

Exam 2
CSS/Hort 430/530
2012

1. In a deoxyribonucleotide, 5' and 3' refer to the
 - a. start site for transcription.
 - b. start site for translation.
 - c. carbons where (respectively) the pyrimidine and purine bases are attached.
 - d. carbons where (respectively) the phosphate and hydroxyl groups are attached.
2. In the S phase of meiosis, DNA replication is
 - a. socialist.
 - b. liberal.
 - c. semiconservative.
 - d. conservative.
3. DNA polymerase synthesizes new deoxyribonucleotide chains in which direction?
 - a. 3' to 5' in the leading strand
 - b. 3' to 5' in the lagging strand
 - c. 5' to 3' in both the leading strand and the lagging strand
 - d. 5' to 3' in the leading strand and 3' to 5' in the lagging strand
4. In higher plants, each chromosome has a single bidirectional origin of DNA replication located at
 - a. the centromere.
 - b. the telomere.
 - c. the dark matter.
 - d. none of the above.
5. The RNA primers that initiate DNA replication in the S phase of mitosis remain in the daughter strands until the organism dies.
 - a. T
 - b. F
6. Okazaki fragments are found on both leading and lagging strands.
 - a. T
 - b. F
7. Transcription of genes located on the 20 chromosomes of maize occurs
 - a. in the cytoplasm.
 - b. in both the nucleus and cytoplasm.
 - c. in the nucleus.
 - d. at the ribosomes.
8. RNA can have informational, functional, and/or regulatory functions
 - a. T
 - b. F
9. In eukaryotes, informational and functional RNAs are
 - a. examples of proteins with quaternary structures.
 - b. always double stranded.
 - c. coded for by genes in the nucleus.
 - d. maternally inherited.

10. A promoter is
- a binding site for RNA polymerase.
 - the signal to end transcription.
 - the same as the start codon.
 - translated as methionine.
11. The segment of a gene that would be most likely to have the sequence TATA ~ 30 bp upstream (5') from the transcription start site is called an intron.
- T
 - F
12. The sequence of the promoter can be found
- in mRNA sequence.
 - in genomic DNA sequence.
 - in the primary amino acid sequence.
 - In all of the above (a-c).
13. If there is a change in the promoter of a gene leading to a loss of the TATA sequence, this could lead to a recessive allele due to failure of transcription of the gene to a mRNA.
- T
 - F
14. The synthesis of the mRNA stops when a stop codon is encountered.
- T
 - F
15. mRNA processing in eukaryotes refers to the addition of a 3' cap, a 5' tail, and removal of exons.
- T
 - F
16. The ATG sequence can be diagnostic of
- a start codon.
 - a stop codon.
 - an intron/exon junction.
 - a 3' UTR
17. Exons are
- always longer than introns.
 - the most likely site of SSRs.
 - a type of mutation.
 - none of the above (a-c)
18. Translation of the mRNAs transcribed from the genes located on the 20 chromosomes of maize occurs in the in the cytoplasm.
- T
 - F
19. The rRNA subunits in ribosomes are transcribed from DNA, but are not translated.
- T
 - F

20. Transfer RNAs (tRNAs)
- are very generic, with each tRNA able to carry at least five different amino acids.
 - consist of 18S and 35S subunits.
 - are coded for by sequences in introns.
 - have anticodons that base pair with codons in mRNA.
21. In the process of translation, the ribosome moves 5' to 3' on the antisense DNA.
- T
 - F

Given the following DNA sense strand – 5'ATG GCC TGG ACT TCA 3'

22. Which is the corresponding DNA antisense strand?
- 5' TAC CGG ACC TGA AGT 3'
 - 3' UAC CGG ACC UGA AGU 5'
 - 3' TAC CGG ACC TGA AGT 5'
 - 5' UAC CGG ACC UGA AGU 3'
23. Which is the corresponding mRNA?
- 3' UAC CGG ACC UGA AGU 5'
 - 5' AUG GCC UGG ACU UCA 3'
 - 5' UAC CGG ACC UGA AGU 3'
 - 3' AUG GCC UGG ACU UCA 5'
24. Which is the correct translation?
- Thr Ser Gly Pro Val
 - Tyr Arg Thr Stop Ser
 - Met Ala Trp Thr Ser
 - Ser Thr Trp Ala Met
25. If you know the amino acid sequence of a polypeptide you can deduce
- several possible DNA sequences for the corresponding gene.
 - the exact DNA code of the corresponding gene.
 - the 5'UTR sequence of the corresponding gene.
 - which stop codon is present in the corresponding gene.
26. In “The gene for fragrance in rice” paper, the authors conclude that the functional basis for the difference between aroma vs. non-aroma alleles is probably due to a premature stop codon in the non-aromatic allele due to a frameshift mutation. This causes aroma to be dominant and lack of aroma to be recessive.
- T
 - F
27. In the case of partial dominance, heterozygotes can be distinguished from the dominant and recessive homozygotes based on phenotype.
- T
 - F

28. The following example showing sequence and codon alignments is an example of a missense mutation.

a. T

b. F

*** CTGGGAGATTATGGCTTTAAG***
 *** CTGGGA-----TAAG*** 11 bp deletion, alignment

*** CTG GGA GAT TAT GGC TTT AAG
 *** CTG GGA TAA G codon alignment

Leu Gly Asp Tyr Gly Phe Lys
 Leu Gly STOP G translation

29. In the case of codominance, the presence of both alleles in a heterozygote can be visualized via electrophoresis.

a. T

b. F

30. The situation where heterozygotes at a locus are most fit - e.g. they have the highest phenotypic value - is called:

a. underdominance

b. overdominance

c. codominance

d. dominance

31. The situation where two phenotypes are determined by the same gene is called

a. codominance.

b. epistasis.

c. linkage.

d. pleiotropy.

32. Epistasis is the consequence of alleles at distinct loci failing to assort independently.

a. T

b. F

33. Epistasis could involve a transcription factor encoded by locus “x” repressing locus “y”.

a. T

b. F

34. In the first unit, and in the unit on “Genes to Phenotypes”, there is the following statement: “Expected and observed ratios in cross progeny will be a function of.” This statement is followed by a list of factors (a – e below). Which of the five factors best describes epistasis?

a. The degree of homozygosity of the parents

b. The generation studied

c. The degree of dominance

d. The degree of interaction between genes

e. The number of genes determining the trait.

35. Which of the following best describes restriction endonucleases:
- Only make blunt cuts in single stranded DNA
 - Only make sticky end cuts in single strand RNA
 - Recognize palindromic sequences of nucleotides
 - Were discovered in a hot spring in Yellowstone National Park
36. If used for a genomic DNA digest, a restriction enzyme with a four-based recognition site will cut more often than a restriction enzyme with an eight-base recognition site.
- T
 - F
37. The purpose for using a vector (such as a plasmid) in making a DNA library is to:
- genetically engineer plants with foreign genes.
 - identify phenotype: genotype associations through marker assisted selection.
 - maintain and increase copy number of specific DNA fragments.
 - make cuts in double stranded DNA at specific recognition sites.
38. There are many types of vectors (e.g. plasmids, phages, BACs, etc.) and a primary difference between these vectors is the size of the DNA insert they can accommodate.
- T
 - F
39. Clones in a cDNA library will be shorter than the original genomic coding sequences because telomeres shorten with each replication.
- T
 - F
40. If you were interested in identifying genes involved only in flower development, you would most likely choose a
- BAC library of genomic DNA
 - cDNA library from root tissue
 - cDNA library made from floral tissue
 - constitutive promoter
41. Two principal methods for designing molecular markers are
- duplication and deletion.
 - promoters and terminators.
 - amplification and hybridization.
 - start and stop codons.
42. The primers that are used for a PCR reaction to amplify genomic DNA consist of
- Taq polymerase.
 - amino acids.
 - deoxyribonucleotides.
 - mRNA.
43. The key step in PCR amplification of genomic DNA is hybridization of DNA to RNA
- T
 - F

44. The temperature cycling used in PCR reactions is needed to alternately allow for double strand DNA denaturation, primer binding, and primer extension.
- a. T
 - b. F
45. A Southern Blot is involves the hybridization of two double stranded DNA molecules.
- a. T
 - b. F
46. The key attribute of dideoxy nucleotides that makes them useful for DNA sequencing is that they have no 3' OH group.
- a. T
 - b. F
47. If you could easily determine the DNA sequence of alleles at 100 loci in one diploid plant that was heterozygous at all loci, how many different alleles would you be able to detect?
- a. 100
 - b. 200
 - c. 400
 - d. 600
48. The genome sizes reported in the Key Gardens database are all based on the actual sequencing of plant genomes.
- a. T
 - b. F
49. Key considerations in Next-Generation, massively parallel, and high throughput DNA sequencing techniques (e.g. 454 and Illumina) are:
- a. Whether to use radioactively or fluorescently labeled dideoxynucleotides
 - b. Whether to determine the DNA sequence in picograms or in Megabases
 - c. Speed, read length, and accuracy
 - d. How many sequencing gels a technician can run in a day
50. In the strawberry genome sequence paper, the term "contig" refers to
- a. The sequence of a complete chromosome, except for the centromeric region
 - b. The sequence of one read (e.g. ~ 100 nucleotides)
 - c. The contiguous sequence of several overlapping reads of DNA sequence
 - d. The n number of chromosomes in *Fragaria*
51. In the context of DNA marker analysis, electrophoresis is used to selectively amplify target DNA sequences.
- a. T
 - b. F
52. A molecular marker based on PCR primers for conserved regions flanking a region of variable length tandem repeats is called a SNP.
- a. T
 - b. F

53. Molecular markers are more useful than morphological markers (naked eye polymorphisms) for construction of high density linkage maps because all types of molecular markers are codominant.
- T
 - F
54. Which of the following is the best example of a SNP-based marker that would be useful for mapping a flowering-time gene in progeny of the cross between two inbred parents?
- A 20 nucleotide deletion in the first intron of the gene in one parent vs. the presence of 20 nucleotides at the corresponding positions in the second parent.
 - Twenty "AT" repeats in the 3'UTR of one parent vs. 10 "AT" repeats in the 3' UTR of the other parent.
 - A "T" in one parent vs. a "C" in the other parent, at the same nucleotide position, in the first exon of the gene.
 - Complete deletion of the gene in one parent vs. presence of the gene in the other parent.
55. RAPD markers are defined by the use of a PCR primer that
- specifically targets promoters
 - is able to function at high temperatures
 - randomly amplifies different size products based on DNA templates of two or more individuals
 - generates very high quality and reproducible data
56. In the case of a codominant molecular marker, the expected phenotypic ratio in the F2 progeny of the cross between two completely inbred lines will be 1:2:1
- T
 - F
57. In the case of a dominant molecular marker, the expected phenotypic ratio in the F2 progeny of the cross between two completely inbred lines will be 3:1.
- T
 - F
58. In the assigned reading on the strawberry genome, the authors present an elegant figure showing synteny between *Fragaria* and *Prunus*. Which of the following best describes the information in this figure?
- Prunus* and *Fragaria* have the same number of chromosomes.
 - Segments of *Prunus* chromosomes have linked loci in the same or similar order as segments of *Fragaria* chromosomes.
 - Each gene in *Fragaria* has an orthologous gene in *Prunus*.
 - Genes in *Fragaria* show pleiotropy whereas those in *Prunus* do not.
59. Marker assisted selection (MAS) is so popular with plant breeders today because
- it allows the breeder to select for traits that cannot be easily, or cheaply, selected based on phenotype.
 - it allows breeders to immediately patent genes.
 - it does not involve PCR.
 - it relies exclusively on morphological markers.

60. The “Putting it all together” example of mapping the *MFT1* gene in the OWBs is an example of capitalizing on
- a. orthology
 - b. ornithology
 - c. western blotting
 - d. synteny