AP® BIOLOGY
2009 SCORING GUIDELINES

Question 3

Phylogeny is the evolutionary history of a species.

(a) The evolution of a species is dependent on changes in the genome of the species. **Identify** TWO mechanisms of genetic change, and **explain** how each affects genetic variation. **(4 points maximum)**

	Identification **(1 point each; 2 points maximum)**	**Explanation** **(1 point each; 2 points maximum)**
DNA (molecular)	Mutation, e.g., point, frameshift, insertions, deletions	Change in nucleotide sequence or amino acid sequence or protein structure or gene expression, or change in phenotype
	Duplication, e.g., gene, chromosome, genome, sympatric speciation	Gene "families," which then diverge by mutation; change in ploidy
	Rearrangement, e.g., gene order, inversions, chromosome fusion, transposons	Chromosome structure altered; change in crossover frequency
Cellular	Crossing over, independent assortment, segregation, nondisjunction (meiosis) Random fertilization (sexual reproduction)	Increase gamete diversity Many possible gamete combinations
Population	Genetic drift or bottleneck or founder effects Gene flow (migration) Geographic isolation or allopatric speciation Nonrandom mating (sexual selection) Sympatric speciation Natural selection	Population allelic/gene frequencies altered or gain or loss of alleles/genes Reproductive fitness/differential success

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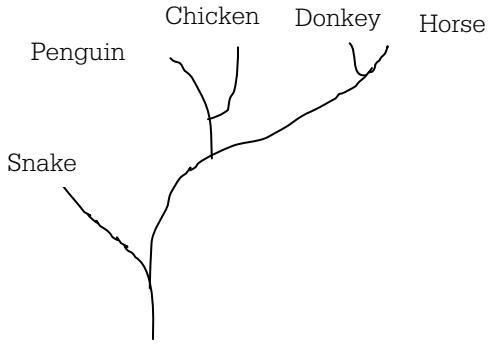
Question 3 (continued)

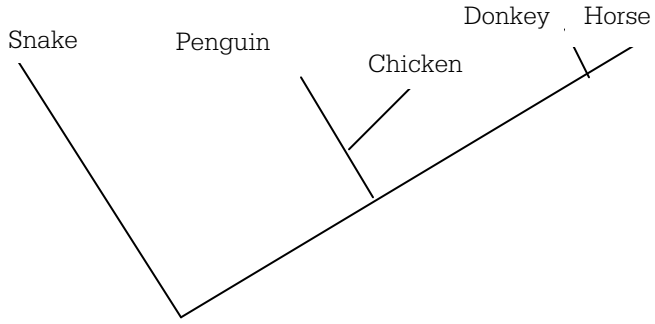
(b) Based on the data in the table below, **draw** a phylogenetic tree that reflects the evolutionary relationships of the organisms based on the differences in their cytochrome *c* amino-acid sequences and **explain** the relationships of the organisms. Based on the data, **identify** which organism is most closely related to the chicken and **explain** your choice. **(4 points maximum)**

THE NUMBER OF AMINO ACID DIFFERENCES IN CYTOCHROME *c*
AMONG VARIOUS ORGANISMS

	Horse	Donkey	Chicken	Penguin	Snake
Horse	0	1	11	13	21
Donkey		0	10	12	20
Chicken			0	3	18
Penguin				0	17
Snake					0

Phylogenetic tree: rooted trees with common ancestor, and with snakes, birds, mammals in correct relative order **(1 point for tree)**





- Cytochrome *c*: the more differences in amino acids of cytochrome *c*, the less closely related, OR fewer differences, more closely related. **(1 point)**
- Penguin is most closely related to chicken. **(1 point)**
- Three amino acids differing between penguin and chicken/penguin has fewest differences from chicken. **(1 point)**

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Question 3 (continued)

(c) **Describe** TWO types of evidence—other than the comparison of proteins—that can be used to determine the phylogeny of organisms. **Discuss** one strength of each type of evidence you described. **(4 points maximum)**

Description **(1 point per box; 2 points maximum)**	**Strength** **(1 point each; 2 points maximum)**
Fossil Observe past organisms	Shows direct evidence of common ancestor, follow evolution (changes over time) from common ancestor
Homology: morphology Organismal structure/form Vestigial structures	Similarities in form(s) show common ancestry/DNA
Homology: embryology/development Morphology of embryos; changes in gene expression during development	Similarities in development show common ancestry/DNA
Homology: reproduction Comparison of reproductive strategies or life cycles: cell division, gamete production, gamete type, etc.	Similarities in reproduction strategies show common ancestry/DNA
DNA sequence Comparison of DNA sequences in specific genes; molecular homologies	Similarities in sequences show common ancestry
Biogeography Analysis of organism distribution(s)	Uses both past and present information to show common ancestry/DNA
Direct observation/behavior Watch organism in natural setting	Similarities in behaviors indicate common ancestry/DNA

3A1

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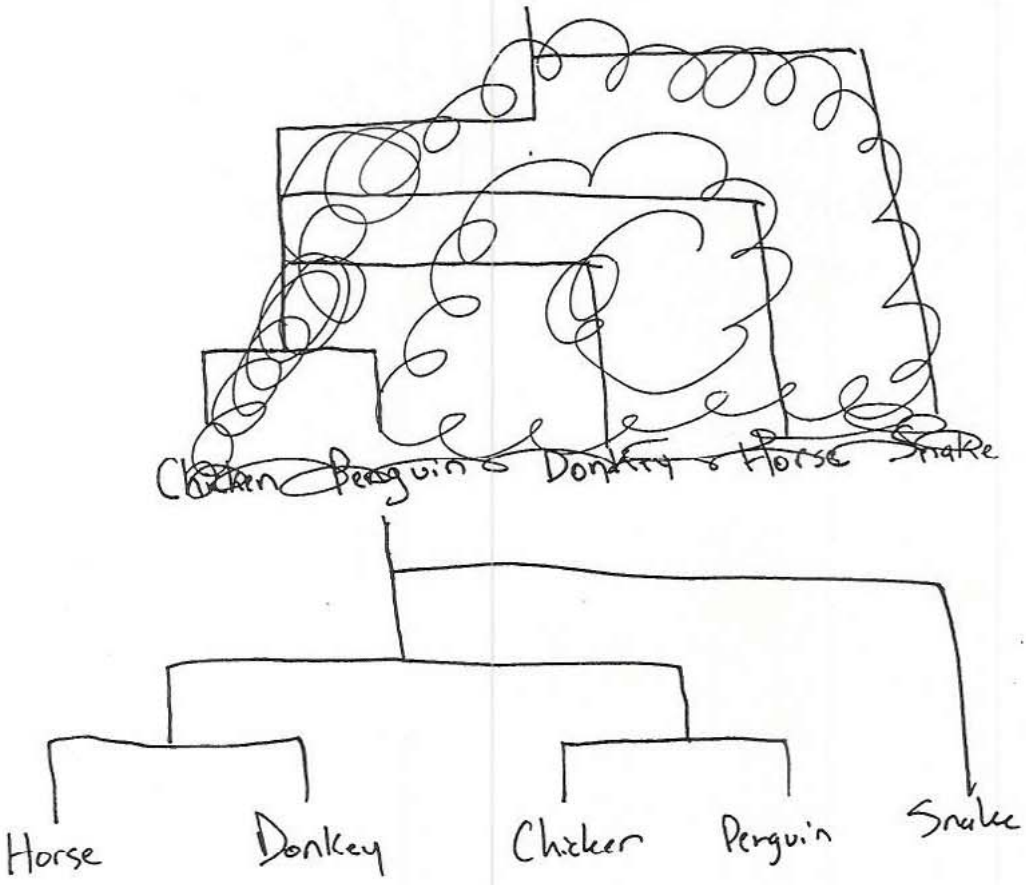
K- Ani.
P- Chord.
C.



Donkey

ADDITIONAL PAGE FOR ANSWERING QUESTION 3

Changing genetics is a key factor in the theory of evolution. An unpredictable factor in this change is mutation. A random change in genetics as an addition, substitution, or deletion can alter an organisms structure or behavior. The ability for these changes to pass on requires that the mutation occur in the sex cells. If an autosomal mutation does not affect the sex cells then it will die with the individual. Mutations can be devestating or extremely helpful to a population depending on the circumstances and can sometimes create a new standard of sexual selection. Geographic isolation, often from changing migration paths or geologic activity can greatly alter the genetics of a population. When brought into a new environment, new challenges are brought to a population. Their adaptations will be different than those in their original habitats or than their counterparts remaining there. Selection of different traits often occurs from predation and new food sources, leaving a genetically and phenotypically different population and consometimes lead to speciation. The genetic similarities in organisms can point to their degree of relation and how recent a common ancestor might be. Based on the differences of the cytochrome-C in these organisms, it would seem that the donkey and horse are very closely related (already obvious from the hybrid viability in the two) as well as the chicken and the penguin. The snake is the furthest related from them all. This makes sense since the donkey and horse are both members of mamonalia and the chicken and penguin both members of Aves. It appears that the penguin is most related to the chicken since it had the fewest diffeneces of cytochrome C (3). Embryology is another way to observe the relation of organisms, especially in mammals. Similarities in embryonic structure and

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appearance support the notion of a more recent common ancestor and can be very uncanny to note in photographs just how similar we are as embryos. Homologous structures of organisms link them together in their adult forms. It's visible in the forearm and hand bones of chordates. The bones in a bat's wing bear striking resemblance and structure to those of the human hand. This also promotes the idea of a common ancestor and can highlight the deviations from it very graphically.

3B1

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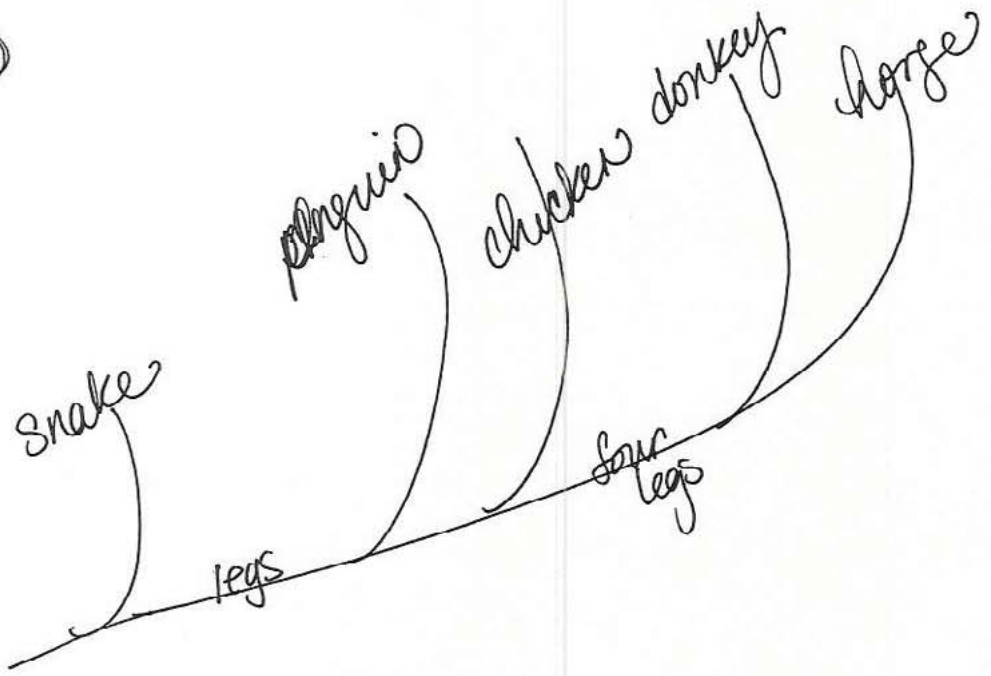
(b)

phylogenetic tree



3B2

ADDITIONAL PAGE FOR ANSWERING QUESTION 3

(a) One mechanism of genetic change is sexual selection over time. In sexual selection, certain phenotypes will give mates an advantage. For example, male peacocks use their bright colors/patterns to attract a female. Ultimately, over time, the most beautiful + bright males will mate more often, therefore making the next generations of males more brightly patterned. Diminishes vara

Another mechanism is simply mutation — as bacteria and viruses are rapidly reproducing, they have a propensity to make errors in their transcription/translation. ~~This~~ If not fatal to the simple organism, the mutation may make it unsusceptible, immune, to human-developed antibiotics because it has now been genetically altered. ~~The happened with~~ ~~and with~~ Sometimes, the greater the variation, the more likely the survival of the species.

(b) The horse & donkey are very closely related, only 1 amino acid difference in cytochrome C meaning that they can even mate together although their offspring (mule) ~~cannot~~ is not fertile. The snake is far removed, having 17+ differences on cytochrome C, but we can also see that physiologically. Snakes do not have legs/limbs or wings. ~~Penguins~~ ~~They are also~~

The penguin is most closely related to the chicken — as you can see, it has only 3 amino acid differences on cytochrome C (compared to 10, 11, 18) which is also shown in phenotypes. Both penguins & chickens have wings, 2 webbed feet, and are ~~approximately~~ in a similar size range

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(although penguins can be much larger). Also, they are born in ~~eggs~~ external eggs.

© Phenotypic structure and behavior/intelligence can be used to determine places on a phylogenic tree.

Phenotypic structures can be useful in organizing a tree, because ultimately proteins create traits and structures determine function, so it covers a wide base/angles of analysis. Phenotypes ~~that~~ are easily visible & in terms of extinct species, many of their only remains are things like bones or imprints in rock (fossils) which are phenotypes but not including DNA to be analyzed.

3C 1

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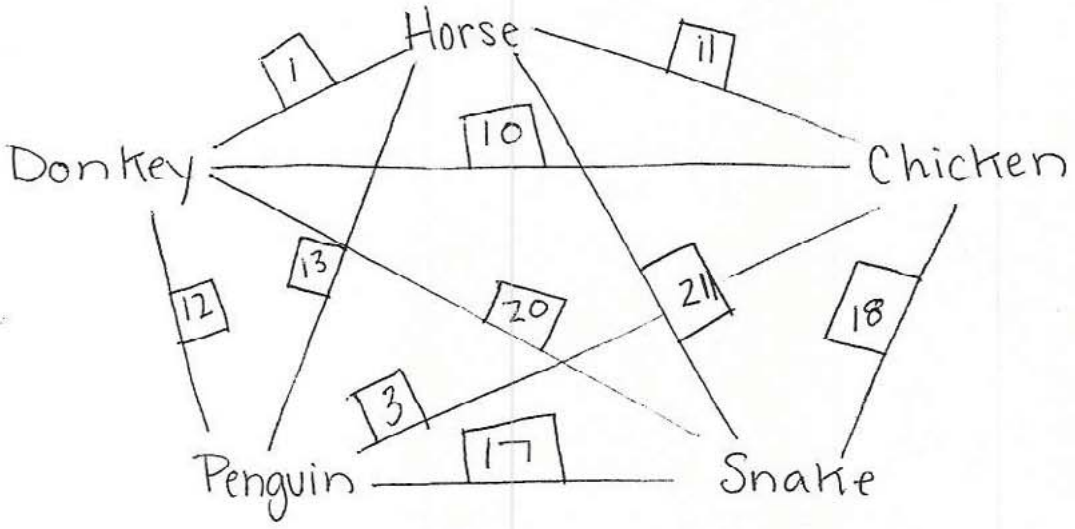
B:



~~Horse~~
~~Donkey~~

Horse / Donkey
↓
Chicken / Penguin
↓
Chicken / Donkey
↓
Chicken / Horse

3C2

A: Deletion in the genetic code of an organism can lead to the development of a new trait, eventually changing the organism and organism's decendants so much they can no longer reproduce with organisms of that species. This means they have become thier own species. Deletion does so by deleting a base pair in the DNA. Depending where the deletion occurs decides how it will effect the animal, if it effects the animal at all.

The same concept accompanies substitution, but instead of deleting a base pair in the genetic code, a base pair is added changing the sequence of base pairs from the point of substitution / deletion forward.

Placement of the substitution or deletion of the base pair can lead to mutation which, if it helps the individual to survive, will be passed on to the decendants of the individual and potentially change the genome of the species.

B: (continued)

The penguin is most closely related to the chicken because it has only 3 differences in thier cytochrome c amino-acid sequence. The next closest difference to the chicken is the donkey (10 differences). Not only are they the most similar on a genetic level, but a penguin resembles a chicken more than the other species presented.

C: Comparing the DNA sequence of organisms can also tell you how closely related species are. It can give you even more information since the original DNA is how the amino acid sequence of chytochrome c is coded for.

Looking at embryonic development also helps you determine the phylogeny of organisms because a way an embryo develops can be very similar to the way another species develops but when both are full grown they look very different and it's hard to

ADDITIONAL PAGE FOR ANSWERING QUESTION 3

see how closely related they might be.

AP® BIOLOGY
2009 SCORING COMMENTARY

Question 3

Overview

A broad understanding of evolution by natural selection is a core principle for learning about phylogenetic relationships and a foundational theme in AP Biology. The first part of this question asked students to identify two ways that genetic change occurs and to explain how each mechanism affects genetic variability. The second part of the question provided details of amino acid differences in the protein known as cytochrome *c*; students were asked to develop a phylogenetic tree among five organisms—horse, donkey, chicken, penguin, and snake—and to identify the species most closely related to the chicken, as shown by the data. The final part of the question required students to discuss two additional (nonprotein) types of evidence that could be used in constructing a phylogeny or evolutionary history of organisms.

Sample: 3A
Score: 10

The response earned the maximum of 4 points in part (a). The response identifies and describes mutation as a mechanism of genetic change by indicating that a mutation can alter an organism's behavior or structure (phenotypes). The response provides a detailed narrative on geographic isolation as a means of altering the genotypes and phenotypes from the original population.

Part (b) required the construction of a phylogenetic tree using the cytochrome *c* amino acid sequence differences among five organisms. The response describes the phylogeny by highlighting the closeness of the donkey–horse and penguin–chicken relationships and indicating that the snake is quite different from the other four species, thus earning 1 point. The response earned 2 points for stating that "the penguin is most related to the chicken since it had the fewest" amino acid differences (three) from the chicken. No points were earned for the tree, which indicates that the horse/donkey and chicken/penguin lineages diverged at the same time.

In part (c) the response earned 2 points by describing embryology as a means to analyze evolutionary relationships in mammals, mentioning structural similarities and explaining that embryonic appearances can indicate a common ancestor. The response earned 1 point for using homologous structures, specifically chordate forearm bones, as evolutionary evidence. An additional point could have been earned for the strength—homologous structures as evidence of a common ancestor—but the response already had earned the maximum of 10 points for the question.

Sample: 3B
Score: 8

In part (a) the response earned the maximum of 4 points. Two points were earned for identifying sexual selection and explaining how it acts as a mechanism of genetic variation. The response provides an example of how the most brightly colored male peacocks "will mate more often," thus passing their genes on to the next generation. Two points were awarded for identifying mutations as means of genetic change and for detailing antibiotic resistance mutations in bacteria.

Question 3 (continued)

In part (b) the response earned the maximum of 4 points. A point was earned for the tree, which, although not completely accurate, has a common ancestor and the species branches in the correct order. The response earned a second point for explaining that the donkey and horse are closely related, based on the cytochrome *c* differences, and clarifying this by indicating that the snake is distantly related due to the large number of differences. The response earned 2 more points by identifying the penguin as the chicken's closest relative because there are three amino acid differences between the two.

In part (c) the response earned no points due to a lack of clear descriptions and strengths.

Sample: 3C
Score: 6

In part (a) the response earned 2 points for identifying and describing mutations as a source of genetic change. The response explains that a mutation changes the sequence of [nucleotide] base pairs.

In part (b) the response identifies the penguin as the closest relative of the chicken, earning 1 point, and explains that "it has only 3 differences in thier [*sic*] cytochrome c amino-acid sequence," earning 1 point. No point was earned for the weblike, unrooted tree.

In part (c) the response earned 1 point for describing the DNA sequence analysis of the cytochrome *c* gene as a type of evidence of phylogenetic comparisons; this is a strength point. A second point was earned for embryological evidence strength, which examines and compares embryo development between species.