chapter 13 Genetics and Biotechnology

section 1 Applied Genetics

Before You Read

Imagine that you could design the perfect dog. What color would it be? Would it be big or small? On the lines below, describe the traits your dog would have. In this section, you will learn how selective breeding produces certain traits.

MAIN Idea

Selective breeding is used to create animals or plants with certain traits.

What You'll Learn

- how inbreeding differs from hybridization
- how to use test crosses and a Punnett square to find the genotypes of organisms

Read to Learn

Selective Breeding

For thousands of years, people have been breeding animals and plants to have certain traits. For instance, some dogs, such as huskies, have been bred to be strong runners. Other dogs, such as Saint Bernards, have been bred to have a good sense of smell.

People have also bred plants, such as tomatoes, apples, and roses, to taste better, resist disease, or produce fragrant flowers. **Selective breeding** is the process used to breed animals and plants to have desired traits. As a result of selective breeding, desired traits become more common.

What is hybridization?

A hybrid is an organism whose parents each have different forms of a trait. For instance, a disease-resistant tomato plant can be crossed with a fast-growing tomato plant. The offspring of the cross would be a tomato plant that has both traits. The hybrid is disease resistant and grows quickly.

Hybridization is the process of making a hybrid organism. Hybridization is expensive and takes a long time, but it is a good way to breed animals and plants with the right combination of traits.

Study Coach

Create a Quiz After you read this section, create a five-question quiz from what you have learned. Then, exchange quizzes with another student. After taking the quizzes, review your answers together.

Reading Check

1. **Name** an advantage of hybridization.

How is inbreeding used?

Inbreeding is another example of selective breeding. **Inbreeding** occurs when two closely related organisms that both display the desired trait are bred. Inbreeding can be used to ensure that the desired trait is passed on. Inbreeding can also eliminate traits that are not desired.

Purebred animals are created by inbreeding. Clydesdale horses are an example of a purebred animal. Clydesdale horses were first bred in Scotland hundreds of years ago. They were bred for use as farm horses that could pull heavy loads. All Clydesdales have the traits of strength, agility, and obedience.

A disadvantage of inbreeding is that harmful traits can be passed on. Harmful traits are usually carried on recessive genes. Both parents must pass on the recessive genes for the harmful traits to appear in the offspring. Inbreeding increases the chance that both parents carry the harmful traits.

Test Cross

Breeders need a way to determine the genotype of the organisms they want to cross before creating a hybrid. They use test crosses to find out the genotype of an organism. In a **test cross**, an organism whose genotype for a desired trait is unknown is crossed with an organism that has two recessive genes for the trait.

Reading Check

2. Explain What is the purpose of a test cross?

_____

_____

_____

When are test crosses performed?

An orchard owner might use a test cross to find out the genotype of a white-grapefruit tree. In grapefruits, white color is a dominant trait and red color is a recessive trait. A red-grapefruit tree has two recessive genes (*ww*). A white-grapefruit tree might have two dominant genes (*WW*), or it might have one dominant gene and one recessive gene (*Ww*).

Picture This

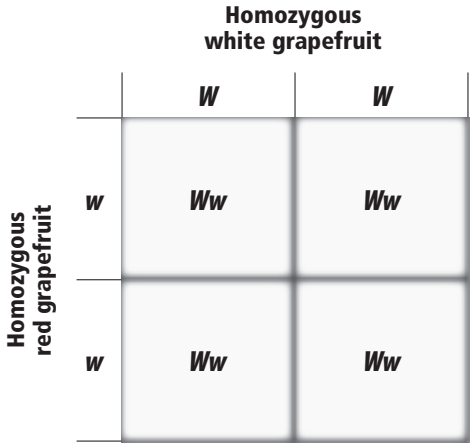
3. Label Fill in the phenotype with the word *white* or *red* for each genotype.

Genotype	Phenotype
Homozygous dominant (*WW*)	
Homozygous recessive (*ww*)	
Heterozygous (*Ww*)	

How does a test cross reveal the genotype?

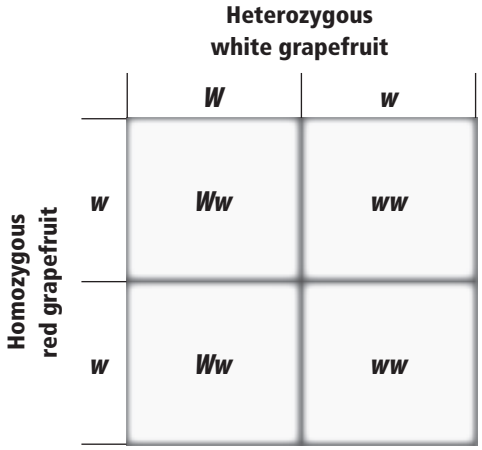
The orchard owner decides to do a test cross to find out the genotype of a white-grapefruit tree. The white-grapefruit tree is crossed with a red-grapefruit tree. The orchard owner uses a Punnett square to understand the results of the cross.

The figure below shows a Punnett square for the test cross if the white-grapefruit tree is homozygous, meaning it has two dominant genes (*WW*). All the offspring from the test cross will be heterozygous, meaning they will have one dominant and one recessive gene (*Ww*). All the offspring of the test cross are white-grapefruit trees.



What if the test cross involved the heterozygous tree?

The figure below shows a Punnett square for the test cross if the white-grapefruit tree is heterozygous (*Ww*). Half the offspring from the test cross will be white (*Ww*). Half the offspring from the test cross will be red (*ww*).



Picture This

4. Evaluate If you planted 100 seeds from this test cross, about how many would be white? How many would be red?

Picture This

5. Calculate If you planted 100 seeds from this test cross, about how many would be white? How many would be red?

chapter 13

Genetics and Biotechnology

section 2 DNA Technology

MAIN Idea

Genetic engineering manipulates recombinant DNA.

What You'll Learn

- the difference between selective breeding and genetic engineering
- how genetic engineering can be used to improve human health

Before You Read

The tools that a chef uses to prepare food differ from the tools a mechanic uses to fix cars. On the lines below, describe a few of the tools you use at home and school. In this section, you will learn about tools scientists use to study DNA.

_____

_____

Mark the Text

Main Ideas As you read, underline or highlight the main ideas in each paragraph.

Read to Learn

Genetic Engineering

For many years, scientists knew the structure of DNA and knew that information flowed from DNA to RNA and from RNA to proteins. In the last few decades, scientists have learned more about how individual genes work by using genetic engineering. **Genetic engineering** is a way of manipulating the DNA of an organism by inserting extra DNA or inserting DNA from another organism.

One example of genetic engineering uses green fluorescent protein (GFP). GFP is a protein made naturally in jellyfish. GFP causes jellyfish to turn green under ultraviolet light. Scientists have inserted the DNA for making GFP into other organisms. This makes the organisms glow.

Reading Check

1. State What do scientists have to do to a gene before they can manipulate it?

_____

_____

_____

DNA Tools

An organism's **genome** is all the DNA present in the nucleus of each cell. Genomes can contain millions of nucleotides in the gene's DNA. In order to study a specific gene, scientists isolate it from the rest of the organism's DNA. Scientists can then manipulate it. To understand how scientists do this, it is helpful to know the DNA tools scientists use.

What are restriction enzymes?

Scientists have found hundreds of restriction enzymes. **Restriction enzymes** are proteins made by bacteria. Each restriction enzyme cuts, or cleaves, DNA at a specific DNA sequence.

How do restriction enzymes work?

One restriction enzyme that is often used by scientists is called *EcoRI*. *EcoRI* cuts DNA containing the sequence GAATTC. After *EcoRI* cuts DNA, it leaves single-stranded ends, called *sticky ends,* as shown in the figure below. DNA that has been cut with *EcoRI* always has the same sticky ends. DNA fragments with sticky ends can be joined with other DNA fragments with complementary sticky ends.

Not all restriction enzymes leave sticky ends. Some restriction enzymes cut straight across both DNA strands, leaving blunt ends. DNA fragments with blunt ends can be joined to other DNA fragments with blunt ends.

How is gel electrophoresis used to separate DNA fragments?

After DNA is cut with a restriction enzyme, the DNA fragments are different sizes. Scientists use **gel electrophoresis** to separate DNA fragments according to the size of the fragments.

DNA fragments are placed on the negatively charged end of a material called gel. An electric current is applied to the gel. The DNA fragments move toward the positive end of the gel. Smaller fragments move through the gel faster than larger fragments. The unique pattern made by the DNA fragment can be compared to the patterns of known DNA fragments for identification. The figure below shows a gel in which DNA has been separated by electrophoresis.

Think it Over

2. Explain Why can two different fragments of DNA cut with *EcoRI* be joined?

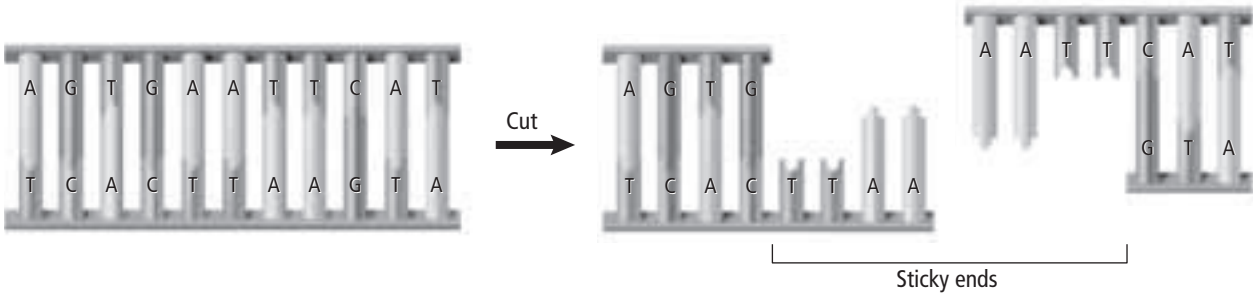
_____

_____

_____

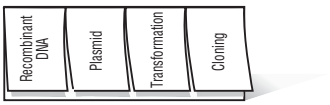
Picture This

3. Analyze Use the figure to explain to a partner how gel electrophoresis works.



FOLDABLES™

Take Notes Make a four-tab Foldable, as shown below. As you read, take notes and organize what you learn about recombinant DNA technology.



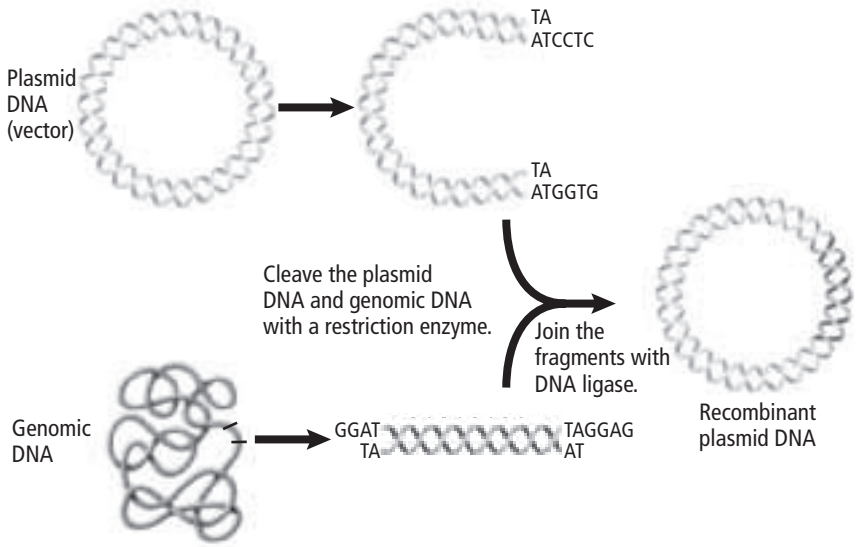
Picture This

4. Identify Circle the carrier in the figure.

Recombinant DNA Technology

Once DNA fragments have been separated using gel electrophoresis, fragments can be removed from the gel. These DNA fragments can then be combined with DNA fragments from another source, as shown in the figure below. This new DNA molecule, with DNA from different sources, is called **recombinant DNA**. Recombinant DNA allows scientists to study individual genes.

Scientists often need to make a lot of recombinant DNA to study it. Scientists use host cells, such as bacteria, to copy the recombinant DNA. A carrier, known as a vector, is used to carry the recombinant DNA into the host cell. One commonly used vector is a small, circular, double-stranded DNA molecule called a **plasmid**. Plasmids can be cut with restriction enzymes. DNA fragments and plasmids cut with the same restriction enzyme can be combined at their sticky ends. An enzyme called **DNA ligase** is then used to join the plasmids and the DNA fragments chemically.



How does transformation occur?

Plasmid DNA can be moved into bacterial cells by **transformation**. Transformation occurs when bacterial cells are heated or given a small electric shock. This creates holes in the plasma membrane of the bacterial cell, enabling the plasmid DNA to enter the bacterial cell.

Plasmids are found naturally in bacteria. When the bacteria reproduce and copy their own DNA, they also copy the plasmid DNA. **Cloning** occurs when bacteria reproduce and copy recombinant DNA molecules.

What is DNA sequencing?

DNA sequencing involves finding out the exact order of the nucleotides that make up an organism's DNA. Knowing the DNA sequence of an organism gives scientists clues about how that organism's genes work. Scientists can compare genes from different organisms. Scientists can also find errors in the DNA. Long DNA molecules must be cut with restriction enzymes before they can be sequenced.

Reading Check

5. Determine How are restriction enzymes used?

How is DNA sequenced?

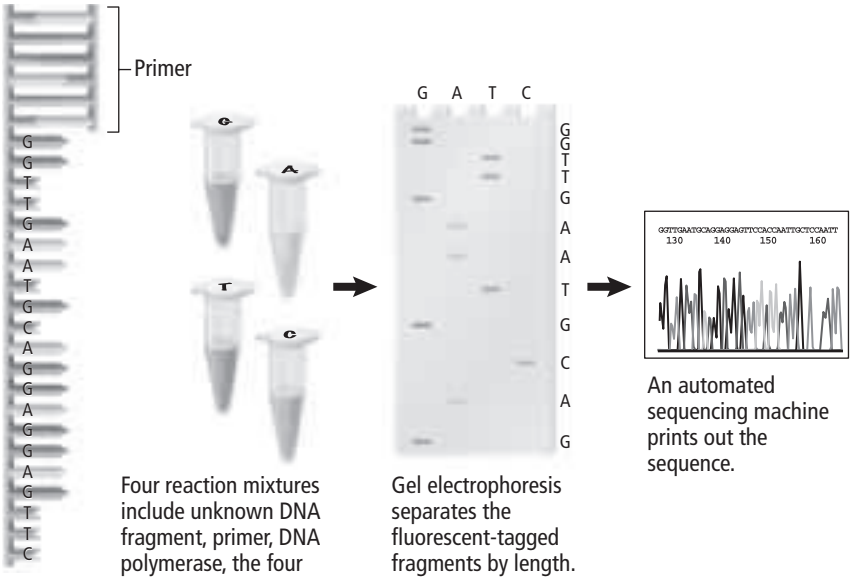
The figure below shows how DNA is sequenced. Scientists mix an unknown DNA fragment, DNA polymerase, and the four nucleotides—A, C, G, and T. Then they add a small amount of the four nucleotides, each tagged with a different color of fluorescent dye.

What stops the growth of a DNA strand?

Usually, when DNA polymerase copies the DNA fragment it will put normal nucleotides on the growing strand. However, sometimes a fluorescent-tagged nucleotide will be added to the strand. Every time these tagged nucleotides are added, the new DNA strand stops growing. This produces DNA strands of different lengths. The tagged fragments are separated by gel electrophoresis. An automated DNA sequencing machine is used to detect the color of each tagged nucleotide. The sequence of the original DNA is determined from the order of the tagged fragments.

Picture This

6. Identify Which step in the process separates DNA fragments by length?



Four reaction mixtures include unknown DNA fragment, primer, DNA polymerase, the four nucleotides, and a different tagged nucleotide.

Gel electrophoresis separates the fluorescent-tagged fragments by length.

An automated sequencing machine prints out the sequence.

What is polymerase chain reaction?

Polymerase chain reaction (PCR) can be used to make millions of copies of a specific region of a DNA fragment. PCR is so sensitive that it can detect a single DNA molecule in a sample. With PCR, scientists can copy a single DNA molecule many times so they can study it.

PCR is a powerful tool used by scientists. Forensic scientists use PCR to identify suspects and victims of crimes. Doctors use PCR to detect diseases such as AIDS.

Reading Check

7. Explain Why is polymerase chain reaction used to make millions of copies of a DNA fragment?

What are the steps of PCR?

Follow the figure below as you read the steps of PCR.

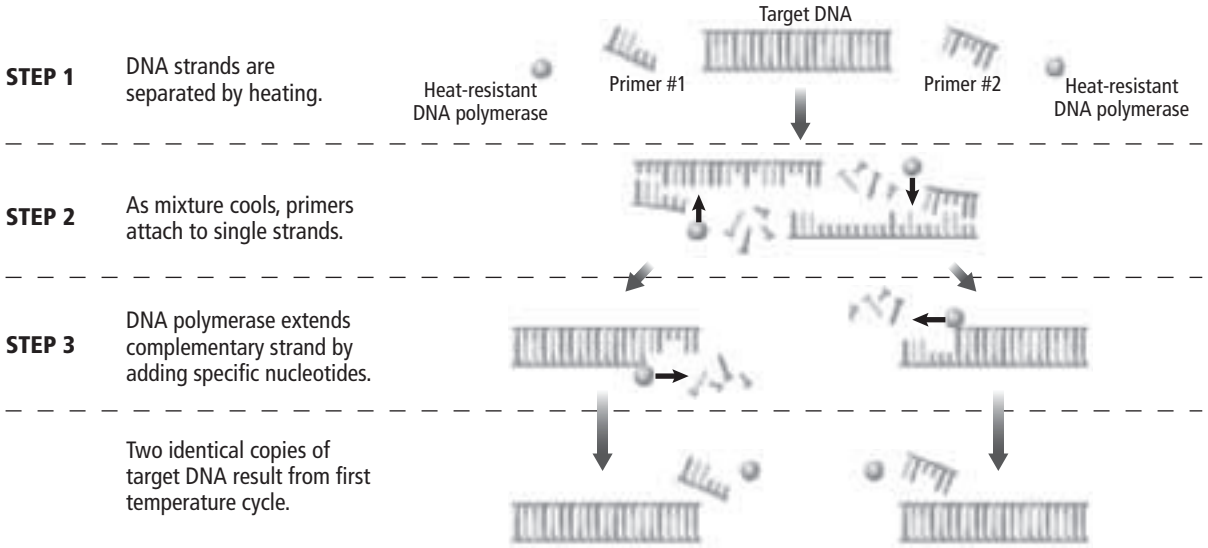
Step 1 Four things are mixed in a small tube: the DNA fragment to be copied, DNA polymerase, the four DNA nucleotides—A, G, C, and T—and two short, single-stranded pieces of DNA called primers. The primers are complements to the ends of the DNA fragment to be copied. The primers are used as starting points for the DNA copies.

Step 2 The tube is placed into a thermocycler. The thermocycler heats and cools the tube over and over again. When the tube is heated, the two strands of the DNA fragment separate. When the tube is cooled, the primers bind to the ends of the separated strands of the DNA fragment.

Step 3 Each primer binds to one strand of the DNA fragment. DNA polymerase then puts the correct nucleotides between the two primers making the copies. The DNA polymerase used in PCR must be able to withstand high heat. It comes from bacteria that live in hot springs, like the ones in Yellowstone National Park.

Picture This

8. Identify Underline the two starting points for the DNA copies.



Biotechnology

Biotechnology is the application of genetic engineering to human problems. Scientists can use biotechnology to produce transgenic organisms. **Transgenic organisms** are organisms that have a gene from a different organism inserted into their DNA. Transgenic animals, plants, and bacteria are used for scientific research, in agriculture, and to treat human diseases.

How are transgenic animals used?

Most transgenic animals are made in laboratories for biological research. Some commonly studied animals are mice, fruit flies, and roundworms. Scientists use these organisms to study diseases and develop ways to treat them.

Transgenic livestock are used to improve the food supply. They also are used to improve health in people. For instance, scientists have engineered goats to make a protein that stops blood from clotting. Doctors use this protein during surgery. Several species of fish have been genetically engineered to grow faster. In the future, transgenic animals might be used as a source of organs for organ transplants in people.

Reading Check

9. Identify one way scientists use transgenic animals.

How are transgenic plants used?

Transgenic crops are grown around the world. Farmers in at least 18 countries grow transgenic corn, soybeans, canola, and cotton on millions of acres. Farmers plant these crops because they are resistant to herbicides and insecticides. For example, farmers now plant genetically engineered cotton. The cotton has been engineered to resist bolls, insects that harm cotton plants.

Scientists have developed other transgenic crops. They are testing these crops in fields. One of these crops is a transgenic rice that is more nutritious than normal rice. Scientists hope to use the transgenic rice to decrease malnutrition in Asian countries. Scientists are also testing crops that are designed to survive extreme weather.

Reading Check

10. Explain What is one trait scientists have engineered into transgenic plants?

Someday, peanuts and soybeans might be developed that do not cause allergic reactions. Transgenic plants might be used to make vaccines or biodegradable plastics.

How are transgenic bacteria used?

Scientists use transgenic bacteria to make insulin, growth hormones, and other medical substances. Transgenic bacteria have been used to protect crops from frost damage and to clean up oil spills. Garbage in some landfills is being decomposed by transgenic bacteria.

chapter 13 Genetics and Biotechnology

section 3 The Human Genome

MAIN Idea

Genomes contain all of the information needed for an organism to survive.

What You'll Learn

- how forensic scientists use DNA fingerprinting
- how human genome information can help diagnose diseases

Before You Read

Scientists now study genes in ways that were not invented 20 years ago. Think of the new technology in your own life. What are some new technologies you use?

_____

_____

Study Coach

Make Flash Cards Make a flash card for each key term in this section. Write the term on one side of the card. Write the definition on the other side. Use the flash cards to review what you have learned.

Read to Learn

The Human Genome Project

A genome is all of the genetic information in a cell. The human genome is all of the genetic information in a human cell. The Human Genome Project (HGP) was an enormous project. One goal was to learn the sequence of the billions of nucleotides that make up human DNA. Another goal was to identify all 20,000 to 25,000 human genes.

The HGP was completed in 2003. Scientists will be working for many years to understand the data.

How was the human genome sequenced?

Human DNA is organized into 46 chromosomes. To determine the human genome, each chromosome was cut. Several restriction enzymes were used to make fragments with overlapping sequences. The fragments were combined with vectors and copied. The overlapping sequences were analyzed to generate a continuous sequence.

As scientists studied the sequences in the human genome, they observed that less than 2 percent of all of the nucleotides in the human genome code for all of the proteins in the body. The rest of the DNA is made of long stretches of repeated sequences called noncoding sequences. Scientists do not yet know the function of these sequences.

Applying Math

1. **Calculate** What percentage of human DNA is not made of genes?

_____

How is DNA fingerprinting used?

The protein-coding sections of DNA are almost identical from one person to the next. The long stretches of noncoding sections of DNA are unique to each individual. **DNA fingerprinting** uses gel electrophoresis to observe the patterns that are unique to each person.

Forensic scientists use DNA fingerprinting to identify suspects and victims in a crime. DNA fingerprinting has been used to convict criminals and free innocent people who were wrongly imprisoned. DNA fingerprinting can be used to identify soldiers killed in war and establish paternity.

When only a drop of blood or a single hair is found at a crime scene, the sample does not contain enough DNA for DNA fingerprinting. Forensic scientists use PCR to copy the DNA and make a larger sample. The DNA is then cut with restriction enzymes and separated by gel electrophoresis. The pattern of the fragments from the sample is compared with DNA samples from known sources, such as a suspect or a victim in a crime.

Identifying Genes

Once the genome has been sequenced, the next step is to identify the genes and determine their functions. Organisms, such as bacteria and yeast, do not have noncoding DNA. Scientists look for DNA sequences called open reading frames (ORFs). ORFs are made of codons—groups of three nucleotides that code for amino acids. ORFs begin with a start codon and end with a stop codon. In between the start and stop codons, ORFs contain at least 100 codons. Scientists have identified over 90 percent of genes in yeast and bacteria by looking for ORFs.

In humans and other complex organisms, the long stretches of noncoding sequence make looking for genes more difficult. Scientists use sophisticated computer programs called algorithms to identify genes.

Bioinformatics

The sequencing of DNA from humans and other organisms has created large amounts of data. It has also led to a new field of study. **Bioinformatics** is the study of how to create and use computer databases to store, organize, index, and analyze this data. Scientists are using bioinformatics to discover new ways to locate genes in DNA sequences and to study the evolution of genes.

Think it Over

2. Identify What is most useful for DNA fingerprinting: protein-coding sequences or noncoding sequences? Explain.

Reading Check

3. Explain What is bioinformatics?

DNA Microarrays

In any cell at any time, some genes are expressed, meaning those genes are making proteins. The rest of the genes are silent. In a different cell or at a different time, other genes will be expressed.

Reading Check

4. Define What does it mean to say a gene is expressed?

_____

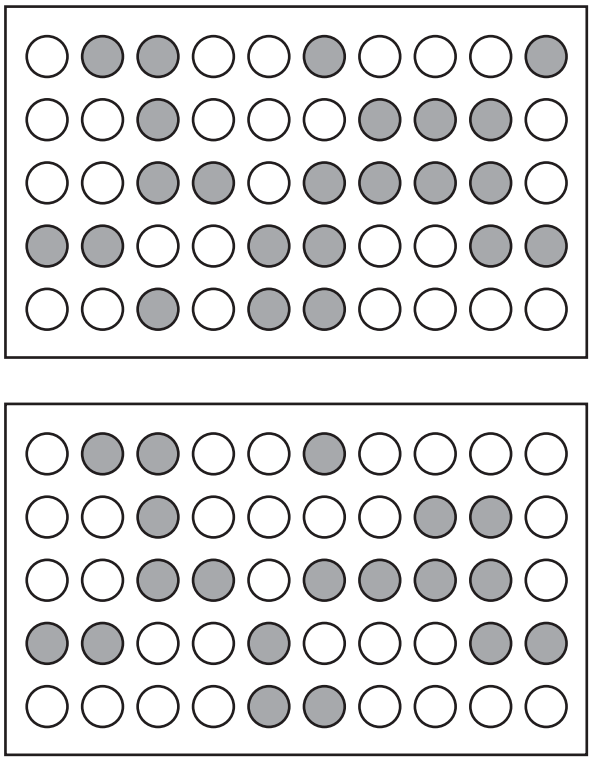
_____

DNA microarrays are tiny microscope slides or silicon chips that contain tiny spots of DNA fragments. One microarray can contain thousands of genes. Scientists use DNA microarrays to study the expression of a lot of genes at once. DNA microarrays are used to study when and where genes are expressed. Microarrays can reveal how gene expression changes under different conditions. Microarrays can be used to compare cancer cells to normal cells. By finding genes that are expressed in cancer cells, scientists can learn more about cancer. They can learn better ways to treat people with cancer.

The figure below shows two DNA microarrays. Each spot represents a different gene. Spots that are white indicate the gene is being expressed. Spots that are black indicate the gene is not being expressed. The top microarray shows the genes that are expressed in a normal cell. The bottom microarray shows the genes that are expressed in a cancer cell.

Picture This

5. Analyze Find the genes that are expressed in the cancer cell but not in the normal cell. Circle the spots that represent those genes.



The Genome and Genetic Disorders

Over 99 percent of all nucleotide sequences are exactly the same from one person to the next. **Single nucleotide polymorphisms**, or SNPs (SNIHPS), are variations in the DNA sequence that occur when a single nucleotide in the genome is changed. A variation is only considered an SNP if it occurs in at least 1 percent of the population.

SNPs can be useful to scientists. Many SNPs do not change how cells function, but SNPs might help scientists find other, nearby mutations that do cause genetic disease. Some SNPs occur near mutations that cause human diseases. Knowing where SNPs occur in the genome might help scientists find mutations that cause diseases.

What is the HapMap project?

A group of international scientists is creating a list of common genetic variations in people. Genetic variations located close together on a chromosome are said to be linked. Linked variations are usually inherited together.

A **haplotype** is a section of linked variations in the human genome. The haplotype map or HapMap project is an international effort to find all the haplotypes. The project will describe what these variations are and show where they are found. The HapMap project will also describe how these variations occur among people within populations and among populations from different areas of the world.

The HapMap project will enable scientists to take advantage of how SNPs and other genetic variations are organized on chromosomes. This will help scientists find genes that cause different types of disease. The HapMap will also help scientists find mutations that affect how a person responds to medicine.

What is pharmacogenomics?

One day people might go to the doctor and have drugs specially prescribed for them based on their genes. **Pharmacogenomics** (far muh koh jeh NAW mihks) is the study of how a person's genes affect his or her response to medicine.

Researchers hope that pharmacogenomics will allow drugs to be custom made for people based on their genetic makeup. Pharmacogenomics might allow doctors to prescribe drugs that are safer, more specific, more effective, and have fewer side effects. Doctors might one day read your genetic code and prescribe drugs made especially for you.

Applying Math

6. Calculate A single nucleotide variation occurs in 7 of every 1000 people. Is this variation an SNP? Why or why not?

Reading Check

7. Define What is a possible benefit of pharmacogenomics?

How does gene therapy work?

Gene therapy is a way of fixing mutated genes that cause disease. Scientists insert a normal gene into a chromosome to replace the mutated gene. The normal gene can then do the work of the mutated gene.

A virus is used as a vector to transfer the normal gene to the cell. The virus releases the recombinant DNA, which contains the normal gene, into the cell. The normal gene inserts itself into the genome and begins functioning.

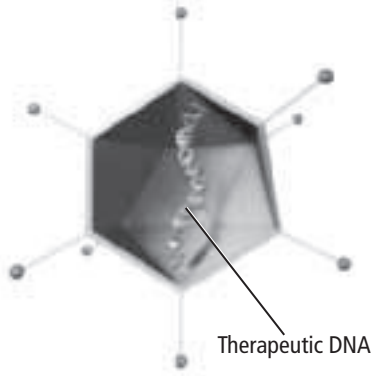
Gene therapy trials are not currently being conducted in the United States. Researchers need to find nontoxic viral vectors before conducting more gene therapy trials.

Picture This

8. Identify How is a normal gene inserted into a cell? (Circle your answer.)

a. by a virus releasing recombinant DNA containing the normal gene

b. by physically removing the mutated gene



Genomics and Proteomics

Genomics is the study of an organism's genome. Following the completion of the human genome sequence in 2003, so much research has become focused on genomics that biologists call this "the genomic era."

Genomics is a powerful strategy for identifying human genes and understanding how they work. Researchers also use genomics to study plants and other organisms, such as rice, mice, fruit flies, and corn, whose genomes have been sequenced.

Genes are important because they are the way cells store information. Proteins are important because they are the machines that make cells run.

Proteomics is the large-scale study and cataloging of the structure and function of proteins in the human body. With proteomics, researchers can study hundreds or thousands of proteins at one time.

Scientists use proteomics to understand human diseases. Scientists expect that proteomics will change the development of medicines to treat diseases such as diabetes, obesity, and atherosclerosis.

Reading Check

9. Define What is proteomics?