the recessive sickle-cell allele along with a normal dominant allele (the sickle-cell alleles are codominant) will have better evolutionary fitness than sickle-cell homozygotes (they usually die young due to the disease) and normal people (many die early from Malaria). Natural selection will thus preserve the mutated allele.

Another mechanism is inbreeding, which increases the frequency of recessive alleles. Since most mutated alleles that cause harmful diseases are recessive, they would increase in frequency as well.

2B,

2. Certain human genetic conditions, such as sickle cell anemia, result from single base-pair mutations in DNA.

   (a) **Explain** how a single base-pair mutant in DNA can alter the structure and, in some cases, the function of a protein.

   (b) **Explain**, using a specific example, the potential consequences of the production of a mutant protein to the structure and function of the cells of an organism.

   (c) **Describe** how the frequency of an allele coding for a mutant protein may increase in a population over time.

a) The structure of proteins depend on several specific interactions between the ~~[redacted]~~ R-groups of a protein, such as disulfide bridges, hydrophobic interactions, and hydrogen bonds. Because each codon (set of three base-pairs) codes for the insertion of one amino acid, a mutation in a single base-pair may (not in all cases) result in the addition of the wrong amino acid by tRNA. Immediately, the primary structure of the protein is incorrect, and the interactions between the base pairs may not allow the polypeptide to bind into a conformation (secondary and tertiary structure) which will no longer fit the function of the specific protein. The functions of proteins, such as enzymes often depend on highly specific interactions between proteins and other molecules (such as the lock-and-key function of enzymes). By altering the primary structure of a protein, a faulty DNA strand may ultimately jeopardize the function of the protein.

b) One specific example of how a mutant protein affects an organism occurs in sickle-cell disease. When a person has this disease, it means that their body is producing incompetent hemoglobin molecules and the individual therefore has a reduced capacity to transport oxygen in their blood.

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2B2

Like most other proteins, the structure of hemoglobin is highly specialized for the optimal transport of oxygen in the blood - a specialization that is dependant on the primary, secondary, tertiary and even quartenary structures of the protein. When hemoglobin is not properly structured and is in a mutant form, it affects red-blood cells by causing them to take on a different structure which reduces their efficiency. Furthermore, since every cell in the body is dependent on an ample supply of oxygen to carry out its metabolic processes, one flaw in protein structure can detrimentally affect the efficiency of every cell in the organism's body and slow down their functions.

c) Although most mutations are bad for an organism, alleles encoding for mutant proteins may be preserved in populations either by natural selection or balancing selection due to heterozygote advantage. In the case of sickle-cell anemia, for example, individuals that show heterozygosity actually have an advantage over others because of an increased resistance to malaria. Therefore, in malaria-rich regions of the world, the mutant allele is preserved and even propegated. Sometimes, a mutant allele codes for a protein which actually increases the individual fitness in an environment. In such cases, natural selection will act on the favorable protein and cause it to be further propegated in subsequent generations.

2C 1

2. Certain human genetic conditions, such as sickle cell anemia, result from single base-pair mutations in DNA.

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(b) **Explain**, using a specific example, the potential consequences of the production of a mutant protein to the structure and function of the cells of an organism.

(c) **Describe** how the frequency of an allele coding for a mutant protein may increase in a population over time.

(a) ~~To produce a protein, the DNA to gene for the~~ To produce a protein, the gene for the protein will dehelix and one strand of the DNA will produce a strand of ~~mRNA~~ mRNA. with ~~the~~ help of RNA polymerase. This ~~process~~ process occures in the neucle. Then the mRNA travels to the ribosome, and tRNAs carring ~~amino ac~~ amino acid will combine with codes on mRNA. Then the polypeptid chain is formed. and ~~hydrogen~~ hychrogen bond may fromed to give the protein conformation.

If a single base-pair is changed, the mRNA, will ~~be~~ ~~diff~~ ~~have~~ has a different point compare to the nomal mRNA. ~~These~~ ~~one~~ This ~~not~~ changes the code on mRNA, and a different amino acid may persent in the polypeptid chain. ~~Bec~~ Because different amino acids ~~has~~ have different -R, so they may form different structure of protein. Because protein's function is highly depend on the conformation of protein, changes of conformation may changes functions.

so, a single base-pair mutant in DNA can alter the structure and function of protein

(b) ~~Color blind ne~~ Colorblind ness is ~~not~~ ~~codes~~ caused by a mutant in protein in human.

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AP® BIOLOGY
2010 SCORING COMMENTARY (Form B)

Question 2

Sample: 2A
Score: 10

This response is well written and clearly organized according to the question, providing examples for several of the statements.

In part (a) 4 points were earned. Three points were earned for the description of a frameshift mutation, how the new codons would code for different amino acids, and how the mutation would affect the protein by changing the amino acid sequence/primary structure. Another point was earned for describing how, in some mutations, different amino acids will have changed interactions (R-groups), thus altering the secondary, tertiary and quaternary structures. Another point could have been awarded for the description of how a mutation could change an enzyme's active and allosteric sites, but the maximum 4 points had already been earned. The response provides an additional example of a substitution mutation.

In part (b) 4 points were earned. One point was earned for describing the sickle cell anemia red blood cells as being sickle-shaped, and a second point was earned for indicating that the cells do not carry oxygen as efficiently as normal cells do. One point was earned for the discussion about the heterozygote advantage owing to malarial resistance, which begins in part (b) and is elaborated in part (c). Another point was earned for the description of the sickle cell allele as recessive, which is found in part (c).

Two points were earned in part (c) for describing how genetic drift/bottleneck and the migration/founder effect alter the allelic frequency. Two points for the description of natural selection and the effect of inbreeding on the allelic frequency could have been awarded, but the response had already reached the 10-point maximum.

Sample: 2B
Score: 7

Four points were earned in part (a). Two points were earned for indicating that each three-base-pair codon "codes for the insertion of one amino acid," and that a mutation in a single base pair could result in the incorrect amino acid being inserted (substitution). A third point was earned for indicating that a mutation could change the primary structure of a protein. The final point came for the indication that a mutation could alter the interaction between an enzyme and another molecule.

In part (b) 2 points were earned for indicating that sickle cell disease reduces the hemoglobin's capacity to carry oxygen. The second of the 2 points was earned for the description, found in part (c) of the response, of the sickle cell anemia resistance to malaria.

One point was earned in part (c) for indicating that the mutant allele can increase an individual's fitness by natural selection, increasing the allele frequency in subsequent generations.

Sample: 2C
Score: 4

In part (a) 4 points were earned. The maximum 3 points were earned for the DNA discussion: 2 points for the description of transcription and translation and the information flow from DNA to mRNA to polypeptide, and a third point for indicating that a point mutation may change the amino acid. The fourth point was earned for stating that amino acids have different R-groups, altering the protein structure.

No points were earned in parts (b) and (c).