along their length) or translation is blocked (if the match between bases is less complete).
b. Evidence indicates that they can do both. miRNAs and siRNAs both affect translation by degrading mRNA or blocking translation. Experiments have shown that siRNAs may silence transcription by changing chromatin structure.

15.7. **a.** RT-PCR: The mRNA from different tissue samples could be isolated. Reverse transcriptase would be used to make cDNA of all the mRNA, and PCR using specific primers could amplify only the gene of interest. Running the samples on a gel would show bands only in the tissues that were expressing the gene. Another possibility would be *in situ* hybridization if the tissues you are studying are readily identified in the whole organism or a section taken from the organism. Labeled probes that are complementary to the mRNA transcribed from that gene would identify tissues in which the gene is expressed.
b. DNA microarray assay: As in RT-PCR, mRNA is isolated from different tissues, and cDNA is made and labeled with fluorescent dye. The cDNA is applied to a microarray (single-stranded DNA fragments of the genes of an organism arranged in a grid). The different cDNA will hybridize with the genes that were expressed in the tissue. The intensity with which the hybridized spots fluoresce indicates the relative amount of mRNA that was in the tissue.

SUGGESTED ANSWERS TO STRUCTURE YOUR KNOWLEDGE

1. **a.** operons
b. promoter
c. operator
d. negative control
e. repressor
f. inactive
g. active
h. corepressor
i. inducer
j. anabolic
k. activate
l. inactivate
m. catabolic
n. cAMP
o. lack of glucose

2. **a.** DNA packing into nucleosomes; histone tail acetylation increases, whereas deacetylation and methylation of tails decreases transcription; methylation of DNA may be involved in long-term inactivation of genes; ncRNAs may promote heterochromatin formation.
b. Specific transcription factors (activators) bind with control elements in enhancers, then interact with mediator proteins and promoter region to form transcription initiation complex; repressors can inhibit transcription.
c. Alternative splicing of primary RNA transcript, 5′ cap and poly-A tail added.
d. Nucleotide sequences in the 3′ UTR affect life span of mRNA, and miRNAs and siRNAs target mRNA for degradation.
e. Repressor proteins and miRNA or siRNA may prevent translation (or short poly-A tail length can allow mRNA stockpiling in ovum); activation of initiation factors begins translation.
f. Protein processing by cleavage or modification; transport to target location; selective degradation of proteins marked with ubiquitin.

ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. b	4. a	7. e	10. b	13. b
2. c	5. b	8. c	11. b	14. d
3. e	6. b	9. b	12. e	

CHAPTER 16: DEVELOPMENT, STEM CELLS, AND CANCER

FOCUS QUESTIONS

16.1. A cell is said to be determined when its developmental fate is set. Its series of gene activations and inactivations has set it on the path to express the genes for tissue-specific proteins. When it produces these proteins and develops its characteristic structure, the cell has become differentiated.

16.2. Bicoid mRNA was shown to be localized at one end of the unfertilized egg; later in development, Bicoid protein occurred in a gradient that was most concentrated in the anterior

cells of the embryo. Also, injection of bicoid mRNA into various regions of early embryos caused anterior structures to form at those sites.

16.3. DNA methylation and histone acetylation help to regulate gene expression. An adult cell must have these epigenetic changes in its chromatin reprogrammed in order to support normal gene expression during development. The DNA of many cloned embryos has been found to be improperly methylated.

16.4. a. Mutations may result in (1) *gene amplification*, in which more copies of the gene are present than normal; (2) *translocation or transposition*, which may bring the gene under the control of a more active promoter or control element; or (3) *point mutation*, resulting in a change in a nucleotide sequence in either a control element that increases gene expression or in the gene that creates a more active or resilient protein.

b. Tumor-suppressor proteins may function in repair of damaged DNA, control of cell adhesion, or inhibition of the cell cycle.

SUGGESTED ANSWERS TO STRUCTURE YOUR KNOWLEDGE

1. Most cytoplasmic determinants are mRNA for transcription factors that are divided by the first few mitotic divisions. They are present in the cells, and their translated product can enter the nucleus and regulate transcription. Inducers must communicate between cells. They are often proteins that bind to cell surface receptors and initiate a signal transduction pathway involving a cascade of enzyme activations, usually leading to the activation of transcription factors within the target cell.

2. Stem cells are undifferentiated cells that can continually divide to form more stem cells or can differentiate into various types of cells. Embryonic stem cells are cells from the blastula stage or earlier that are able to continually divide and differentiate into many, if not all, different types of cells. Adult stem cells are present in small numbers in various tissues and can divide to form a limited number of cell types. Induced pluripotent stem cells have been transformed from differentiated cells by the introduction of copies of "stem cell" master regulatory genes. These cells may be able to function as ES cells. Yes, we can consider the cells of the apical meristem of shoots and roots to be stem cells in that these undifferentiated, continually dividing cells can develop into all types of plant tissues.

ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. e	4. d	7. c	9. e
2. a	5. e	8. e	10. b
3. c	6. b		

CHAPTER 17: VIRUSES

FOCUS QUESTIONS

17.1. 1. Phage attaches to host cell and injects DNA.
2. Phage DNA forms a circle. Certain factors determine which cycle is entered.
3. New phage DNA and proteins are synthesized and self-assemble into phages.
4. Bacterium lyses, releasing phages.
5. Phage DNA integrates into bacterial chromosome, becoming a prophage.
6. Bacterium reproduces, passing prophage to daughter cells.
7. Large population of infected bacteria forms.
8. Occasionally, prophage exits bacterial chromosome and begins lytic cycle.

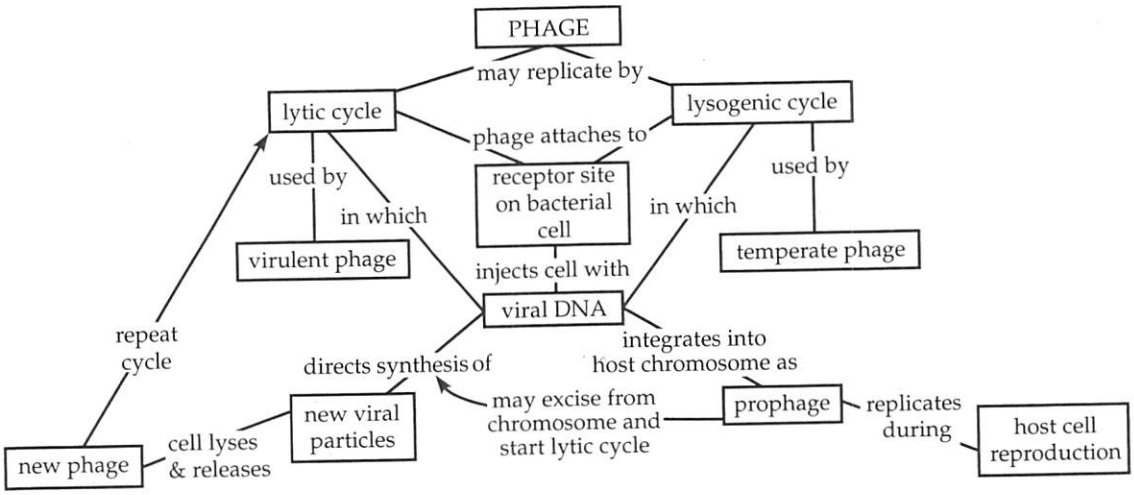
a. phage DNA
b. bacterial chromosome
c. new phages
d. prophage
e. replicated bacterial chromosome with prophage

17.2. RNA → DNA → RNA; viral reverse transcriptase, host RNA polymerase

17.3. Viral particles spread easily through plasmodesmata, the cytoplasmic connections between plant cells. As there are no cures for plant viral diseases, reducing the spread of infection and breeding resistant varieties are the best approaches.

SUGGESTED ANSWERS TO STRUCTURE YOUR KNOWLEDGE

1.



2. **a.** DNA
b. RNA
c. protein capsid
d. host cell
e. bacterium
f. lytic or lysogenic cycle
g. animal
h. membraneous envelope
i. reverse transcriptase
j. plant
k. plasmids or transposons

ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. b	**4.** a	**7.** b
2. c	**5.** d	**8.** c
3. e	**6.** b	**9.** b

CHAPTER 18: GENOMES AND THEIR EVOLUTION

FOCUS QUESTIONS

18.1. Microbial species—metagenomics enables the sequencing of a mixture of DNA from an environmental sample without the need to grow each species separately in the lab.

18.2. Comparing nucleotide and amino acid sequences may reveal matches with other genes of known function or reveal common amino acid domains for which a function is known and can identify similarities with closely or distantly related species that help trace a species' evolutionary history.

18.3. **a.** the archaean *Archaeoglobus fulgidus* (1,130/Mb); humans (7/Mb)
b. rice, *Oryza sativa* (40,600); the bacterium *Haemophilus influenzae* (1,700)
c. a plant, *Fritillaria assyriaca* (124,000 Mb); *H. influenzae* (1.8 Mb)
d. less than 21,000; alternative splicing of exons can allow each gene to code for more than one polypeptide; post-translational processing can also alter polypeptides

18.4. They are first transcribed into RNA; thus, the original retrotransposon remains in place. Reverse transcriptase converts the RNA to DNA, which is inserted into another site in the genome.

18.5. 1. D; 1.5
2. I; 20
3. H; 5
4. B; 44
5. E; 10
6. G; 17
7. C; 15
8. F; 5–6
9. A; 3

18.6. The lysozyme gene, which codes for a bacterial infection-fighting enzyme, was present in the last common ancestor of birds and mammals. After their lineages split, the gene underwent a duplication event in the mammalian lineage, and a copy of the lysozyme gene evolved into a gene coding for a protein involved in milk production.

18.7. **a.** Exon shuffling can happen through an error in meiotic recombination, which may occur between two homologous transposable elements, or by the inclusion or tagging along of an exon with a transposable element, which moves a copy of the exon to a new location.
b. Exons often code for domains of a protein. Providing a new domain to a protein may enhance or change its function.

18.8. The homeobox codes for a DNA-binding homodomain, while other domains specific to each regulatory gene interact with transcription factors to recognize particular enhancers or promoters and thus control different batteries of developmental genes.

SUGGESTED ANSWERS TO STRUCTURE YOUR KNOWLEDGE

1. Many non-protein-coding sequences are highly conserved across species, indicating that they perform some important, but as yet unidentified, function. Much of this DNA is transcribed into RNA molecules, some of whose functions are being discovered.
a. Transposable elements include transposons, which are DNA segments, and retrotransposons, which are produced from RNA transcribed into DNA. These transposable elements are very common and move DNA to new locations in the genome.
b. *Alu* elements are about 300 nucleotides long and make up about 10% of the human genome. Some are transcribed into RNA, but their function is unknown. They may provide alternate splice sites for RNA processing.
c. L1 sequences are long retrotransposons that rarely move about. They are found in many introns and may help regulate gene expression.
d. Simple sequence DNAs are highly repetitive tandem sequences found at centromeres and telomeres of a chromosome. They appear to have structural functions in organizing chromatin. Sequences with fewer repetitions are called STRs (short tandem repeats) and are used in genetic profiling.
e. Pseudogenes are remnants of genes that are no longer functional because mutations have altered their regulatory sequences.

2. Chromosome duplication provides additional copies of genes that may undergo mutation and produce new proteins. Rearrangements of chromosome sections, such as duplications, inversions, and translocations, may create reproductive barriers between populations that lead to the formation of new species. Errors during meiosis can lead to duplications of genes or exons, or exchange of exons, providing genetic material that may take on related or novel functions. Transposable elements can facilitate recombination between different chromosomes, can disrupt genes or control elements, and can carry genes or exons to new locations.

ANSWERS TO TEST YOUR KNOWLEDGE

Multiple Choice:

1. c	**4.** d	**7.** e	**10.** d
2. d	**5.** b	**8.** e	**11.** b
3. a	**6.** a	**9.** c	**12.** d

CHAPTER 19: DESCENT WITH MODIFICATION

FOCUS QUESTIONS

19.1. **a.** **1.** E f
2. A b
3. B e
4. C d, g
5. F a
6. D c
7. G g
b. a, f, d, b, e, g, c

19.2. Observation 1: Members of a population vary in their inherited traits.
Observation 2: All species can produce more offspring than the environment can support, and many offspring do not survive.