Exam 3 PBG 430/530 2014

1. You read that the genome size of a recently discovered plant is 213 Mb and that in this species 2n = 6. This means that there are 213 Mb of DNA in a cell that is
   a. n (e.g. gamete)
   b. 2n (e.g. embryo)
   c. 3n (e.g. endosperm)

2. In a diploid species that is 2n = 24, the "F" gene is 2 kb long. Which of the following statements is most true?
   a. Many alleles at the F locus are possible in a sample of 1,000 plants of this species, but only two alleles will occur in any single plant
   b. In a population of 1,000 plants of this species, only two alleles at the F locus are possible
   c. If there are different alleles at the F locus, there is no way to study their inheritance
   d. If you produce doubled haploids from the cross of the F1 derived from FF x ff the expected genotypic ratio for alleles at the F locus is 3:1

3. If you self an F1 plant for three generations, what % of the original heterozygosity would you expect to be retained in any one progeny? Assume each of the parents of the F1 was completely homozygous.
   a. 100%
   b. 50%
   c. 33%
   d. 25%
   e. 12.5%

4. Saffron is only found in its triploid state, and must be clonally propagated. What source of heritable phenotypic variation is most likely to be found in a plant's progeny?
   a. Independent assortment
   b. Segregation
   c. Mutation
   d. Centromere shortening

5. While Chi-Squared tests have been around for a while (>100 years!), they are still one of the best methods for determining if alleles at a locus defined by a SNP are showing the expected segregation ratio.
   a. True
   b. False

Use the following example for questions 6 -10. In peas, flower color can be controlled by two unlinked loci, A and B, where at least at least one dominant allele must be present at each locus for the flower to be purple, otherwise the flower is white. Two heterozygous pea plants (AaBb X AaBb) are crossed.

6. What is the expected ratio of purple to white flowered progeny? It may help to complete a punnett square. ***However, this is not required***

a. 1:1
b. 1:3
c. 9:7
d. 15:1
e. 9:3:3:1

7. If doubled haploid progeny were made from one of the heterozygous parents, what would the expected ratio of purple to white progeny be?
a. 1:1
b. 1:3
c. 9:7
d. 15:1
e. 9:3:3:1

8. This trait is
a. qualitative
b. quantitative

9. The interaction between these genes can be described as
a. synteny
b. crossover interference
c. epistasis
d. pleiotropy

10. In your doubled haploid progeny, you notice a slight difference between your expected and observed colored progeny, and you decide to conduct a chi-squared test to determine if this difference is significant. How many degrees of freedom will you use in this test?
a. 1
b. 2
c. 3
d. Impossible to know given this information

11. In monoecious plants, each individual plant only has one gender, while in dioecious plants, each plant has both male and female parts.
    a. True
    b. False

12. "Perfect" flowers have both male and female parts.
    a. True
    b. False

13. The eight nuclei in a single embryo sac have
    a. different genotypes, as determined by the tetrad of microspores
    b. the same genotypes

14. Which example would best demonstrate pleiotropy?
    a. In barley, plant height is controlled by many genes as well as environmental factors
    b. In barley, genes for qualitative disease resistance and awn type are so close they are difficult to separate in a breeding population
    c. In barley, a single locus affects both grain starch formation and beta glucan content

15. Telomere shortening progresses over the life of an individual because
    a. the edges of chromosomes are less protected from oxidants, and therefore more prone to mutation events
    b. during DNA replication, the end of the chromosome is not replicated in the lagging strand
    c. telomerase slowly digests the edges of chromosomes

16. In 2014, linkage maps can be made from
    a. SNPs
    b. INDELs
    c. microsatellites
    d. all of the above

17. Before DNA marker data were available,
    a. researchers were not able to construct linkage maps
    b. linkage maps were made using naked-eye polymorphisms
    c. researchers had to assemble a plant's entire genome to know the distance between genes

18. You determine that the linkage maps of Fragaria and Prunus have blocks of the same loci in the same order but have different numbers of chromosomes. This is an example of
    a. analogy
    b. xenology
    c. homoeology
    d. synteny

Consider the following data from the cross of completely homozygous *Agape nectaria* plants. The data are from a doubled haploid population consisting of 96 plants. Based on these data, answer questions 19-21.

Genotype	RRSS	RRss	rrSS	rrss
Observed number of plants	10	37	40	9

19. What is the most likely explanation for these data?
    a. High rates of mutation are occurring in these plants
    b. The R and S loci show independent assortment
    c. The R and S loci are linked

20. Based on these data, which genotypes most likely represent the non-parental classes?
    a. RRSS and rrss
    b. RRSS and RRss
    c. RRss and rrSS
    d. RrSs and RrSs

21. The distance (in percent recombination) between the R and S loci is
    a. 19/77=24.7%
    b. 9.5/96=9.9%
    c. 19/96=19.7%

22. If the percent recombination between two loci is 20%, the centiMorgan (cM) value will be
    a. larger than the percent recombination
    b. smaller than the percent recombination
    c. basically the same as percent recombination

23. In a deoxyribonucleotide, 5’ and 3’ refer to the carbons where (respectively) the phosphate and hydroxyl groups are attached.
    a. True
    b. False

24. DNA is useful for storing genetic data because it
    a. can be replicated and is capable of change
    b. often acts as an enzyme in addition to storing information
    c. has strong phosphodiester bonds that help stabilize the nucleus

25. DNA polymerase synthesizes new DNA chains in which direction?
    a. 5' to 3' in the leading and lagging strands
    b. 5' to 3' in the leading strand and 3' to 5' in the lagging strand
    c. From the centromeres to the telomeres

26. Which of the following elements of a gene best describes the promoter?
    a. Region between transcription start site and start codon
    b. Region between start codon and stop codon
    c. 3' nucleotide sequence that signals the end of translation
    d. Binding site for RNA polymerase

27. Which of the following elements of a gene best describes the coding sequence?
    a. Region between transcription start site and start codon
    b. Region between start codon and stop codon
    c. 3' nucleotide sequence that signals the end of translation
    d. Binding site for RNA polymerase

28. Which of the following elements of a gene best describes the stop codon?
    a. Region between transcription start site and start codon
    b. Region between start codon and stop codon
    c. 3' nucleotide sequence that signals the end of translation
    d. Binding site for RNA polymerase

29. Where would you most likely see active transcription of genes?
    a. Euchromatin
    b. Constitutive heterochromatin
    c. Epigenetically silenced chromatin

30. In the process of translation, the ribosome moves
    a. 5' to 3' on the mRNA
    b. 3' to 5' on the mRNA
    c. 5' to 3' on the antisense DNA
    d. Towards the magnetic north pole, unless in the southern hemisphere

31. For any given polypeptide chain, except those containing only Met and Trp, the exact DNA sequence cannot be determined
    a. True
    b. False

32. Across the genome, a reasonable way to estimate the length of the polypeptide chains that arise from translation is to divide the number of nucleotides transcribed by three
    a. True
    b. False

For questions 33-35, given the following DNA sense strand:

5’ ATG TAC CGG ACC TGA 3’

33. Which is the corresponding DNA template (antisense) strand?
    a. 5’ TAC ATG GCC TGG ACT 3’
    b. 3’ TAC ATG GCC TGG ACT 5’

34. Which is the corresponding mRNA?
    a. 3’ AUG UAC CGG ACC UGA 5’
    b. 5’ AUG UAC CGG ACC UGA 3’

35. Which is the correct translation?
    a. Ser Pro Gly His Val
    b. Met Tyr Arg Thr STOP
    c. Met Arg Tyr Thr STOP
    d. STOP Thr Arg Tyr Met

36. Homologous chromosomes pair during
    a. mitosis
    b. meiosis
    c. mitosis and meiosis

37. The C-value paradox refers most correctly refers to
    a. The fact that polyploids always have bigger genomes than diploids
    b. Chromosomes architecture varies greatly between eukaryotes and prokaryotes
    c. At a given ploidy level (e.g. when comparing two different diploids) genome size is not related to chromosome number or the number of genes

38. According to the assigned reading, the conservation of DNA sequence in non-coding DNA in two distantly related organisms implies that
    a. non-coding DNA has a functional role
    b. non-coding DNA has no functional role
    c. the amount of non-coding DNA is directly related to evolutionary complexity

39. A recessive trait can be due to
    a. complete deletion of a gene
    b. deletions or insertions of multiple nucleotides at key regions of a gene
    c. nucleotide substitutions at key regions of a gene
    d. all of the above

40. In the S phase of meiosis, DNA replication is
    a. conservative
    b. semiconservative
    c. liberal
    d. communist

41. You are trying to determine whether a DNA sequence is a gene. What sequence would help confirm that it is a gene if found 30bp upstream (5') from the transcription start site?
    a. AAAAAAA
    b. TATA
    c. GATTACA
    d. GCGCGC
    e. ATG

42. mRNA processing in eukaryotes refers to
    a. 3' caps, 5' tails, and exon removal
    b. 5' caps, 3' tails, and intron removal
    c. folding
    d. coupling of the ribosomal subunits

43. Which of the following is most true when it comes to extracting plant genomic DNA for sequencing?
    a. Longer fragments of DNA are better – restriction enzymes can then be used to cut the long fragments into target lengths
    b. Shorter fragments are better so that you do not need to use restriction enzymes

44. Which of the following two elements are essential for making cDNA from mRNA?
    a. A 5'cap and TAQ polymerase
    b. A 3' poly-A tail and reverse transcriptase
    c. An oligo corresponding to the target promoter and RNA polymerase
    d. Micron beads, adapters, and emulsion PCR

45. An "oligo", as used in PCR, refers to
    a. The RNA primers that initiate DNA replication during the S phase
    b. The naturally occurring DNA nucleotide variants found most often in 5' UTRs
    c. Nucleotides lacking a 3' OH group used in chain termination sequencing
    d. Synthetic DNA primers that are designed and produced in order to amplify target DNA regions

46. Restriction enzymes are such useful molecular tools because
    a. They cut up bacteria that invade and contaminate sterile cell cultures
    b. They cut DNA at defined recognition sequences and the longer the target sequence the more often it occurs in any given sample of DNA
    c. They make molecular biology more exciting because you never know at what DNA sequence they will cut
    d. They cut DNA at defined recognition sequences and the shorter the target sequence the more often it occurs in any given sample of DNA

47. If you use a methylation sensitive restriction enzyme you will be more likely to
    a. not make cuts in non-coding and/or low expression regions of the genome
    b. make cuts in non-coding and/or low expression regions of the genome
    c. make cuts every 400 nucleotides
    d. make cuts only in single stranded DNA

48. A cloning vector, such as a plasmid, is used to construct libraries for whole genome sequencing using both Sanger sequencing and Illumina next generation sequencing.
    a. T
    b. F

49. Which of the following vectors would you choose for cloning large (~ 200 kb) genomic DNA fragments?
    a. Bacterial plasmid
    b. Bacterial artificial chromosome (BAC)

50. If your goal is to study promoter and dark matter sequences, what type of library would you use?
    a. cDNA
    b. gDNA
    c. rRNA
    d. tRNA

51. Which of the following best describes three cyclic steps in PCR, in the correct order?
    a. Denaturing DNA to make it single stranded, primer annealing, synthesis of a new DNA strand
    b. Primer annealing, denaturing DNA to make it single stranded, synthesis of a new DNA strand
    c. Synthesis of a new DNA strand, primer annealing, denaturing DNA to make it single stranded

52. TAQ polymerase is so special and useful for PCR because
    a. It can replicate DNA faster than any other polymerase
    b. It can create amino acid strands complimentary to RNA strands
    c. It can synthesize new DNA strands, form a DNA template at high (~ 70^0C) temperatures
    d. It can synthesize new DNA strands, form a DNA template at low (~ 7^0C) temperatures

53. After 30 cycles of PCR, approximately how many copies of your target sequence do you expect for each starting DNA strand with your target region:
    a. Tens
    b. Hundreds
    c. Thousands
    d. Billions

54. Dideoxy sequencing is also known as chain termination sequencing because
    a. The dideoxy nucleotide prevents further synthesis of DNA due to the lack of a free 5' carbon
    b. The dideoxy nucleotide prevents further synthesis of DNA due to the lack of a free 3' OH
    c. The dideoxy nucleotide prevents further synthesis of DNA due to the lack of a nitrogen-containing base (e.g. A,T, C, or G)
    d. Chain termination is the same as sequencing by synthesis

55. Illumina and 454 sequencing are based on
    a. sequencing by synthesis
    b. chain termination
    c. nanopores

56. Why does the OSU Center for Genomics Research and Biocomputing (CGRB) Central Services Lab continue to offer Sanger sequencing?
    a. It is the cheapest sequencing technology available
    b. It is the fastest sequencing technology available
    c. It does not involve dideoxy nucleotides
    d. It is still a gold standard for accuracy and read length

57. In the context of DNA sequencing, what is a contig?
    a. A set of overlapping DNA fragments
    b. The number of nucleotides per centiMorgan
    c. The amount of DNA sequence that is found in one read
    d. A mature mRNA in which introns have been removed

58. Which of the following "omes" relates to the DNA sequence of expressed genes?
    a. Genome
    b. Exome
    c. Proteome
    d. Metabolome

59. According to the assigned reading on Illumina sequencing, if your plant has a genome size of ~3,000 Mb how long would it take to sequence 5 different accessions?
    a. One day
    b. One week
    c. One year

60. According to the assigned reading on Illumina sequencing, the first human genome was sequenced using capillary electrophoresis and took approximately how long and at what cost?
    a. One year and 3 million USD
    b. 5 years and 30 million USD
    c. 10 years and 3 billion USD
    d. 100 years and 30 billion USD

61. According the assigned reading on PCR, the PCR technique is both a thermodynamic and an enzymatic process
    a. True
    b. False

62. According the assigned reading on PCR, the length of a standard PCR primer is
    a. ~ 5 nucleotides
    b. ~ 25 nucleotides
    c. ~ 250 nucleotides
    d. ~ 500 nucleotides

63. In the assigned reading on "Biology's Dry Future", a maize geneticist reported that genetic factors controlling disease resistance and flowering time were found in non-coding DNA. This means that
    a. There are important regulatory regions in non-coding DNA that affect the expression of genes that encode proteins associated with disease resistance and flowering time phenotypes
    b. There are no genes for disease resistance and flowering time – these phenotypes are determined only by the environment
    c. Non-coding regions are monomorphic in terms of their DNA sequence

64. According to the assigned reading on sequencing the genome of the woodland strawberry, at what approximate level of coverage was the woodland strawberry sequenced?
    a. 3X
    b. 30X
    c. 300X
    d. 3,000X

65. According to the assigned reading on sequencing the genome of the woodland strawberry, the genome of this plant was assembled *de novo* and anchored to a linkage map. This means that
    a. The DNA for each chromosome (linkage group) was isolated and sequenced
    b. DNA from the whole genome was sequenced and matching sequences were then identified in the genome sequence and in markers on the linkage map
    c. Markers in each linkage group were sequenced and then connected to form a genome sequence
    d. Oligonucleotide pseudomolecules were synthesized that match each linkage group

66. All useful and polymorphic molecular markers are in exons
    a. T
    b. F

67. A perfect marker is
    a. Linked to the gene of interest
    b. Unrelated to the gene of interest
    c. In the gene of interest

68. Molecular breeding based on DNA markers and transgenics both use the tools of biotechnology. The two approaches differ in that:
    a. DNA markers involve the gene gun (biolistic transformation) whereas transgenics are made using Agrobacterium
    b. Molecular breeding uses markers to find target genes in a crop (or its relatives) and to track these genes in sexually derived cross progeny whereas transgenics involves the non-sexual transfer of genes
    c. Developing DNA markers requires a whole genome sequence whereas transgenics only requires knowing about the target gene
    d. Molecular markers were used to select for the glyphosate resistant enzyme encoded by the C4EPSPS found in rare varieties of wild corn and transgenic technologies were used to find the gene in the wild corn.

69. Monomorphic markers are
    a. Not informative for linkage map construction
    b. Useful for identifying regions of the genome that may indicate shared ancestry in two individuals
    c. Both of the above
    d. None of the above

70. In order to detect a dinucleotide simple sequence repeat (microsatellite) polymorphism in genomic DNA of your favorite plant, which of the following is required?
    a. All plant specimens need to have the same unique DNA sequences flanking the variable length repeat
    b. All plant specimens need to have different DNA sequences flanking the variable length repeat
    c. A restriction enzyme is required that cuts every two nucleotides in the repeat region of each plant specimen
    d. A labeled probe to detect RNA: DNA hybridization

71. SNPs – and other molecular markers – can be used to generate maps. Which of the following are examples of the utility of linkage maps?
    a. Determine evolutionary relationships
    b. Find the genome location of target genes
    c. Determine how many base pairs a target gene is from the centromere
    d. A and b, above
    e. All of the above

72. Unwanted gene flow from crops to weedy relatives is only an issue with transgenics. It is not a concern when alternative alleles are induced by mutation or introduced using sexual crossing.
    a. T
    b. F

73. In the C4 EPSPS transgene example described in class, the CAMV35S promoter was used. This means that:
    a. The promoter was discovered in cauliflower and it limits expression of the gene to leaves of the corn plant
    b. The promoter is 35 times faster than the previous model and it introduces a premature stop codon in the target gene
    c. The promoter occurs naturally in a virus and in transgene constructs it leads to constitutive expression of genes put under its control
    d. The promoter occurs naturally in a virus and it is a key component of the CRSPR and CIBUS genome editing techniques

74. The key difference between transgenics and cisgenics is that
    a. Transgenics have the promoter controlling the transgene on one chromosome and the transgene coding region on a different chromosome whereas cisgenics have the promoter and transgene fused in a single construct
    b. Transgenics always have selectable markers and cisgenics never have selectable markers
    c. Most GMO crops in production today were derived by cisgenics, not transgenics
    d. Cisgenics involves non-sexual transfer of genes from the same or closely related species whereas transgenics involves non-sexual transfer of genes from species that are not sexually compatible

75. Both hemizygotes and homozygotes for the C4 EPSPS gene still produce an enzyme that is inhibited by glyphosate but both types are resistant to the herbicide.
    a. T
    b. F

76. Transgenes and naturally occurring genes have the same essential components: promoter, coding region, and terminator sequence
    a. T
    b. F

77. The principal reason for using an antibiotic selectable marker is to make the tissue cultures resistant to contamination by bacteria
    a. T
    b. F

78. After particle bombardment, reporter genes are used to kill cells that do not carry the target transgene
    a. T
    b. F

79. The principal advantage of Agrobacterium-mediated transformation over biolistic transformation is that it usually introduces fewer copies of the transgene.
    a. T
    b. F

80. If you suspected gene flow from a creeping bentgrass plant with the C4 EPSPS gene (which confers resistance to glyphosate) to a wild relative that is susceptible to the herbicide, how could you determine if the F1 hybrid carried the transgene?
    a. PCR for the transgene in the F1
    b. Spraying the F1 with roundup herbicide
    c. Selfing the F1 and spraying the cross progeny with roundup herbicide
    d. PCR for the transgene in the selfed progeny of the F1
    e. All of the above

81. Genome editing is a technology that requires information about target genes in order to make specific changes in them that will result in changes in phenotype
    a. T
    b. F

82. The Clearfield wheat varieties that are resistant to herbicide were developed using CRSPR technology.
    a. T
    b. F

83. Both CRSPR technology and restriction enzymes are based on naturally occurring bacterial defense systems
    a. T
    b. F

84. One of the drawbacks to the CRSPR genome editing technology is that it can only be applied to exons
    a. T
    b. F

85. If a polyploid has ~ 90,000 genes and a diploid ancestor has 30,000 genes, the polyploid will, on average, be 3 times as productive as the diploid ancestor
    a. T
    b. F

86. A key difference between and aneuploids and euploids is that
    a. Aneuploids have exact multiples of the x chromosome number
    b. Euploids have exact multiples of the x chromosome number
    c. Aneuploids originate from interspecific hybridization and euploids do not
    d. Aneuploids do not have spindle fibers

87. In the case of an autotetraploid, the statement “only two alleles are possible at a locus but many alleles are possible in a population” is no longer correct in what sense?
    a. There may be up to four different alleles at a locus in an individual plant
    b. Only four alleles are possible in a population of the autotetraploid individuals
    c. Both a and b, above
    d. Neither a nor b, above

88. Allopolyploids arise through the
    a. Spontaneous doubling of homologous chromosomes within a species
    b. Interspecific hybridization and chromosome doubling

89. Homoeologous chromosomes are found in both autopolyploids and allopolyploids
    a. T
    b. F

90. Homoeologous chromosomes are examples of complete, or nearly complete synteny
    a. T
    b. F

91. In both autopolyploids and allopolyploids, bivalent pairing is the key to full fertility
    a. T
    b. F

92. Bread wheat (2n = 6x = 42) is an allopolyploid that was created by humans through the intentional and sequential hybridization of various diploid ancestors, starting approximately 10,000 years ago in the New World.
    a. T
    b. F

93. If you have a species that is 2n = 2x = 14 (RR) and your cross it with a related hexaploid species (2n = 6x = 42; AABBDD) the F1 will be
    a. Sterile
    b. Have 42 chromosomes
    c. Both a and b, above
    d. Neither a nor b, above

94. In the preceding question, if the ABDR plant undergoes chromosome doubling, the resulting plant will be
    a. Diploid
    b. Tetraploid
    c. Hexaploid
    d. Octaploid

95. If you wanted to breed a seedless triploid watermelon you would cross
    a. 2x x 2x
    b. 2x x 3x
    c. 2x X 4x

96. The cultivated banana is sterile because it is
    a. Self-incompatible
    b. Male sterile
    c. Triploid
    d. Epigenetically silenced

97. A haploid plant is sterile because it has 1 homologous chromosome per nucleus
    a. T
    b. F

98. The advantage of doubled haploids for plant breeding and genetics is that by doubling the chromosome number you make plants that are
    a. Homozygous at all loci
    b. Heterozygous at all loci

99. Doubled haploids can only be made from diploids – not from polyploids
    a. T
    b. F

100. In hybrid corn production, doubled haploids are used to
    a. Create true breeding F1 plants, identical to those that would result from apomixis
    b. Create true breeding completely inbred corn varieties so that farmers do not have to buy hybrid seed each year
    c. Accelerate the development of completely homozygous inbred parent that are then crossed to produce F1 hybrid seed