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Test Bank for Molecular Cell Biology 7th Edition by Lodish and Berk and Kaiser and Krieger and Bretscher and Ploegh and Amon and Scott

Chap6. Genes, Genomics, and Chromosomes

6.1 *Eukaryotic Gene Structure*

1. Which of the following is a typical feature of prokaryotic genes?

a.polycistronic messenger RNAs

b.complex transcription

units c.introns

d.a and c

Ans: a

2. The chicken lysozyme gene is considered to be a solitary gene because

a.it contains no introns.

b.it is not present on a chromosome.

c.it is represented only once in the haploid genome.

d.none of the above

Ans. c

3. All the following statements about complex transcription units are true except:

a.They can have multiple poly(A) sites.

b.They can generate multiple mRNAs.

c.They can generate multiple polypeptides.

d.They are common in bacteria.

Ans: d

4. In eukaryotes, tandemly repeated genes encode

a.rRNAs.

b.cytoskeletal

proteins. c.b-globin.

d.all of the above

Ans. A

5. Short micro RNAs

(miRNAs) a.code for proteins.

b.are common in bacteria but not eukaryotes.

c..are involved in regulation of gene expression.

d.have no known function.

Ans: c

6.2 *Chromosomal Organization of Genes and Noncoding DNA*

6. Which of the following organisms has the greatest amount of DNA per cell?

a.chicken

b.fruit fly

c.tulip

d.human

Ans: c

7. All the following statements about microsatellite DNA are true except: a.It consists of a repeat length of 1–13 base pairs.

b.It can cause neurological diseases such as myotonic dystrophy.

c.It can occur within transcription units.

d.all of the above

Ans: d

8. Which of the following classes of repetitious DNA is most abundant in the human genome?

a..simple-sequence DNA

9. non-LTR transposons

c.LTR transposons

d.DNA transposons

Ans: b

6.3 *Transposable (Mobile) DNA Elements*

9. All the following steps are performed by the enzyme transposase during nonreplicative transposition of bacterial insertion sequences except

a.excision of the IS element from the donor DNA molecule.

b.introduction of staggered cuts into the target DNA molecule.

c.ligation of the IS element to the target DNA.

d.synthesis of DNA to fill in the single-stranded gaps.

Ans: d

10. Which of the following is not a mobile DNA element?

a.transposon

b.long terminal repeats (LTR)

c.long interspersed elements (LINES)

d.insertion sequence (IS) elements

Ans: b

11. Which of the following mobile elements is a retrotransposon?

a.yeast Ty element

b.bacterial IS sequence

c.Drosophila P element

d.maize activator (Ac) element

Ans: a

12. SINES (short interspersed elements)

a.are approximately 300 base pairs long.

b.are LTR containing retrotransposons.

c.are present in over 1 million copies in the human genome.

d.a and c

Ans: d

13. Mobile DNA elements likely contributed to the evolution of higher organisms by the

ageneration of gene families by gene duplication.

a..creation of new genes by exon shuffling.

b.formation of more complex regulatory regions.

c.all of the above

Ans: d

6.4 *Organelle DNAs*

14. All of the following statements about mitochondrial DNA are true except:

a.Mammalian mitochondrial DNA contains introns.

b.In mice, 99.99 percent of mitochondrial DNA is maternally inherited.

c.Mitochondrial DNA encodes rRNAs and tRNAs.

d.The human mitochondrial genome is smaller than the yeast mitochondrial genome.

Ans: a

15. In mammals, the RNA sequence AUA CUC UGA is translated as a.Met-Leu-Trp in the nucleus and Met-Leu-Trp in mitochondria. b.Met-Leu-Trp in the nucleus and Ile-Leu-stop in mitochondria.

16. Ile-Leu-stop in the nucleus and Met-Leu-Trp in mitochondria.
17. Ile-Leu-stop in the nucleus and Ile-Leu-stop in mitochondria.

Ans: c

6.5 *Genomics: Genome-wide Analysis of Gene Structure and Expression*

16. Which of the following pairs of proteins are considered to be paralogous?

a.yeast a-tubulin and yeast b-tubulin

b.yeast a-tubulin and worm a-tubulin

c.fly b-tubulin and human b-tubulin

d.worm b-tubulin and human a-tubulin

Ans: a

17. How many genes are estimated to be in the human genome?

a.25,000

b.35,000

c..75,000

d.100,000

Ans: a

18. Open reading frame (ORF) analysis is not effective in identifying genes in higher eukaryotes because of the presence of

a.promoters.

b.enhancers.

c.introns.

d.repetitious DNA.

Ans: c

19. Which of the following evidence is indicative of the presence of a gene in an unknown DNA sequence?

a.alignment to a partial cDNA sequence

b.sequence similarity to genes of other organisms

c.ORF consistent with the rules for exon and intron

sequences d.all of the above

Ans: d

6.6 *Structural Organization of Eukaryotic Chromosomes*

20. All the following statements are true about a nucleosome except:
21. It contains an octamer core of histones.

b It is about 10 nm in diameter.

1. It is the “string”-on -ofa-str ing”the “beadsappearance.
2. It contains approximately 150 base pairs of DNA.

Ans: c

21. DNA that is transcriptionally active

a.is more susceptible to DNase I digestion. b.is

tightly packed into a solenoid arrangement.

c.contains unacetylated histones.

d.is more condensed than nontranscribed DNA.

Ans: a

22. All of the following can be found in chromatin except

a.DNA.

b.histones.

c.RNA. d.transcription

factors.

Ans: c

23. Which of the following statement(s) is (are) true of a eukaryotic chromosome?

a.It is a linear structure.

b.It consists of a single DNA molecule.

c.It can contain greater than a billion base pairs of DNA.

d.all of the above

Ans: d

24. In mammals, X-chromosome inactivation

a.occurs in half the diploid cells of the adult female.

b.results from the ionization of the X-chromosome.

c.is considered an epigenetic event.

d.b and c

Ans. c

6.7 *Morphology and Functional Elements of Eukaryotic Chromosomes*

.

Ans: d

26. Chromosome painting involves

a.staining chromosomes with Giemsa reagent.

b.hybridizing fluorescent probes to chromosomes.

c.hybridizing radioactive probes to chromosomes.

d.a and b

Ans: b

27. All the following statements about heterochromatin except:

a.It is a dark-staining area of a chromosome.

b.It is usually transcriptionally active.

c.It is often simple sequence DNA. d.It is a region of condensed chromatin.

Ans: b

PART B: Testing on the Concepts

6.1 *Eukaryotic Gene Structure*

29. Give a functional definition of a gene.

Ans: A gene consists of the entire DNA sequence required for synthesis of a functional protein or RNA molecule. In addition to the coding regions or exons, a gene includes transcription control regions, such as enhancers, and other critical noncoding regions such as poly(A) sites and splice sites. Sometimes essential control regions can even be located in introns.

30. What is the advantage of complex transcription units over simple transcription units?

Ans: A complex transcription unit can be processed into multiple mRNAs that can code for different proteins. A simple transcription unit can code for only one RNA and one protein. Complex transcription units allow for a greater diversity of proteins from the same number of genes.

6.2 *Chromosomal Organization of Genes and Noncoding DNA*

31. Describe the general organization of protein coding genes in the yeast and human genomes.

Ans: In yeast, the protein coding regions are closely spaced along the DNA sequence. In contrast, in the human genome, only a small fraction of the DNA encodes for protein. Thus, the density of protein coding genes per length of DNA is higher in yeast than it is in humans. Put another way, the human genome contains a much higher proportion of noncoding to coding sequences than the yeast genome.

32. Describe the proposed mechanism discussed in this chapter for the origin of gene families.

Ans: A gene family consists of a set of duplicated genes that encode proteins with similar but not identical amino acid sequences. An example of a gene family is the genes encoding the b-like globins. The different genes in the gene family probably arose by duplication of an ancestral gene, most likely as a result of an unequal crossover during meiotic recombination. Over time,

these duplicated genes accumulated random mutations. In some cases, a protein with a slightly different function emerged; in other cases, the mutations led to a nonfunctional gene known as a pseudogene.

33. What is the underlying mechanism behind why gene mutations that lead to Huntington's disease act as dominant

Ans: The mutations that lead to Huntington'sexamplesof disease expanded microsatellite repeats. In the case of the H a triplet CAG repeat in the first exon. Expansion of this repeat results in
synthesis of long stretches of polyglutamine. Over time, the protein products that contain long stretches of polyglutamine aggregate. Protein aggregation leads to neuronal cell death, which in turn gives rise to the symptoms of Huntington's disease. These microsatellite mutations the presence of aggregated protein causes symptoms, even though some normal protein is produced from the normal allele.

6.3 *Transposable* (*Mobile) DNA Elements*

34. Describe the two major pathways for transposition of mobile elements.

Ans: Mobile elements fall into two major classes. Insertion sequences and transposons move via a DNA intermediate, whereas retrotransposons transpose via an RNA intermediate. DNA elements encode a transposase enzyme, which catalyzes the transposition event. A retrotransposon is first transcribed into RNA, which is then used as a template for synthesis of double-stranded DNA by the action of the retrotransposon-encoded enzyme, reverse transcriptase. The resulting double-stranded DNA is then integrated into the host genome.

35. Review the experimental evidence that the yeast Ty element transposes through an RNA intermediate.

Ans: In Experiment 1 (see Figure 10-14 on text page 231), a plasmid was constructed which expressed a Ty element from a galactose-inducible promoter. Yeast cells, transformed with the Ty element plasmid, showed an increased frequency of transposition when plated on galactose-containing medium compared to galactose-free medium. This result demonstrated that transcription into an RNA intermediate is required for Ty transposition. The second experiment used a plasmid containing a Ty element with an intron from an unrelated yeast gene. The transposition events were found to lack the intron, which suggested that transpositon with Ty elements involves an RNA intermediate from which the intron was removed by RNA splicing.

6.4 *Organelle DNAs*

36. Describe the evidence that supports the bacterial ancestry of mitochondria.

Ans: Both mitochondrial and bacterial DNA are circular molecules. Mitochondrial ribosomes resemble bacterial ribosomes in their RNA and protein compositions, size, and sensitivity to various antibiotics. The drug chloramphenicol, but not cycloheximide, blocks protein synthesis by both mitochondrial and bacterial ribosomes, whereas cytoplasmic ribosomes are resistant to chloramphenicol and sensitive to cycloheximide.

6.5 Genomics: Genome-wide Analysis of Gene Structure and Expression

37. Bioinformatics can be used to categorize genes that are homologous, paralogous, and orthologous. What determines whether a gene is the homolog, paralog, or ortholog of another gene?

Ans. For example, the tubulin genes belong to a large gene family, of which all members contain very similar nucleotide sequences, which in turn encode proteins with similar amino acid sequences. The earliest eukaryotic cells probably contained one ancestral gene, which was later duplicated and diverged into ancestral a- and b-tubulin genes. As new species evolved, the a- and b-tubulin genes diverged to form new a- and b-tubulin genes. Since the sequences of all tubulin genes are remarkably similar, suggesting that they arose from a common ancestral gene, they are considered to be homologous to each other. The a and b genes that diverged as a result of a duplication are defined as being paralogs. The a-tubulin (or b-tubulin) genes in different species of animals are likely to encode proteins with the same function and are considered to be orthologs.

38. Briefly describe what tool you might use to compare the amino acid sequence of a newly discovered protein to the amino acid sequences of known proteins.

Ans: You might use a publicly available computer program such as BLAST. According to the National Library of Medicine, which maintains this database and program, “The Basic Local Alignment Search Tool (of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.”

6.6 *Structural Organization of Eukaryotic Chromosomes*

39. Describe how modification of histone tails can control chromatin condensation.

Ans: The amino termini of histones, which are known as histone tails, extend from the structure of the nucleosome. Positively charged lysine side chains present in the histone tails may interact with linker DNA or other nucleosomes. Acetylation of the lysine side chains neutralizes the positive charges, thereby eliminating the potential interaction with the negatively charged DNA phosphate groups. Thus, acetylation of histones makes the chromatin less likely to form a condensed structure. Deacetylation of the histones once again allows the positively charged lysines to interact with the DNA phosphate groups, leading to chromatin condensation.

6.7 *Morphology and Functional Elements of Eukaryotic Chromosomes*

40. Why is there a need for a specialized structure at the ends of eukaryotic chromosomes and for the enzyme telomerase?

Ans: Because all known DNA polymerases elongate DNA in the 5′ to 3′ direction, all require a RNA or DNA primer to initiate synthesis. As the replication fork approaches the end of the chromosome, DNA synthesis on the leading strand continues to the end of the chromosome without a problem. However, because the lagging strand is synthesized discontinuously, it cannot be replicated in its entirety. When the RNA primer is removed, a short segment of DNA remains single-stranded with no way to make this region double-stranded. If there were no specialized mechanism for replicating DNA at the ends, then the chromosome would shorten with each round of replication. Telomerase is the enzyme that completes the synthesis of the DNA at the telomeres.