# Module B
## Continuity and Unity of Life

# Unit 6
## Genetics

Genetic information passes on the instructions for building and operating an organism from one generation to the next. This unit will help you review how genes are inherited, how they may be altered or mutated to increase variability, and how they are engineered through human intervention.

1 Genes and Inheritance Genetic information is inherited according to particular patterns. In this lesson, you will review the patterns of inheritance, including dominant, recessive, co-dominant, incomplete dominant, sex-linked, polygenic, and multiple alleles. You will also review the functional relationships between DNA, genes, alleles, and chromosomes and their roles in inheritance.

2 Mutations and Chromosome Abnormalities Genetic information may be altered in various ways. In this lesson, you will review processes that alter genetic information, including crossing-over, nondisjunction, duplication, translocation, deletion, insertion, and inversion. You will also review ways that genetic mutations alter the DNA sequence and may result in genotypic and phenotypic variations within a population.

3 Genetic Engineering Genetic engineering is the control of genetic variability through technology and human intervention. In this lesson, you will review the impacts of selective breeding, gene splicing, cloning, genetically modified organisms, and gene therapy on such diverse fields as medicine, forensics, and agriculture.

LESSON 1

# Genes and Inheritance

BIO.B.1.2.2, BIO.B.2.1.1

Remember that a gene is a region of DNA that codes for a specific protein. Genes come in different versions, called **alleles.** An organism's alleles, along with its environment, determine that organism's traits. In most cases, traits are **polygenic,** meaning that they are determined by a number of different genes located on different chromosomes. More rarely, a single gene will determine a single trait. In the 1800s, Gregor Mendel discovered the basic rules of inheritance by studying single-gene traits in pea plants.

## Dominant and Recessive Alleles

Just as there are different versions of a trait—for example, tall and short pea plants—there are different versions, or alleles, of the genes that determine those traits. The gene that determines height in pea plants has two different alleles—one causing a tall **phenotype** and one causing a short phenotype.

The body cells of most sexually reproducing organisms contain two alleles of each gene. An organism may have inherited two identical alleles or two different alleles for a gene. The combination of alleles in an organism's cells is its **genotype.** If a pea plant inherits two **dominant** alleles (*TT*), it expresses the dominant phenotype. If it inherits two **recessive** alleles (*tt*), it expresses the recessive phenotype. Genotypes with two matching alleles are described as *homozygous.*

| Genotype | | Phenotype |
|---|---|---|
| *TT* | homozygous dominant | tall |
| *Tt* | heterozygous | tall |
| *tt* | homozygous recessive | short |

A *heterozygous* organism inherits one of each allele. Because a dominant allele masks the effects of the recessive allele, this organism will show the dominant phenotype. The table describes the effects of genotype for a gene with alleles *T* and *t* on phenotype.

Remember that a gamete contains only one chromosome of each pair. Therefore, it contains one of the two alleles making up the organism's genotype. A homozygous pea plant (*TT* or *tt*) can produce gametes with only one allele. Half of the gametes produced by a heterozygote (*Tt*) have the *T* allele, and half have the *t* allele.

A **gene** is a DNA sequence that specifies a protein. An **allele** is a version of a gene. Each sexually reproducing organism inherits two alleles of each gene.

A **polygenic trait** is determined by many different genes.

In the 1800s, Gregor Mendel founded the field of genetics with his studies on pea plants. The traits Mendel studied are determined by single genes.

A **genotype** is the combination of alleles of a particular gene. A **phenotype** is the appearance of a trait.

Dominant alleles are often represented by capital letters and recessive alleles by lowercase letters.

A **dominant** allele is expressed if the individual inherits just a single copy of the allele.

A **recessive** allele is expressed only if the individual inherits two copies of the allele.

*Homozygous* means "same alleles" and *heterozygous* means "different alleles."

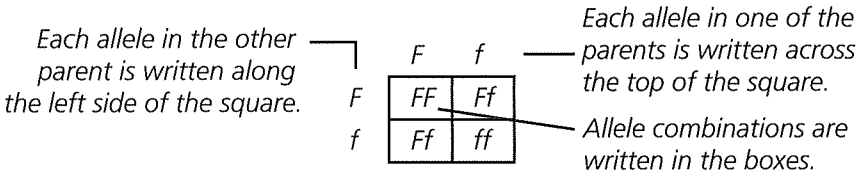
If a gamete contains an allele, that allele must also be present in the organism's body cells.

In fruit flies, the allele for normal-sized wings (*W*) is dominant to the allele for small wings (*w*). A fly that has normal wings breeds with a fly that has small wings. Several offspring have small wings, and others have normal wings. Identify the genotype of each of the parent flies.

The small-wing phenotype is expressed only in individuals that have two *w* alleles. Therefore, the small-wing parent must have the *ww* genotype. The small-wing offspring must have inherited one *w* allele from each parent. Therefore, each parent must have at least one *w* allele. The normal-wing parent must have one *W* allele, because it has normal wings. The normal-wing parent must therefore be heterozygous, or *Ww*.

## Predicting Inheritance

Scientists use *Punnett squares* to show the possible allele combinations and phenotypes of the offspring of a given set of parents. Punnett squares also show the probability that each offspring will have a given genotype. The diagram below shows an example for a human trait: the genetic disease cystic fibrosis. The alleles for this trait are the dominant *F* (no cystic fibrosis) allele and the recessive *f* (cystic fibrosis) allele.




In this example, the probability that an offspring will be heterozygous is 50%. The probability that an offspring will be homozygous recessive is 25%, and the probability that an offspring will be homozygous dominant is 25%. Therefore, the probability that each child of these parents will have cystic fibrosis is 25%. Note that a Punnett square cannot be used to predict the genotype or phenotype of a specific offspring.

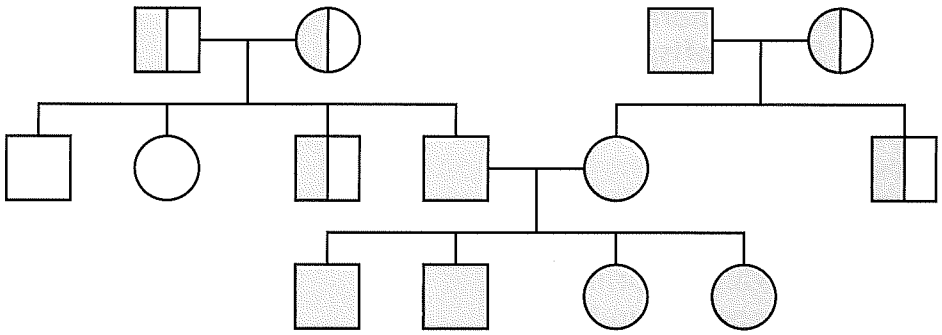
A *pedigree* chart can be used to trace inheritance of a trait through multiple generations of related individuals. In a pedigree, males are typically represented by squares and females are represented by circles. Shaded shapes indicate that the individual has the trait in question. Half-shaded shapes indicate the individual is a *carrier* of the trait but does not express the trait. A horizontal bar directly connecting two individuals represents a set of parents. A horizontal bar joining short vertical branches represents all the offspring of a set of parents.

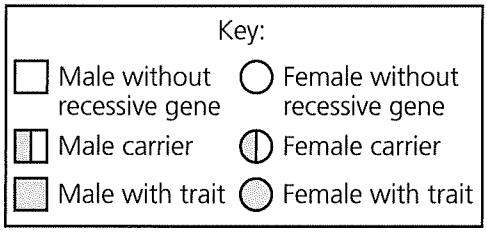
Cystic fibrosis is an example of a genetic disease that is caused by a mutation in a single gene. This gene codes for a specific cell protein, which is involved in the transport of chloride ions across the cell membrane. The mutation produces a faulty protein.

Not all traits are governed by a single gene. Some traits, such as height in humans, are affected by multiple genes. In addition, some genes produce proteins that affect multiple traits.

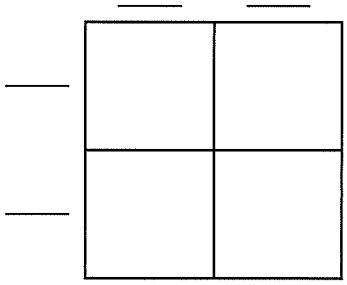
In a pedigree, the *carrier* of a recessive disease may be represented by a half-shaded shape. Carriers are heterozygous.

**INHERITANCE OF A TRAIT OVER THREE GENERATIONS**






Look at the pedigree chart above. Complete the Punnett square below for the first (left) couple in the top row of the chart. Determine the probability of inheriting each genotype and phenotype. Do the results of the Punnett square differ from the pedigree for the four children of this couple? Explain.



As carriers, each parent is heterozygous, and the completed Punnett square looks like this:

| | *A* | *a* |
|---|---|---|
| *A* | *AA* | *Aa* |
| *a* | *Aa* | *aa* |

The genotypes (and phenotypes) are, *AA* (normal), *Aa* (carrier), *aa* (disease), and *Aa* (carrier). The actual genotypes and phenotypes observed in this couple's offspring are, from left to right in the pedigree chart: *AA* (normal), *AA* (normal), *Aa* (carrier), and *aa* (disease). Although there was a 50% chance of being a carrier, only one of the four offspring is a carrier. Despite only a 25% chance of having the *AA* genotype, two offspring have this genotype. The results differ because a Punnett square allows you to predict the chances of inheriting a genotype, and can tell you which genotypes are impossible, but it cannot specify exactly which alleles an individual will inherit.

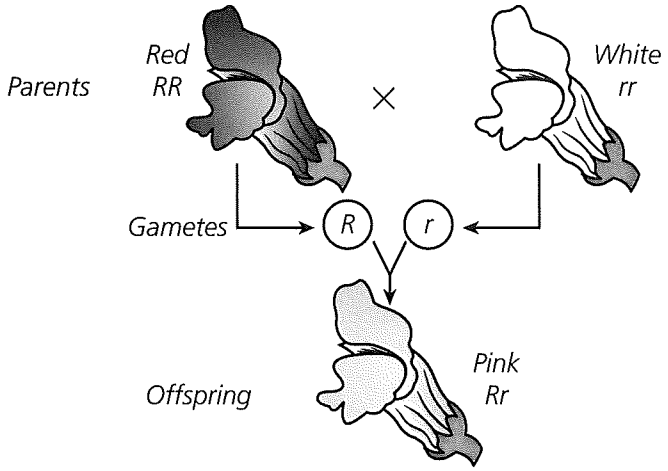
All multicellular organisms are eukaryotes, so all multicellular organisms have cells with nuclei and membrane-bound organelles.

Predictions from Punnett squares are accurate for very large numbers of offspring, such as the hundreds produced in fruit fly crosses.

# Incomplete Dominance, Co-Dominance, and Multiple Alleles

Not all genes have one dominant and one recessive allele. Some alleles may show **incomplete dominance,** meaning that a heterozygous individual has a phenotype that differs from those with either homozygous genotype. The inheritance of flower color in snapdragons is an example of incomplete dominance. The allele *R* results in the red flower phenotype and the allele *r* results in white flowers. However, heterozygous flowers are pink. This phenotype is "in between" the dominant and recessive phenotypes.

In **incomplete dominance,** the heterozygous phenotype is "in between" the homozygous phenotypes.




**Snapdragon flower color shows incomplete dominance. The pink color of the offspring is "in between" the colors of the parents.**

Alleles may also show **co-dominance,** meaning that heterozygotes express *both* the dominant and recessive phenotypes, rather than a blend of the two. For example, some cattle have a *roan* coat, which is made up of white and colored hairs. Roan cattle have one allele for white hair and another for reddish-brown hair. Roan cattle have one of each allele, and both types of hair. Notice that the heterozygous phenotype is not tan or light red hair. Rather, both phenotypes are expressed completely.

An organism heterozygous for **co-dominant alleles** expresses *both* of the homozygous phenotypes.

Some genes have more than two possible alleles. ABO blood type in humans is one example of a **multiple-allele** trait. Within the human population, there are three blood type alleles: $I^A$, $I^B$, and *i*. Each person has only two of the possible three alleles. Instead of three possible genotypes, multiple alleles produce a larger number of genotypes.

A gene may have **multiple alleles** in the population, even though each individual still carries only two alleles.

The ABO blood type gene is also an example of co-dominance. Blood type is determined by the presence of a carbohydrate group attached to a protein on the surface of red blood cells. Different carbohydrate groups result from the $I^A$ and $I^B$ alleles. If both alleles are present, the individual has type AB blood. These alleles are both dominant to the *i* allele, which results in a surface protein with *no* attached carbohydrate and type O blood.

ABO type is just one of many different ways to classify blood types. People can also be Rh factor positive or negative. ABO and Rh blood types are important in medicine.

This table summarizes the phenotypes associated with each of the six possible human blood-type genotypes.

| Genotype | Phenotype |
|---|---|
| $I^AI^A$ | type A blood |
| $I^BI^B$ | type B blood |
| $I^AI^B$ | type AB blood |

| Genotype | Phenotype |
|---|---|
| $I^Ai$ | type A blood |
| $I^Bi$ | type B blood |
| $ii$ | type O blood |

**A child has type O blood. If the child's mother has type A blood, what are all the possible genotypes and phenotypes of the father?**

A $ii$ only

B $ii$ and $I^Ai$

C $ii$, $I^Ai$, and $I^Bi$

D $ii$, $I^Ai$, $I^AI^A$, and $I^Bi$

Choice D is incorrect; the father cannot have type AB blood ($I^AI^B$), because he would then have to pass on one dominant allele to his child. We know that the type O child has no dominant alleles ($ii$). Choice A is incorrect because the father needs only one $i$ allele to pass on to his child. Choice B is incorrect because genotype $I^Bi$ is also possible, as it includes at least one $i$ allele. Choice C is correct; the father may have genotypes $ii$ (type O), $I^Ai$ (type A), or $I^Bi$ (type B).

Other genes may also result in type O blood. For example, a gene may prevent the carbohydrate group from being made at all. In rare cases, two AB parents may have a type O child.

## Sex-Linked Traits

In humans and many other animals, a single pair of chromosomes, called the *sex chromosomes,* determines an individual's sex. The human sex chromosomes are the X chromosome and the Y chromosome. An XX individual is female, while an XY individual is male.

The X chromosome is much larger, and contains many more genes, than the Y. Most genes on the X chromosome determine traits that have nothing to do with being male or female. Males, who have only one X chromosome, therefore have only one allele of each of these genes. Traits governed by the genes on a sex chromosome are called **sex-linked traits.**

A **sex-linked trait** is determined by genes on either the X or Y chromosome.

Non-sex chromosomes are called *autosomes.*

Hemophilia, a blood-clotting disorder, is determined by a single gene on the X chromosome. The allele for the disorder is recessive. A female will have hemophilia only if both of her X chromosomes have the recessive alleles. In contrast, a male needs only one recessive allele to have hemophilia. He has only one X chromosome, and there is no other allele to possibly mask the disorder.

A father with hemophilia will pass the recessive allele to all of his daughters. Assuming that the mother is homozygous dominant, the daughters will be carriers of (heterozygous for) the disorder. However, they may pass the recessive allele to male children.

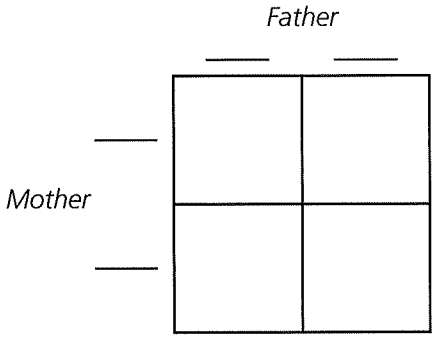
Recessive sex-linked traits governed by genes on the X chromosome are observed more often in males than in females.

A man with hemophilia and a woman who has no history of the disease in her family plan to have a child. The parents' genotypes are $X^hY$ and $X^HX^H$.

A Complete the Punnett square to show the possible genotypes of offspring.

B Determine the probability of a child inheriting hemophilia.

C How would this probability differ if the mother had hemophilia instead of the father?




For part A, write each of the parents' chromosomes on the outside of the Punnett square and fill in the boxes with the genotypes. The completed square should look like this:

| | $X^h$ | Y |
|---|---|---|
| $X^H$ | $X^HX^h$ | $X^HY$ |
| $X^H$ | $X^HX^h$ | $X^HY$ |

For part B, the probability of a child having hemophilia is zero. The boys will inherit the male Y chromosome, which does not carry the recessive hemophilia allele. However, because each daughter *must* inherit the father's X chromosome with its recessive *h* allele, all of the daughters will be heterozygous, or carriers. For part C, if the mother had hemophilia instead of the father, her genotype would be $X^hX^h$. Any male child of the couple would have hemophilia and any daughter would be a carrier.

## IT'S YOUR TURN

**Please read each question carefully. For a multiple-choice question, circle the letter of the correct response. For a constructed-response question, write your answers on the lines.**

1 The gene for seed shape in pea plants has two alleles, resulting in either smooth or wrinkled peas. A pea plant with one *smooth* allele and one *wrinkled* allele produces only smooth peas. Based on this information, which conclusion can be drawn?

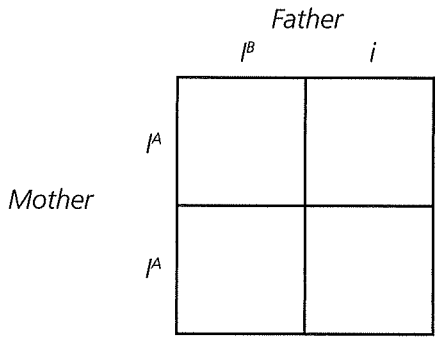
A Both alleles are co-dominant.

B One allele is incompletely dominant.

C The allele for smooth seeds is recessive.

D The allele for wrinkled seeds is recessive.

***Complete the Punnett square below to help you answer questions 2 and 3.***




2 Which of the following describes the parents' phenotypes?

A The father has type O blood, and the mother has type B blood.

B The father has type B blood, and the mother has type A blood.

C The father has type O blood, and the mother has type A blood.

D The father has type B blood, and the mother has type AB blood.

3 Which of the following correctly predicts their child's chance of inheriting a blood type?

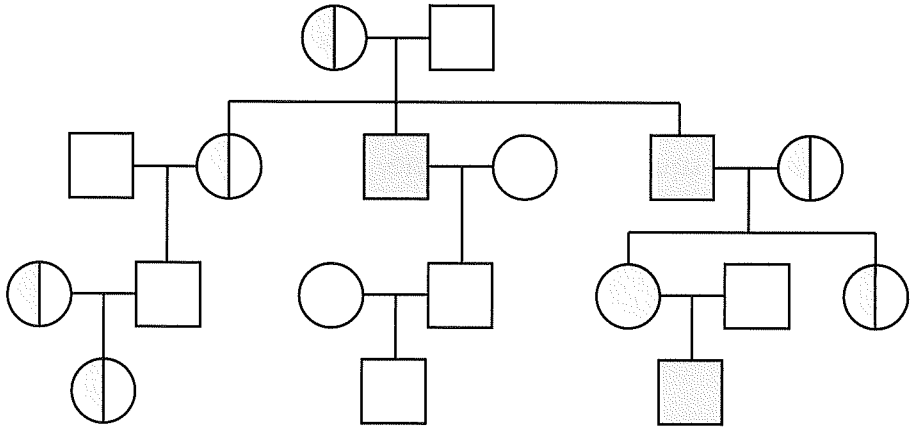
A The child has a 0% chance of inheriting the B blood type.

B The child has a 25% chance of inheriting the A blood type.

C The child has a 50% chance of inheriting the O blood type.

D The child has a 75% chance of inheriting the AB blood type.

***Use the pedigree chart below to answer question 4.***



4 What is the **most likely** pattern of inheritance for the trait indicated by the shaded figures?

A simple recessive

B simple dominant

C X-linked recessive

D X-linked dominant

5 Fruit flies normally have red eyes. A recessive allele causes some fruit flies to have purple eyes. Which statement describes the purple-eyed offspring of a red-eyed parent and a purple-eyed parent?

A The offspring has two recessive alleles located on the same chromosome.

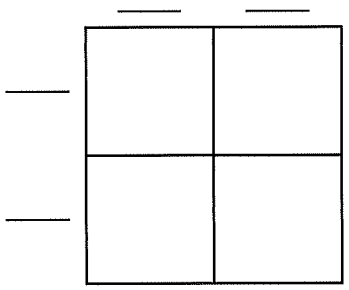
B The offspring has two chromosomes with a recessive allele present on each.

C The offspring has one dominant and one recessive allele located on the same chromosome.

D The offspring has one chromosome with a dominant allele and one chromosome with a recessive allele.

6 Red-green color blindness is the inability to distinguish the colors red and green. The gene for this trait is located on the X chromosome. The allele for normal color vision ($X^B$) is dominant and the allele for color blindness ($X^b$) is recessive. A color-blind woman and a man with normal color vision plan to have their first child.

A Complete the Punnett square for the couple.



B Identify the phenotypes represented in the Punnett square and percentage probability for each phenotype.

C The woman has an ultrasound and determines that the child is male. Has the probability of having a color-blind child changed? Explain.

LESSON 2

# Mutations and Chromosome Abnormalities

BIO.B.2.1.2, BIO.B.2.3.1, BIO.B.3.1.3

For most genes, there exist at least two alleles in a population's "gene pool." Alleles that are not passed on to offspring can be lost from a population. New alleles result from mutations in genes and chromosomes. A **mutation** is a permanent change in genetic material that may be passed from parents to offspring. Mutations are the source of genetic variety within populations and species.

A **mutation** is a change in a DNA sequence. Mutations are the source of the different alleles found in a species or population.

## Mutations in Genes

DNA encodes genetic information that specifies how proteins should be assembled. The sequence of bases (A, C, G, and T) in a gene spells out the order of amino acids in the protein. A mutation in the DNA sequence of a gene can result in a different protein being made, or even no protein at all. The type and severity of the change in the protein depends on the type of mutation that has occurred.

Mutations can occur in any cell of the body. However, only mutations in the cells that give rise to gametes may be passed on to offspring.

Recall that amino acids are represented by triplets of bases called *codons*. Sometimes, a single amino acid may be represented by more than one codon. For example, the codons TTA and TTG both code for the amino acid leucine (LEU). What would happen if the base G in the sequence below mutated to an A? The gene sequence would be different, but the same protein would be made. Because this type of mutation does not cause a change in the protein, it is called a *silent mutation*.

A codon is a set of three nucleotide bases that specify an amino acid.

Original protein sequence: ARG — **LEU** — HIS — MET — TYR
**Original DNA sequence:** CGA — TT**G** — CAC — ATG — TAT
↓
**New DNA sequence:** CGA — TT**A** — CAC — ATG — TAT
New protein sequence: ARG — **LEU** — HIS — MET — TYR

A *silent mutation* in DNA does not change the resulting protein.

What if the second base in the same codon were changed to a C? The new codon specifies a different amino acid. When the protein is assembled, the amino acid serine will be substituted for leucine. This may have a positive, negative, or neutral effect on phenotype. Because the "meaning" of the codon changes, this type of mutation is called a *missense mutation*.

Original protein sequence: ARG — **LEU** — HIS — MET — TYR
**Original DNA sequence:** CGA — TT**G** — CAC — ATG — TAT
↓
**New DNA sequence:** CGA — T**C**G — CAC — ATG — TAT
New protein sequence: ARG — **SER** — HIS — MET — TYR

A *missense mutation* changes one amino acid in the resulting protein.

*Stop* codons tell the ribosome that it has reached the end of the gene sequence on the mRNA strand. A *nonsense mutation* is one that changes a codon into a *stop* codon. This ends translation before the entire protein is assembled, resulting in a shortened protein.

A *nonsense mutation* inserts a *stop* codon and shortens the resulting protein.

Original protein sequence: ARG — LEU — HIS — MET — TYR
Original DNA sequence: CGA — TTG — CAC — ATG — TAT
↓
New DNA sequence: CGA — TAG — CAC — ATG — TAT
New protein sequence: ARG — *stop* —

Some mutations insert or delete nucleotides in a gene. If three (or a multiple of three) bases are added or removed, the number of codons changes slightly. However, if the number of inserted or deleted bases is *not* a multiple of three, this changes how the bases are grouped into codons. This is called a **frame-shift mutation,** and it results in changes to the amino acids assembled after the mutation.

A **frame-shift mutation** changes how bases are grouped into codons, or the *reading frame* of the gene.

Original protein sequence: ARG — LEU — HIS — MET — TYR
Original DNA sequence: CGA — TXG — CAC — ATG — TAT
↓
New DNA sequence: CGA — TGC — ACA — TGT — ATC
New protein sequence: ARG — CYS — THR — CYS — ILE

A mutation causes six nucleotides to be inserted at one location into the DNA that encodes a protein. How may the resulting protein be affected?

A It may gain two amino acids or it may lose two amino acids.

B It will have different amino acids starting at the mutation site.

C It may gain two amino acids or it may be shortened at the mutation site.

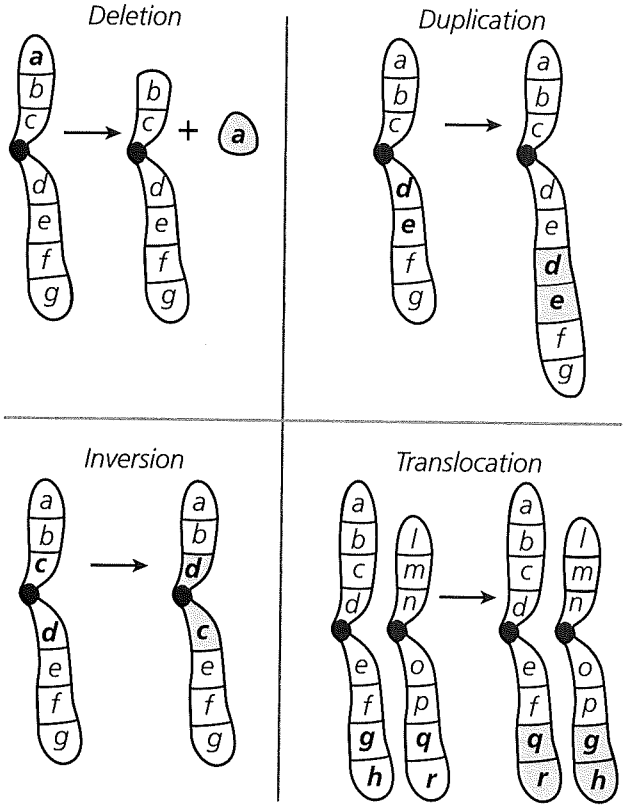
D It will have two different amino acids but the same number of total amino acids.

The insertion of six nucleotides adds two codons to the DNA sequence. The protein can lose two amino acids only if bases are removed rather than added; choice A is incorrect. The protein has different amino acids starting at the mutation site only if a frame-shift occurs. However, because six is a multiple of three, the remaining bases will be grouped as they were originally and the remaining protein will be the same; choice B is incorrect. Only missense mutations, in which bases are changed rather than added, can alter two amino acids while conserving the total number of amino acids; choice D is incorrect. Choice C is correct; if the codons specify amino acids, two amino acids will be added, but none will be lost. If one of the codons is a stop codon, the protein will be shortened at the mutation site.

## Chromosomal Mutations and Rearrangements

Just as the bases making up a gene may be altered, so can entire chromosomes. Pieces of a chromosome may be deleted, duplicated, inverted, or swapped among different chromosomes.

A chromosomal *deletion* occurs when a segment of chromosome is lost, removing tens or hundreds of genes. In contrast, a *duplication* occurs when a part of the chromosome is repeated. These genes occur twice on the chromosome. In an *inversion,* a chromosome segment is flipped in the reverse direction.




**Chromosomes as well as genes can undergo mutation in several ways.**

Sometimes, a segment of one chromosome may move to join another chromosome. This is called a **translocation.** A translocation may involve a single segment moving to a new location, or two segments of different chromosomes may trade places.

A chromosomal *deletion* removes a large segment of genetic material.

A chromosomal *duplication* causes genes to be repeated on the same chromosome.

A chromosomal *inversion* flips the order of genes on a chromosome.

A chromosomal **translocation** moves segments from one chromosome to another, sometimes exchanging genetic material between two chromosomes.

Chromosomal mutations that occur in normal body cells may disrupt the cell cycle and lead to cancer.

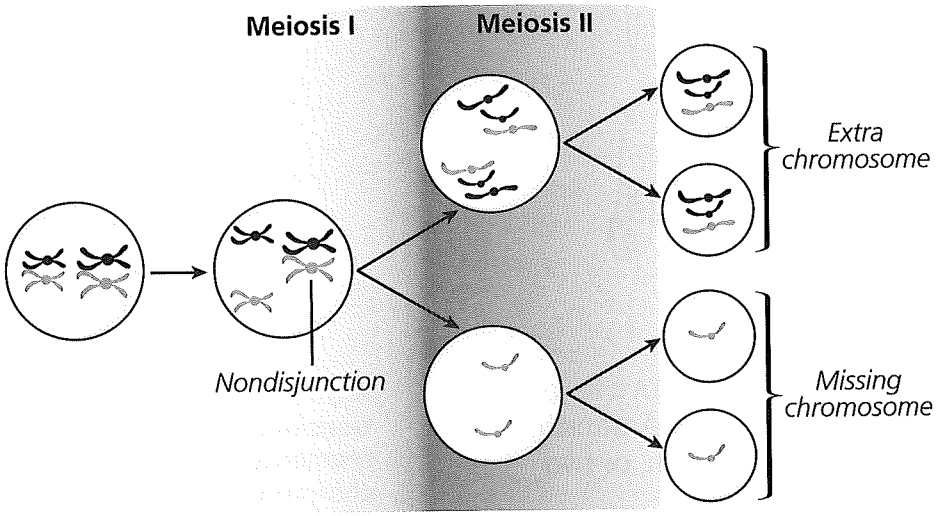
Which types of chromosomal mutations are likely to have more severe effects, and which are likely to have less severe effects, on the health of the individual? Explain.

Deletions and duplications are likely to have more severe health consequences, while inversions and translocations are likely to have less severe effects. A deletion or duplication changes the number of alleles present for the genes involved. An inversion or translocation simply moves alleles without deleting them, keeping their numbers the same.

## Changes in Chromosome Number

Every species has a characteristic number of chromosomes. A missing or extra chromosome alters this number and causes medical conditions ranging from moderate to severe. Abnormal chromosome numbers result from errors that may occur during either stage of meiosis.

In meiosis I, pairs of homologous chromosomes exchange genetic material (cross-over) and then segregate into different daughter cells. If the chromosomes in a pair fail to separate properly, each daughter cell ends up with one more or fewer chromosomes than normal. The failure of chromosomes to properly separate is called **nondisjunction.**



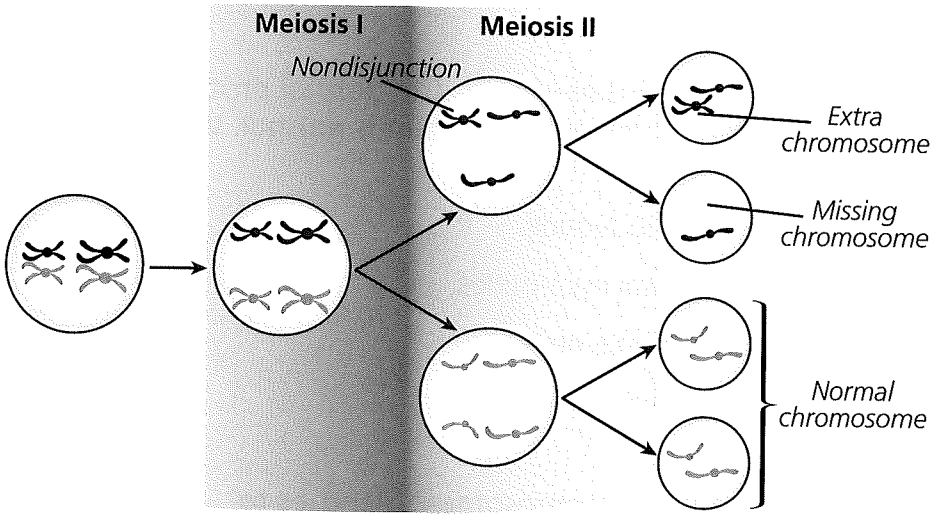

**If disjunction occurs during meiosis I, the daughter cells have either an extra chromosome or a missing chromosome.**

Meiosis is the cell division process that produces gametes (egg and sperm cells). In meiosis, the pairs of homologous chromosomes separate and each daughter cell has half the normal number of chromosomes.

**Nondisjunction** is the failure of chromosomes or chromatids to separate during meiosis or mitosis.

Chromosome number abnormalities are usually so severe that the embryo is miscarried. One exception is Down syndrome, caused by an extra copy of chromosome 21.

In meiosis II, pairs of sister chromatids separate into different daughter cells. Here, too, nondisjunction can occur if sister chromatids remain together.




**If disjunction occurs during meiosis II, the daughter cells may have an extra chromosome, a missing chromosome, or the normal number.**

During the formation of a human gamete, the homologs of chromosome 18 pair up and crossing-over occurs between them. However, they fail to separate when the cell divides. How will this affect the gametes that form?

When a nondisjunction event occurs in meiosis I, one of the daughter cells gains both homologs and the other lacks any. All of the gametes that form have either one extra chromosome or one missing chromosome.

## IT'S YOUR TURN

**Please read each question carefully. For a multiple-choice question, circle the letter of the correct response. For a constructed-response question, write your answers on the lines.**

1 A mutation results in a protein that is one-third as long as the normal protein. However, the amino acid sequence for the translated part of the protein is normal. Which best describes the mutation that occurred?

A It was a silent mutation that altered a single nucleotide.

B It was a missense mutation that inserted several nucleotides.

C It was a nonsense mutation that replaced a single nucleotide.

D It was a frame-shift mutation that deleted several nucleotides.

2 Alagille syndrome results when a segment of chromosome 2 attaches to chromosome 20, and a segment of chromosome 20 attaches to chromosome 2. What type of chromosomal mutation causes this disorder?

A deletion

B duplication

C inversion

D translocation

***Use the diagram to answer question 3.***

**PARTIAL KARYOTYPE FROM INFANT BODY CELL**


3 A full karyotype is an image of all the chromosomes present in a cell, while a partial karyotype shows only some of the chromosomes. The partial karyotype shown above is from an infant born with a rare disorder. Only chromosomes 10, 11, 17, and 18 are shown. Which event caused the disorder?

A nondisjunction

B chromosome duplication

C separation of sister chromatids

D segregation of homologous chromosomes

***Use the table and diagram below to answer question 4.***

**DNA CODONS FOR SEVERAL AMINO ACIDS**

| Amino Acid | Codons |
|---|---|
| Arginine (ARG) | CGA, CGC, CGG, CGT, AGA, AGG |
| Asparagine (ASP) | GAC, GAT |
| Glycine (GLY) | GGA, GGC, GGG, GGT |
| Glutamic acid (GLU) | GAA, GAG |
| Isoleucine (ILE) | ATA, ATC, ATT |
| Proline (PRO) | CCA, CCC, CCG, CCT |
| Tyrosine (TYR) | TAC, TAT |

**MUTATION IN A GENE SEQUENCE**

Original DNA sequence: TAT — ATC — CCG — GAC — GAA

↓

New DNA sequence: TAT — ATC — CCC — GGA — CGA

4 The mutation shown occurs in a skin cell of a coyote belonging to a population in the Northeastern United States. The mutation has a neutral effect on the cell.

A Identify the type of mutation and describe how it affects the protein that is produced in the skin cell.

B Will the mutation be passed on to the coyote's offspring? Explain.

C If the mutation were passed on to offspring, how would it affect the gene pool of the coyote population?

LESSON 3

# Genetic Engineering

BIO.B.2.4.1

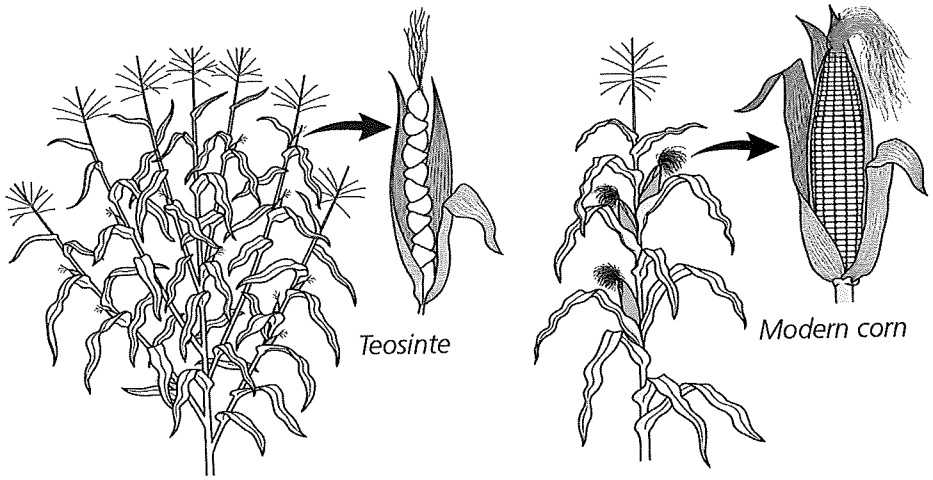
Only recently have people discovered the ability to manipulate the *genomes* of other organisms by taking genes from one species and placing them in other species. This activity is so new that we are still debating whether it is safe and ethical to do so. However, humans have less directly changed organisms' genomes since prehistoric times, giving us our familiar crops, livestock, and pets.

Technology now allows us to sequence entire genomes. A *genome* refers to all the genetic information contained in the chromosomes of a species.

## Selective Breeding vs. Genetic Engineering

Since the dawn of civilization, humans have altered the genes of plant and animal species. By choosing and breeding organisms with useful traits, people transformed wild species into the livestock and crops that we still use today. For example, teosinte, a wild grass with small, tough seeds, was bred to produce ears of larger, tender kernels familiar to us as corn. By planting only the most desirable teosinte seeds, farmers selected for traits that differed from those of the rest of the species. Over time, the plant grown by the farmers was transformed into a genetically distinct species that we know as corn. This type of transformation is called **selective breeding.**

In **selective breeding,** people choose only organisms with desirable traits to reproduce, making the alleles for these traits more common. Selective breeding is also called *artificial selection.*




**Wild teosinte is the ancestor of domestic corn.**

A *hybrid* is a cross between two breeds or two closely related species. Crossing two varieties of wheat, for example, may result in a better wheat variety.

While selective breeding takes many generations and requires only simple tools, technological advances have allowed scientists to manipulate organisms' genes directly. Scientists have tools that allow them to remove a gene from one species and insert it into the genome of another, combine parts of genes in new ways, and use genes to improve medicine and agriculture. The use of technology to manipulate and change genes is called **genetic engineering.**

**Genetic engineering** involves directly inserting, removing, or altering an organism's DNA.

One use of genetic engineering is to make corn crops resistant to pests. The European corn borer is an insect that lays eggs on corn plants. The larvae then feed on the corn leaves, damaging the crop and causing it to produce poorer-quality ears of corn. To combat this pest, scientists turned to *Bacillus thuringiensis* (*Bt*), a species of soil bacteria that makes a protein that is deadly to the corn borer. By taking the protein's gene from *Bt* and inserting it into the cells of corn plants, scientists created a **genetically modified organism,** or **GMO.**

A **genetically modified organism (GMO)** contains DNA from other organisms. GMOs are also called *transgenic* organisms because they contain *transgenes,* or genes from other species.

Genetically modified organisms, such as *Bt* corn, raise safety and environmental concerns. Although the transgenic protein in *Bt* corn has been found safe for both humans and wildlife, consumers still want GMO foods to be labeled so that they may decide for themselves whether to consume it.

The impact of GMOs on the environment is also a concern. The *Bt* protein is very specific to European corn borers. Reducing this insect's numbers may increase those of its competitors or have other unintended effects on the ecosystem.

Which is **most likely** an example of a genetically modified organism?

A a blue violet that is grafted to an African violet

B a hybrid dog crossbred from a pug and a beagle

C a bacterium that contains DNA from another bacterium

D a microorganism that develops resistance to an antibiotic

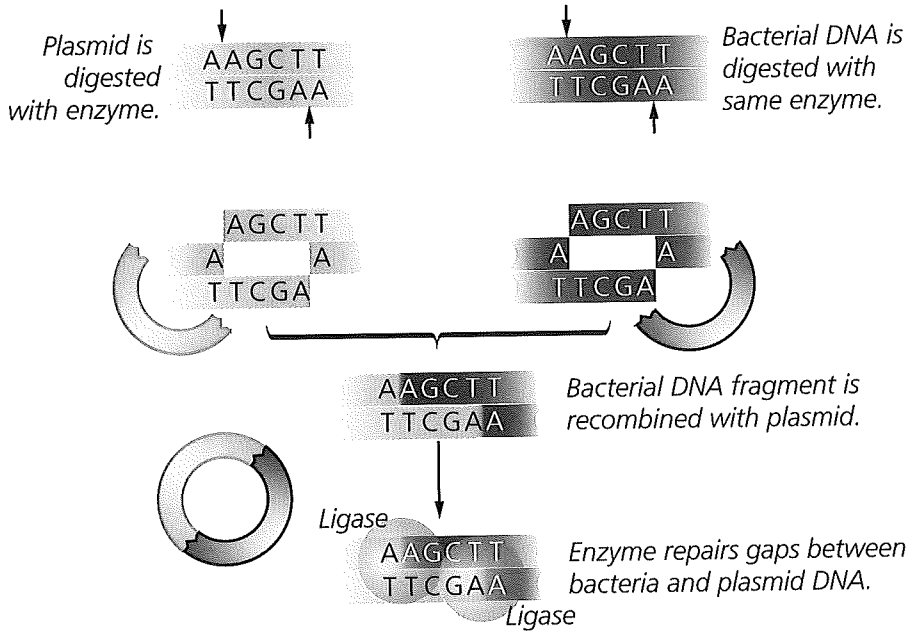
A genetically modified organism contains DNA that has been introduced, using technology, from another source. Grafting two violets does not change their DNA, so choice A is incorrect. Producing a hybrid dog does not involve introducing DNA from another species, so choice B is incorrect. Antibiotic resistance develops from selection on an existing mutation, so choice D is incorrect. Choice C, a bacterium with foreign DNA, is most likely to be a GMO.

## Gene Splicing

Genes, which are pieces of DNA, can be moved from place to place using enzymes. Special enzymes are able to digest, or cut, DNA at specific base sequences. For example, the enzyme *Hin*dIII (hindy-three) recognizes the sequence AAGCTT. If this sequence occurs on both ends of a gene, the enzyme can be used to cut the gene out of the surrounding DNA.

An enzyme is a protein that catalyzes a reaction. Enzymes are used to cut DNA at specific sites and bind pieces of DNA together.

The gene can then be inserted into a *plasmid,* a naturally occurring piece of circular DNA that is exchanged between bacterial cells. Scientists take advantage of plasmids as vehicles for recombinant DNA. Cutting the plasmid with the same enzyme allows the gene to insert itself into the plasmid. Cutting and recombining a gene in this way is known as **gene splicing.**




**Gene splicing cuts a gene out of the surrounding DNA and inserts it into a plasmid. Enzymes cut and bond pieces of DNA.**

Inserting a gene into a plasmid makes it more useful. The plasmid can be inserted into bacteria or other organisms. To make GMO corn, scientists inserted the plasmid with the *Bt* gene into cultured corn plant cells and allowed the cells to incorporate the DNA into their genomes. Plants grown from these genetically modified cells contain the *Bt* transgene in each of their cells.

Why does using the same enzyme to digest DNA allow the DNA to combine?

The enzyme produces ends that have complementary base pairs, allowing the ends of different pieces of DNA to join together.

## Genetic Engineering and Health

Recombinant DNA is useful in making vaccines. Vaccines work by exposing a person's immune system to a *pathogen,* such as a virus or bacterium. Once exposed, the immune system is able to recognize that pathogen and will quickly attack and destroy it should it infect the person again. Vaccines expose a person to a pathogen without actually transmitting the disease. Exposure to

In **gene splicing,** DNA is cut apart and recombined in different ways. *Recombinant DNA,* combined from several sources, is created in this way.

Notice that the sequence recognized by the enzyme is the same on both DNA strands. Although the rest of the DNA is different, the ends have identical single-stranded regions. This allows different pieces of DNA, cut by the same enzyme, to be joined together.

The cellular machinery of bacteria is used to do much of the work of genetic engineering. For example, inserting a plasmid into a single bacteria and allowing it to divide results in a population of cells that contain the plasmid. The cells can then be destroyed to remove the plasmid copies.

Scientists can grow plant and animal cells as single cells in nutrient-containing liquid. These are known as *cell cultures.*

*Pathogens* are disease-causing organisms. They include viruses and bacteria.

even a small part of the pathogen, such as a single protein, is enough to give a person immunity.

Scientists use recombinant DNA to make vaccines. They isolate the gene for a protein from the virus or bacteria and place the recombinant DNA into another cell, such as a yeast cell. The yeast cell incorporates the recombinant DNA into its own genome and expresses the gene. The protein it produces is used to vaccinate against the pathogen.

More recently, scientists have tried using genetic engineering to treat people with genetic disorders. Cystic fibrosis, for example, is caused by a mutation in the gene for an ion channel protein. This causes mucus to build up in the lungs and other organs. Every cell in a cystic fibrosis patient's body has the nonfunctioning allele, although not every cell needs to produce the protein.

Genetic engineering is also used to produce the insulin hormone, which is a protein. The gene for human insulin is cut and spliced into a plasmid, which is then taken up by bacteria cells. The bacteria make the hormone, which is processed and sold as medicine.

**Gene therapy** tries to insert functional genes into the cells that need them. Of course, it is difficult to place recombinant DNA into the nuclei of human cells. Scientists must first determine an appropriate *vector* (vehicle) that can deliver the DNA into patients' cells. For cystic fibrosis, scientists have tried using a modified cold virus. By placing a working copy of the gene into the virus, and allowing the virus to enter the lungs, scientists hope that the gene will insert itself into the lung cells' genetic material. An effective gene therapy for cystic fibrosis is still being developed.

**Gene therapy** changes the DNA of a person with a genetic disease by introducing working genes into cell nuclei.

Which disorder would be the **best** target for gene therapy?

A type II diabetes, which is influenced by diet and genetics

B high blood pressure, which is influenced by multiple genes

C hemophilia, which is caused by a gene on the X chromosome

D Lyme disease, which is caused by bacteria transmitted by ticks

Because gene therapy replaces a nonfunctioning gene, the best target is a disease caused by a single, known gene. Type II diabetes and high blood pressure are influenced by multiple genes and/or unidentified genes, and so would make poor targets for gene therapy. Lyme disease is caused by a pathogen, rather than a gene. Hemophilia, choice C, is the best target for gene therapy because it is caused by a single gene.

## DNA Technology in Forensics

One major application of genetic technology is in **forensics,** the investigation of crimes. Both criminals and victims leave DNA evidence at the scene of a crime and, possibly, on each other. Each individual has a sort of DNA "fingerprint."

**Forensics** is the use of science and technology to investigate and solve crimes.

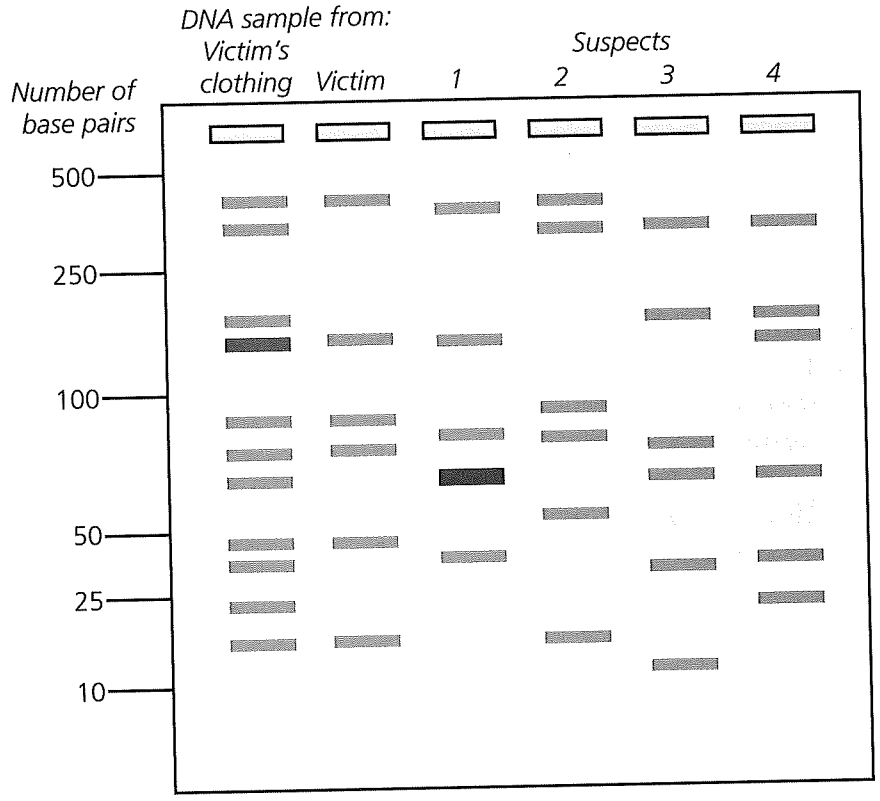
Amazingly, most of the DNA in the human genome is identical from one person to the next. Only a very small percentage varies. In order to identify individuals on the basis of DNA, scientists need to examine variable regions of the genome. One type of variable region consists of short, repeated DNA sequences (STRs) that are not part of a gene. Each repeat consists of between two and five bases. They are arranged end-to-end and repeat a different number of time in different individuals. For example, the STR sequence GATA may repeat between 6 and 15 times.

Allele 1: GATAGATAGATAGATAGATA
Allele 2: GATAGATAGATAGATAGATAGATAGATAGATAGATAGATA...

**Two alleles of the STR GATA show different numbers of repeats.**

STRs occur in thirteen different *loci* (places in the genome), providing a good source of measureable variation for forensics. While two people may share the same alleles at one locus, they are less likely to do so at two loci, and even less likely at more loci. Therefore, examining STRs at several different loci allows investigators to distinguish the DNA from different individuals.

To examine STRs, investigators make multiple copies of the DNA at different STR loci. They use *gel electrophoresis* to separate the DNA fragments on the basis of size. By matching individuals' DNA with blood samples, investigators can determine the source of blood, saliva, or hair found at a crime scene.




**This electrophoresis gel shows DNA from three different STR loci, each represented by two alleles. The DNA on the victim's clothing comes from more than one source.**

STR stands for *short tandem repeat.* These nongenetic DNA sequences differ among individuals, making them useful in identification.

CODIS is the FBI database that stores DNA fingerprints. CODIS stores information on alleles at 13 different STR loci for each person on file.

Sometimes, there is little or poor-quality DNA at a crime scene. *Polymerase chain reaction,* or PCR, is a technique that makes multiple copies of even miniscule amounts of DNA. Making multiple copies of DNA fragments allows them to be visualized on an agarose gel.

*Gel electrophoresis* separates DNA by size. DNA that has been amplified by PCR is loaded into the little "wells" at the top of the electrophoresis gel. An electric current applied to the gel causes the DNA fragments to move toward the other end. Small fragments move more quickly than larger fragments.

DNA fingerprinting is also used to determine paternity (identify the father of an infant).

Examine the electrophoresis gel image on page 152. The victim of this crime wounded the suspect, whose blood stained the victim's clothing. Which suspect is the source of the DNA?

A 1

B 2

C 3

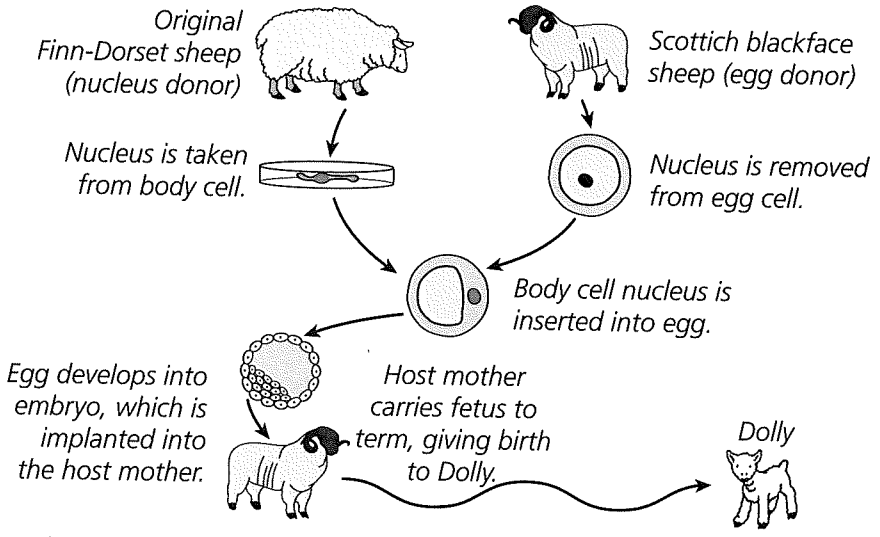
D 4

The DNA on the victim's clothing comes from multiple sources. One source is the victim: Notice how all the DNA fragments from the victim also appear on the clothing. Ignore these fragments, and match the remaining fragments with one of the suspects. The DNA from suspect 4 matches the remaining fragments. Choice D is correct.

## Cloning

Normally, a sexually reproducing organism inherits its genes from different parents and is genetically distinct from both of them. In contrast, reproductive **cloning** attempts to create animals that are genetically identical. All of the genes and chromosomes in the clone must be from the original animal.

To clone a mammal, scientists use a nucleus from one of the animal's body cells. They also need an egg cell to accept the nucleus and a host mother to gestate the offspring. The nucleus is removed from the egg cell, and the nucleus from the original animal's cell is inserted into the egg. The egg cell now has a full set of chromosomes. It is allowed to develop into an embryo, which is then inserted into the uterus of the host mother. The resulting offspring is genetically identical to the animal that donated the nucleus.




**Three different animals were used in the cloning of Dolly.**

Reproductive **cloning** is the creation of a genetically identical organism. The first cloned animal, Dolly the sheep, was born in 1996.

Dolly the sheep was cloned through *somatic cell nuclear transfer* (SCNT). The somatic (body) cell's nucleus is transferred to an egg cell, and must be specially treated to encourage it to develop. Cloning Dolly required creating several hundred embryos in this way, most of which were not successful.

Cloning animals is still a difficult process and most cloned embryos do not develop successfully. Despite this, there are several reasons why people might want to clone an animal. A farmer might want more of a certain livestock animal with particularly good traits, or a person might want a clone of a favorite pet that has passed away. However, because the environment also influences development, a cloned animal's phenotype will not be identical to the original in every way.

Another reason for cloning has to do with preserving endangered species and bringing back extinct species. Ecologists worry, however, that cloning will discourage people from protecting endangered species' habitats. Habitat destruction is the leading cause of species decline. If animals can simply be cloned, why be concerned with habitat protection? So far, however, cloning has not played a major role in wildlife conservation.

Creating a clone of an extinct species is especially difficult because an intact cell nucleus is needed. The wooly mammoth is one species that scientists have considered cloning. Scientists are trying to isolate viable cells from frozen mammoths. The nucleus of a mammoth cell would need to be transferred to a donor egg from a suitable, closely related species, which would then need to act as the host mother. Even if cloning a mammoth were successful, it is not certain how well the animal would survive outside of captivity.

In 2001, scientists cloned a cowlike animal called a gaur. Gaurs are endangered and the scientists hoped that cloning would help preserve the species. However, the cloned gaur died soon after birth due to unrelated causes.

Mitochondria contain their own DNA. A fertilized egg's mitochondria are contributed by the egg cell, but not the sperm cell. Which two sheep in the diagram on page 153 have identical mitochondrial DNA?

A the egg donor and Dolly

B the host mother and Dolly

C the egg donor and the host mother

D the original Finn-Dorset sheep and Dolly

Dolly inherits mitochondrial DNA from the mitochondria in the egg cell. These mitochondria are identical to those in the egg donor. Choices B and D are incorrect because neither the original sheep nor the host mother contribute an egg cell. Choice C is incorrect because, although these are both Scottish blackface sheep, they do not necessary have the same mitochondria. Choice A is correct.

## IT'S YOUR TURN

**Please read each question carefully. For a multiple-choice question, circle the letter of the correct response. For a constructed-response question, write your answers on the lines.**

1 Which of the following is **not** an example of genetic engineering?

A An agricultural scientist creates a hybrid strain of rice by crossing two rice varieties.

B A biology student inserts plant DNA into bacteria to determine its role in the cell cycle.

C A vaccine manufacturer inserts a plasmid containing a gene from a virus into yeast cells.

D A medical researcher isolates a functional copy of a muscular dystrophy gene for gene therapy.

2 Which is the **most** challenging step in developing effective gene therapy for human diseases?

A determining the DNA sequence for the gene

B delivering the gene into the cells of the body

C splicing the functional gene involved in the disorder

D determining which disorders can be cured by gene therapy

3 A scientist uses enzymes to splice genetic DNA into a plasmid, and then inserts the plasmid into a cell. Which of the following is **most likely** an application of this process?

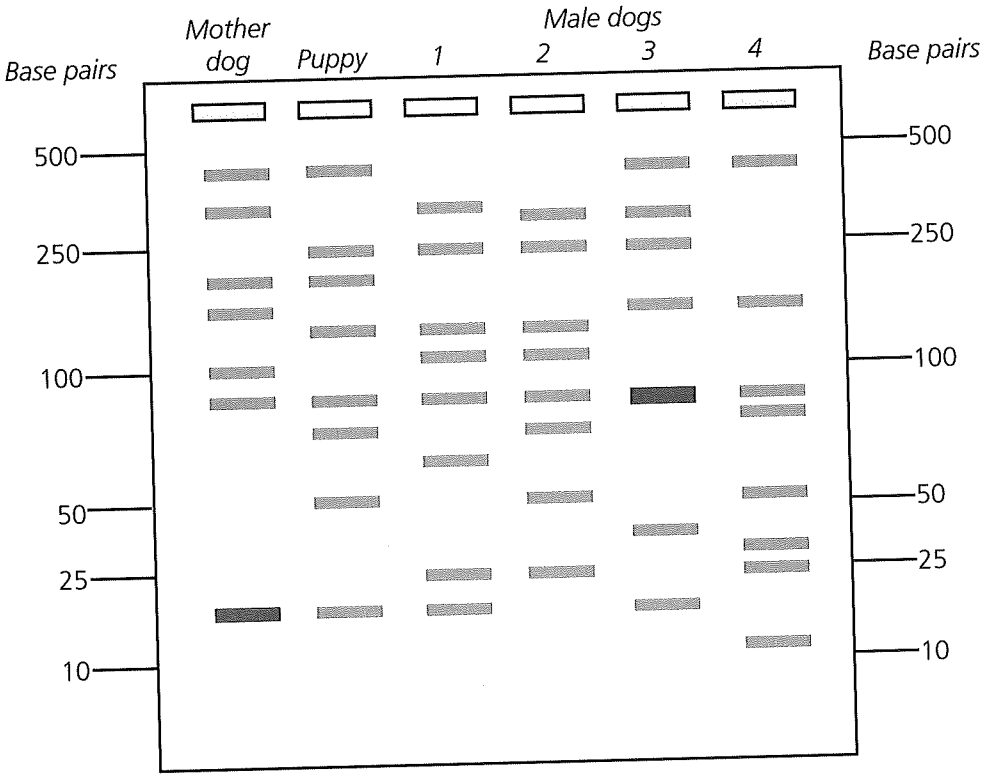
A producing an exact genetic clone of a prized racehorse

B producing a vaccine against the human papillomavirus

C determining which of several rice varieties should be crossed

D determining whether a suspect's blood was present at a crime scene

***Use the diagram below to answer question 4.***




4. A purebred dog has a litter of puppies. The dog's owners are not sure which dog is the father of the puppies. They hire a scientist to identify the father through DNA fingerprinting. The scientist takes blood samples from four dogs and examines STRs at several different loci. She amplifies the amount of DNA at each STR and separates the resulting DNA fragments using gel electrophoresis. The resulting gel, with DNA fragments visible as bands at different locations, is shown above.

   A. How many STR loci were examined by the scientist? Explain. (Keep in mind that a single STR locus has two alleles.)

B Why are the DNA bands located at different positions in each lane?

C Which male dog is the puppy's father? Explain your choice.