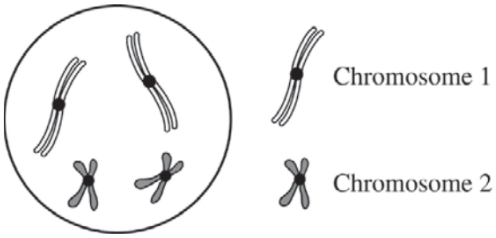
AP BIO Unit 5 Released FRQs

2016 #7

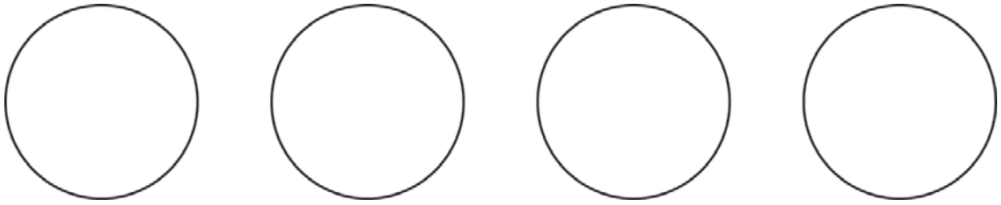


7. In a certain species of plant, the diploid number of chromosomes is 4 (2n = 4). Flower color is controlled by a single gene in which the green allele (*G*) is dominant to the purple allele (*g*). Plant height is controlled by a different gene in which the dwarf allele (*D*) is dominant to the tall allele (*d*). Individuals of the parental (P) generation with the genotypes *GGDD* and *ggdd* were crossed to produce F_1 progeny.

   (a) **Construct** a diagram below to depict the four possible normal products of meiosis that would be produced by the F_1 progeny. Show the chromosomes and the allele(s) they carry. Assume the genes are located on different chromosomes and the gene for flower color is on chromosome 1.

   (b) **Predict** the possible phenotypes and their ratios in the offspring of a testcross between an F_1 individual and a *ggdd* individual.

   (c) If the two genes were genetically linked, **describe** how the proportions of phenotypes of the resulting offspring would most likely differ from those of the testcross between an F_1 individual and a *ggdd* individual.

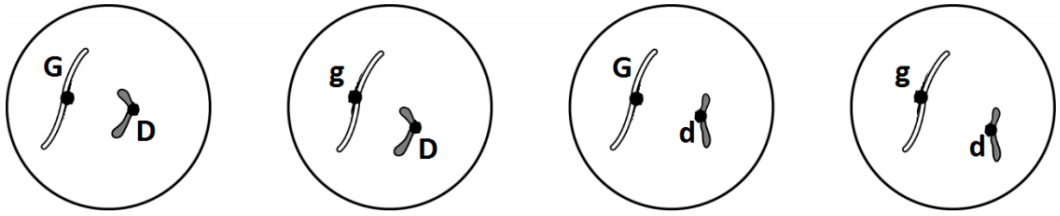


2016 #7 Answer Key

(a) **Construct** a diagram below to depict the four possible normal products of meiosis that would be produced by the F_1 progeny. Show the chromosomes and the allele(s) they carry. Assume the genes are located on different chromosomes and the gene for flower color is on chromosome 1. **(1 point)**

Construct diagram (1 point)

- Diagram must include all of the following:
  - Each cell has one unduplicated chromosome 1 (with G or g).
  - Each cell has one unduplicated chromosome 2 (with D or d).
  - Genotype combinations should be: GD, Gd, gD, gd.



(b) **Predict** the possible phenotypes and their ratios in the offspring of a testcross between an F_1 individual and a *ggdd* individual. **(1 point)**

Prediction (1 point)

- 1 green dwarf: 1 green tall: 1 purple dwarf: 1 purple tall

(c) If the two genes were genetically linked, **describe** how the proportions of phenotypes of the resulting offspring would most likely differ from those of the testcross between an F_1 individual and a *ggdd* individual. **(1 point)**

Identify difference (1 point)

- The majority/greater than 50 percent would have the parental plant phenotypes
- Greater than 25 percent would be green dwarf plants and greater than 25 percent would be purple tall plants
- Less than 25 percent would be green tall plants and less than 25 percent would be purple dwarf plants

2014 #8

8. 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.

2014 #8 Answer Key

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. (**3 points maximum**)

(a) **Provide** ONE piece of evidence that would indicate new genetic variation has occurred in the engineered flies. (**1 point**; LO 1.10)

Piece of evidence

- New phenotypes
- Different DNA sequence
- New genotypes
- Chromosomal differences
- Different mRNA sequence
- Protein with different amino acid sequence

(b) **Describe** ONE mechanism that could lead to genetic variation in the engineered strain of flies. (**1 point**; LO 3.28)

Describe mechanism

- Sexual reproduction produces offspring with new combinations of alleles/traits
- Meiosis produces new combinations of alleles/traits
- Crossing over produces new combinations of alleles/traits
- Independent assortment produces new combinations of alleles/traits
- Random fertilization produces new combinations of alleles/traits
- Immigration/gene flow introduces new alleles/gene sequences
- Viral infection inserts DNA into genome
- Nondisjunction causes anomaly in chromosome number
- Chromosomal rearrangements (e.g., large deletions, duplications, translocations, inversions, transposons, etc.) inactivate genes or result in multiple copies of genes
- Radiation or chemicals or mutagens induce mutations/changes in DNA

(c) **Describe** how genetic variation in a population contributes to the process of evolution in the population. (**1 point**; LO 1.25)

Description

- Genetic variation is the basis of phenotypic variation that can be acted upon by natural selection
- Without genetic variation, there is no phenotypic variation on which natural selection can act

2013 #5

5. The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

	Relative Amino Acid Position									
Species	1	2	3	4	5	6	7	8	9	10
I	Val	His	Leu	Val	Glu	Glu	His	Val	Glu	His
II	Val	His	Leu	Lys	Glu	Glu	His	Val	Glu	His
III	Val	His	Leu	Val	Glu	Glu	His	Val		
IV	Val	His	Leu	Val	Arg	Trp	Ala	Cys	Met	Asp

(a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III.

(b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction.

2013 #5 Answer Key

(a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III. **(2 points maximum)**

Explanation: **1 point per row**
NOTE: Specific names of mutation types are not required.

Species	Genetic Change in DNA / Bases	Result of Change to Polypeptide / Protein
II	mutation / substitution / point mutation / missense mutation	an amino acid change only at position 4 (Val to Lys)
III	mutation (e.g., substitution / insertion / deletion / point mutation / frameshift mutation / nonsense mutation) that introduces a stop codon after the codon for Val	termination of the polypeptide after the Val at position 8

(b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction. (**2 points maximum**)

Predicted Change (**1 point maximum**)	Justification of Prediction (**1 point maximum**)
Protein may have a different structure and a change in function.	Change in amino acid sequence of the protein starting at position 5 could alter the overall structure or local structural regions, interfering with function of the protein.
Protein may have a different structure and no change in function.	Change in amino acid sequence alters the shape / conformation / folding / binding region / regulatory region of the protein, but does not affect the critical functional region(s) of the protein.
Protein structure and function may not be affected.	Change in amino acid sequence does not alter the protein shape / conformation / folding and does not alter function.

2010 #3

3. A new species of fly was discovered on an island in the South Pacific. Several different crosses were performed, each using 100 females and 100 males. The phenotypes of the parents and the resulting offspring were recorded.

Cross I: True-breeding bronze-eyed males were crossed with true-breeding red-eyed females. All the F_1 offspring had bronze eyes. F_1 flies were crossed, and the data for the resulting F_2 flies are given in the table below.

F_2 Phenotype	**Male**	**Female**
Bronze eyes	3,720	3,800
Red eyes	1,260	1,320

Cross II: True-breeding normal-winged males were crossed with true-breeding stunted-winged females. All the F_1 offspring had stunted wings. F_1 flies were crossed, and the data for the resulting F_2 flies are given in the table below.

F_2 Phenotype	**Male**	**Female**
Normal wings	1,160	1,320
Stunted wings	3,600	3,820

Cross III: True-breeding bronze-eyed, stunted-winged males were crossed with true-breeding red-eyed, normal-winged females. All the F_1 offspring had bronze eyes and stunted wings. The F_1 flies were crossed with true-breeding red-eyed, normal-winged flies, and the results are shown in the table below.

Phenotype	**Male**	**Female**
Bronze eyes, stunted wings	2,360	2,220
Bronze eyes, normal wings	220	300
Red eyes, stunted wings	260	220
Red eyes, normal wings	2,240	2,180

(a) What conclusions can be drawn from cross I and cross II? **Explain** how the data support your conclusions for each cross.

(b) What conclusions can be drawn from the data from cross III? **Explain** how the data support your conclusions.

(c) **Identify** and **discuss** TWO different factors that would affect whether the island's fly population is in Hardy-Weinberg equilibrium for the traits above.

2010 #3 Answer Key

(a) What conclusions can be drawn from cross I and cross II? **Explain** how the data support your conclusions for each cross. **(4 points maximum)**

Conclusion for cross I (1 point maximum)	**Possible explanations for cross I (1 point maximum)**
• Bronze dominant/red recessive • Autosomal (non-sex-linked)	• All F_1 /heterozygotes express dominant trait (bronze). • F_2 shows 3:1 ratio (bronze:red/dominant:recessive). • Equal distribution of F_2 phenotypes for both genders.
Conclusion for cross II (1 point maximum)	**Possible explanations for cross II (1 point maximum)**
• Stunted dominant/normal recessive • Autosomal (non-sex-linked)	• All F_1 /heterozygotes express dominant trait (stunted). • F_2 shows 3:1 ratio (stunted:normal/dominant:recessive). • Equal distribution of F_2 phenotypes for both genders.

(b) What conclusions can be drawn from the data from cross III? **Explain** how the data support your conclusions. **(4 points maximum)**

Conclusion for cross III (1 point per bullet; 2 points maximum)	**Explanation for cross III (1 point per bullet; 2 points maximum)**
• Genes linked • Crossing over • Genes 10 map units apart	• Not a 1:1:1:1 ratio (as predicted by independent assortment). • Not a 1:1 ratio/two recombinant phenotypes (unexpected). • Frequency of recombinant phenotypes was 10 percent (setup equation OK)/parental phenotypes (bronze/stunted and red/normal) are represented in 90 percent of offspring.

(c) **Identify** and **discuss** TWO different factors that would affect whether the island's fly population is in Hardy-Weinberg equilibrium for the traits above. **(4 points maximum)**

Identification (1 point per bullet; 2 points maximum)	**Discussion of effect (1 point per bullet; 2 points maximum)**
• Large population	• Minimized genetic drift.
• Random mating	• No gene pool change due to mate preferences.
• No mutation	• No new alleles in population.
• No immigration/emigration/ migration (no gene flow)	• No gene pool change by addition/loss of alleles.
• No natural selection	• No alleles favored or disfavored by environment.

2010B #2

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.

2010 B #2 Answer Key

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.

2004 #1

1. Meiosis reduces chromosome number and rearranges genetic information.

   (a) **Explain** how the reduction and rearrangement are accomplished in meiosis.

   (b) Several human disorders occur as a result of defects in the meiotic process. **Identify** ONE such chromosomal abnormality; what effects does it have on the phenotype of people with the disorder? **Describe** how this abnormality could result from a defect in meiosis.

   (c) Production of offspring by parthenogenesis or cloning bypasses the typical meiotic process. **Describe** either parthenogenesis or cloning and **compare** the genomes of the offspring with those of the parents.

2004 #1 Answer Key

(a) **Explain** how the reduction and rearrangement are accomplished in meiosis.
(5 points maximum)

REDUCTION
1 point: **(homologous) chromosomes pair, then separate** and move to opposite poles during 1st meiotic division
1 point: **chromatids separate** during 2nd meiotic division

OR

1 point: two rounds of cell (nuclear) division but only one replication of the chromosomes

REARRANGEMENT
1 point: **crossing over** (in proper context)
1 point: **random alignment (independent assortment)** of tetrads
1 point: **elaboration (e.g.: correct mechanism/description or consequences** of one of the above) *

*NOTE: Diagrams that are clearly labeled and are described in the essay portion are acceptable and may receive a point

(b) Several human disorders occur as a result of defects in the meiotic process. **Identify** ONE such chromosomal abnormality; what effects does it have on the phenotype of people with the disorder? **Describe** how this abnormality could result from a defect in meiosis.
(4 points maximum)

CHROMOSOMAL ABNORMALITY
1 point: **Identify** one condition by name or description (e.g.: Down or trisomy 21; Turner or XO; fragile X; cri-du-chat or 5p-; etc.)
1 point: **Phenotype** of the example given above

DESCRIBE
1 point: **Name or identify the meiotic event** (e.g.: nondisjunction, unequal crossing over, inversion, mispairing)
1 point: **Description** of the meiotic event *

(c) Production of offspring by parthenogenesis or cloning bypasses the typical meiotic process. **Describe** either parthenogenesis or cloning and **compare** the genomes of the offspring with those of the parents.
(3 points maximum)

CLONING OR PARTHENOGENESIS
1 point: **Definition**
- **Parthenogenesis**: development of an unfertilized egg into an adult; often the adult is haploid

OR

- **Cloning**: using a somatic cell or cells from a multicellular organism to make one or more genetically identical individuals (or inducing a diploid body cell of an organism to revert to its embryonic state and then develop into a complete adult organism without fertilization)

1 point: **Description** of an example or the process in a plant or animal (parthenogenesis is rare in plants)
1 point: **Comparison** of the genomes of offspring and parents (e.g. identical for cloning)