**Exam 3 Plant Genetics 2011**

1. Considering the case of “Roundup Ready” sugarbeet seed production in the Willamette Valley, which of the following gene flow mechanisms is the most likely?
	1. Sugar
	2. Prions
	3. Eggs
	4. Pollen
2. If there is gene flow between a homozygous diploid Roundup Ready plant and a homozygous non-Roundup Ready plant of the same species, the phenotype of the hemizygous F1 generation will be:
	1. Segregating 1:1 for Roundup resistance: susceptibility
	2. Segregating 3:1 for Roundup resistance: susceptibility
	3. All Roundup resistant
	4. All Roundup susceptible
3. You cross two of the hemizygous F1 plants described in question # 2. In the F2, what do you expect?
	1. Quantitative inheritance
	2. Qualitative inheritance
	3. Low heritability
	4. Epistasis
4. A homozygous allohexaploid Roundup Ready plant pollinates a homozygous allohexaploid non-Roundup Ready plant of the same species. The hemizygous F1 plant is self-pollinated. What phenotypic ratio do you expect in the F2? Assume bivalent pairing.
	1. Segregating 9:3:3:1 for Roundup resistance: susceptibility
	2. Segregating 3:1 for Roundup resistance: susceptibility
	3. All Roundup resistant
	4. All Roundup susceptible
5. An autotetraploid Roundup Ready plant with one copy of the EPSPS gene pollinates an autotetraploid non-Roundup Ready plant of the same species. Assume bivalent pairing. You expect all F1 plants to be resistant to Roundup.
	1. T
	2. F
6. You create a transgenic autohexpaloid obligate apomict with one copy of the EPSPS gene. This plant sets 100 seeds. What is your expectation for the phenotypes of plants grown from these seeds?
	1. Segregating – some plants Roundup resistant and others susceptible
	2. All plants susceptible to Roundup
	3. All plants resistant to Roundup
	4. No expectations – anything could happen
7. In most angiosperms, the chloroplasts are maternally inherited. If you created a transgenic plant with the EPSPS gene in the chloroplast rather than the nucleus, what would you expect in terms of the Roundup reaction phenotype in the progeny of this plant?
	1. Segregation
	2. Independent assortment
	3. All progeny will be like the mother plant
	4. Crossovers at pachynema
8. You create a transgenic plant in a dioecious species, where the male is XY and the female is XX. You “insert” a gene conferring resistance to insects on the Y chromosome. What phenotypes do you expect in the progeny of your transgenic male crossed with a non-transgenic female?
	1. All females susceptible and all males resistant
	2. All females resistant and all males susceptible
	3. All males and all females resistant
	4. All males and all females susceptible
9. What is the most likely number of genes in a diploid plant (at the n level, which is the usual convention for stating the number of genes)?
	1. 15,000
	2. 30,000
	3. 60,000
	4. 120,000
10. The genome size of the green bean is approximately 587 Mb while that of the Ponderosa pine is approximately 23,668 Mb. Which of the following statements best describes this situation?
	1. Small plants always have smaller genome sizes than big plants
	2. Gymnosperms always have smaller genome size than angiosperms
	3. There is no direct relationship between genome size and the size of an organism
	4. The Ponderosa pine will have a higher Mb:cM ratio than the green bean.
11. The two alleles at a locus (where the locus corresponds to the location of a gene on a chromosome) in a diploid organism
	1. May be identical in DNA sequence
	2. May differ in DNA sequence for only one nucleotide
	3. May differ in DNA sequence for multiple nucleotides
	4. May differ in that the gene is present on one homolog and completely missing on the other homolog
	5. All of the above
12. The two alleles at a locus (where the locus is defined as a molecular marker based on PCR and electrophoresis)
	1. May show codominance
	2. May show dominance
	3. May show epistasis
	4. None of the above
	5. A and B above
13. It is possible that alleles at two different loci could show both epistasis and independent assortment.
	1. T
	2. F
14. The source of new alleles (as defined by difference in DNA sequence) is
	1. Recombination between loci
	2. Mutation
	3. Epigenetics
	4. Translocations involving breakage and reunion of non-homologous chromosomes

**Use the following information to answer questions 15 – 17.** You have 100 F2 chile pepper plants in your garden. They were grown from seed you obtained by selfing F1 hybrid plants. The F1 plants all had red peppers and were tall. Your goal is to develop a homozygous red pepper/dwarf height variety. You record the following data on the F2:

* + - 57 red pepper and tall plants
		- 17 red pepper and dwarf plants
		- 19 green pepper and tall plants
		- 7 green pepper and dwarf plants
1. What is the most likely explanation for the observed F2 phenotypes?
	1. Height and color are the pleiotropic effects of a single gene
	2. Height and color are the results of epistasic interactions
	3. Height and color are quantitative traits, each determined by many genes
	4. Height is controlled by alleles at one locus and color by alleles at another locus
2. If you calculate a chi square test for the chile pepper color/height data, how many degrees of freedom would you use to determine if you will accept or reject your hypothesized ratio?
	1. 1
	2. 2
	3. 3
	4. 4
3. You save 100 seeds harvested from the 17 red pepper/dwarf plants. You plant the 100 seeds and grow the F3 generation. Which of the following is the most realistic expectation?
	1. All plants will meet your goal of being homozygous for red color and dwarf height
	2. Some plants will meet your goal of being homozygous for red color and dwarf height
	3. No plants will meet your goal of being homozygous for red color and dwarf height
4. The genome sizes of cocoa and strawberry fall into which of the following ranges?
	1. 100 - 500 Kb
	2. 100 - 500 Mb
	3. 1,000 – 5,000 Mb
	4. 10,000 – 50,000 Mb
5. Sex determination in plants that do not have perfect flowers is based on the selective abortion of floral organs.
	1. T
	2. F
6. Cross-pollination has so many disadvantages that most plants are either self-incompatible hermaphrodites or are obligate apomicts.
	1. T
	2. F
7. Self-incompatibility is a mechanism for ensuring that plants achieve high levels of homozygosity at a maximum number of loci
	1. T
	2. F
8. In the case of the maize T cytoplasm, male sterility and susceptibility to Southern Corn Leaf Blight are the pleiotropic effects of a gene located in the
	1. Nucleus
	2. Mitochondrion
	3. Chloroplast
	4. Ribosome
9. Each autosome during the G1 stage of mitosis consists of
	1. Only dark matter
	2. A single DNA molecule
	3. Pure heterochromatin
	4. 100 centiMorgans, which equals exactly 500 Mb of DNA
10. Histone proteins are
	1. The building blocks of ribosomal subunits
	2. Formed in the nucleolus
	3. Found in both heterochromatic and euchromatic regions of interphase chromosomes
	4. Not encoded by genes
11. The key role of colchicine in the production of doubled haploids is that it
	1. Prevents the formation of centromeres
	2. Prevents the formation of telomeres
	3. Prevents meiosis
	4. Prevents the formation of spindle fibers
12. The nucleolus is
	1. the nucleus of a mitochondrion
	2. the site of assembly of ribosomes
	3. the membrane surrounding the nucleus
	4. responsible for epigenetic silencing of genes
13. If you have a cDNA library, it is most likely to contain
	1. DNA sequences present in euchromatin
	2. DNA sequences present in the dark matter between genes
	3. DNA sequences present in heterochromatin
	4. All of the above
14. Homologous and homoeologous chromosomes pair in both mitosis and meiosis
	1. T
	2. F
15. A plant = 2n = 2x = 30. The total number of chromatids migrating to each pole at Anaphase of mitosis will be
	1. 15
	2. 30
	3. 45
	4. 60
16. A plant = 2n = 4x = 60. The total number of chromatids migrating to each pole at Anaphase of mitosis will be
	1. 15
	2. 30
	3. 45
	4. 60
17. An allotetraploid plant is 2n = 4x = 28. Assume no homoeologous pairing. The total number of pairs of homologous chromosomes (bivalents) at Pachynema of meiosis will be
	1. 7
	2. 14
	3. 28
	4. 56
18. A plant = 2n = 2x = 30. The total number of chromosomes in each of the four microspores in the tetrad is
	1. 15
	2. 30
	3. 45
	4. 60
19. Segregation of alleles at a locus and independent assortment of alleles at two or more loci may occur during mitosis in facultative apomicts.
	1. T
	2. F
20. Independent assortment of alleles at two or more loci can be determined by
	1. Random alignment of non-homologous chromosomes at Metaphase I
	2. Crossover between homologous chromosomes at Pachynema
	3. A and B above
	4. None of the above
21. If an organism is 2n = 2x = 20, and you have data from 2,000 markers providing complete genome coverage scored on a population of 100 doubled haploid plants, you should show how many linkage maps?
	1. 5
	2. 10
	3. 20
	4. 40
22. If an allotetraploid organism is 2n = 4x = 40, and you have data from 4,000 markers providing complete genome coverage scored on a population of 100 doubled haploid plants, you should show how many linkage maps?
	1. 5
	2. 10
	3. 20
	4. 40

***Information for Questions 37 - 40***

Chromosome 3 of *Capsicum burnem* is reported to be 150 centiMorgans long. The R and H loci are shown near each other on the chromosome 3 linkage map. One locus controls pod color (alleles R\_ and rr determine red and green respectively) and the other controls flavor (alleles H\_ and hh determine hot and mild flavor, respectively). You score the two traits in 100 doubled haploid progeny derived from the F1 of the cross between two inbred parents. You record the following numbers of plants in each category:

|  |  |  |  |
| --- | --- | --- | --- |
| Red and mild  | Red and hot  | Green and mild  | Green and hot  |
| 35 | 10 | 10 | 45 |

1. The “parental” classes are
	1. Red/hot and Green/mild
	2. Red/mild and Green/hot
	3. Not identifiable given these data
2. Because the two loci are reported to be on the same chromosome, you want to see if they are linked in your cross. To do so, you would divide
	1. The parental classes/100
	2. The non-parental classes/100
	3. The non-parental + parental classes/100
3. If you calculated that the frequency of recombination is 20%, would you conclude that the report of the two loci being on the same chromosome is wrong?
	1. Yes
	2. No
4. You expect your calculated recombination % to be
	1. Lower than the cM value
	2. The same as the cM value
	3. Higher than the cM value
	4. The cM value multiplied by 0.150
5. Crossing over is such a potent source of genetic variation because it always leads to the gain or loss of chromatin.
	1. T
	2. F
6. Consider two distantly related species, such as wheat and rice. Comparing linkage maps of the two species is most useful for assessing which of the following
	1. Orthology
	2. Homology
	3. Homoeology
	4. Synteny
7. Homoeology is an example of complete synteny
	1. T
	2. F

**Use the following cartoon of a deoxyribonucleotide to answer questions 44 - 46.**

1. The nitrogen-containing bases (A,T,C, or G) will be attached to which carbon?
	1. 1’
	2. 2’
	3. 3’
	4. 4’
	5. 5’
2. The phosphate group will be attached to which carbon?
	1. 1’
	2. 2’
	3. 3’
	4. 4’
	5. 5’
3. If this was a dideoxy nucleotide, an OH group would not be present at which carbon?
	1. 1’
	2. 2’
	3. 3’
	4. 4’
	5. 5’
4. Mutations caused by DNA replication errors are relatively rare because
	1. Restriction endonucleases remove incorrect bases from the 3’ end of a developing strand
	2. Helicases have endonuclease activity and remove incorrect bases at replication forks
	3. Some polymerases have exonuclease activity and can remove incorrect bases from the 3’ end of a developing strand
	4. Telomerase repairs mutations at the telomeres
5. At a bidirectional replication fork, leading strands are
	1. Where new strands are synthesized 3’ to 5’
	2. Always on top
	3. Where Okazaki fragments occur
	4. Where new strands are synthesized 5’ to 3’

**Use the following information to answer questions 49 – 51**

 The following sequence is for the sense (non-template) DNA strand:

5’ atg gac aca 3’

1. Which is the correct antisense (template) strand sequence?
	1. 5’ tac ctg tgt 3’
	2. 3’ tac ctg tgt 5’
	3. 3’ atg gac aca 5’
	4. 5’ atg gac aca 3’
2. Which is the correct mRNA sequence?
	1. 5’ aug gac aca 3’
	2. 5’ uac cug ugu 3’
	3. 3’ uac cug ugu 5’
	4. 3’ aug gac aca 5’
3. Based on this sequence, you can tell that it came from an exon and not an intron
	1. T
	2. F
4. RNA differs from DNA in that
	1. It is usually single stranded
	2. It contains triose rather than deoxyribose
	3. It contains the base adenine rather than thymine
	4. It is always single stranded
5. tRNA is an example of informational RNA
	1. True
	2. False
6. mRNA consists of 28S and 5.8S subunits
	1. True
	2. False
7. When RNA has a regulatory role, as in RNAi, this involves
	1. Methylating the DNA
	2. Introducing premature stop codons
	3. Removing genes from the DNA
	4. Degrading mRNA transcripts
	5. Removing 3’ caps and 5’ tails
8. Where would you expect to find a TATA box?
	1. 5’UTR
	2. Promoter
	3. Intron
	4. Exon
	5. 3’UTR
9. You are interested in the sequence of the promoter and introns in the BAD2 gene of rice. Which type of library would be most suited for finding this information?
	1. CDS
	2. Genomic
	3. cDNA
	4. Lend-lease
10. In a transgene construct, the stop codon is an essential component because it signals the end of transcription.
	1. T
	2. F
11. All eukaryotic genes have introns
	1. T
	2. F
12. Your local supplier of useful genetic information offers you AFLP genotyping service. This service would be most useful for
	1. Detecting INDELs based on microsatellites
	2. Characterizing consensus promoter sequences
	3. Detecting EPSPS gene flow
	4. Characterizing the degree of genetic diversity in garlic clones collected from around the world
13. The following example showing sequence and codon alignments, as well as the translated protein, is an example of what type of mutation?
	1. Frameshift
	2. Missense
	3. Silent
	4. Nonsense

	

**Use the following information to answer questions 64 - 66** The following diagram illustrates the results of electrophoresis of PCR products, representing two possible alleles at the *VRN-H1* locus, from genomic DNA of Parent 1(P1), Parent 2 (P2), and the F1 derived from crossing P1 x P2.

|  |
| --- |
| P1 P2 F1---- -------- ---- |

1. The electrophoresis of these PCR products reveals marker alleles that show
	1. Epistasis
	2. Complete dominance
	3. Overdominance
	4. Codominance
2. If the basis of the polymorphism between P1 and P2 is the length of intron 1, which parent has the shorter intron 1?
	1. P1
	2. P2
	3. Neither one – the parents have the same length intron 1
3. If you developed doubled 96 haploids (DH) from the F1 of this cross, what would you expect?
	1. All the DH lines would have 2 bands, like the F1
	2. The DH lines would have bands like P1, P2, and the F1 in a 1:1:2 ratio
	3. About half the DH lines would have the P1 band and the other half would have the P2 bands
	4. The DH lines would show bands different from those observed in the parents
4. Southern Blot
	1. Technique based on hybridization of labeled single strand DNA probe and single strand target DNA
	2. Technique for specifically amplifying a target sequence of DNA
5. Restriction enzyme
	1. Thermostable DNA polymerase
	2. Cuts DNA at specific recognition sequence
6. The alternation of generations refers to
	1. teen: parent epistasis.
	2. the progeny of controlled crosses between gymnosperms.
	3. hemizygosity of transgenes.
	4. the haploid and sporophytic stages of plant life cycles.
7. If a plant breeder is going to cross two genetically different varieties to study the genetics of a trait that is important in the endosperm, it does matter which parent is used as the female.
	1. T
	2. F
8. Allopolyploids arise from
	1. Intra-specific hybridization
	2. Inter-specific hybridization
9. In a certain population of wheat, the heritability of kernel weight is calculated to be 30%. This means:
	1. Environmental effects are responsible for 30% of the observed variation
	2. Environmental effects are responsible for 70% of the observed variation
	3. Genetic effects are responsible for 70% of the variation
	4. None of the above
10. The heritability of stem length in the “A x B” barley population is calculated to be 0. This means that in this experiment differences in stem length among barley plants in the population are due to causes other than genetics (i.e. soil nutrition, water availability, etc)
	1. T
	2. F
11. Following up on question # 71, which of the following is true?
	1. The heritability of stem length in all barley populations will be 0
	2. If you did a better job of controlling environmental variation in a subsequent experiment involving the A x B population, the heritability might increase
	3. Heritability is so difficult to calculate that it is of little practical utility
	4. Stem length is a qualitative trait and therefore has no heritability
12. Which of the following features best describes marker data based on DNA-level polymorphisms?
	1. Highly influenced by the environment
	2. Epigenetic modifications
	3. Quantitative inheritance
	4. Qualitative inheritance
13. A quantitative trait locus (QTL) is:
	1. The location of a single gene or multiple genes determining a quantitative trait
	2. A gene determining a quantitative trait
	3. A molecular marker for a quantitative trait
	4. A gene or molecular marker determining a qualitative trait
14. If you want to do an association mapping analysis to detect QTL for fruit color intensity in tomato, which of the following would you use?
	1. Fruit color intensity and genotypic data from an array of unrelated plants
	2. Fruit color intensity and genotypic data from plants derived from a single cross
	3. Genotypic data and pedigree data from unrelated plants
	4. Sequencing mRNA from two plants differing in fruit color intensity
15. You develop a doubled haploid (DH) rice population from the F1 of the cross between variety A (tall) and variety B (short). You run 1,000 molecular markers on the population and you find that alleles at one of the marker loci - “SSR\_1” - show a non-random relationship with the phenotype: the average height of DH lines with the SSR\_1 allele from parent A is statistically different from the average height of DH with the SSR\_1 allele from parent B. Which of the following statements is true?
	1. SSR\_1 is a QTL for plant height in this population
	2. SSR\_1 is not linked to a QTL responsible for plant height in this population
	3. SSR\_1 is, beyond the shadow of a doubt, in the gene responsible for plant height in this population
	4. SSR\_1 is linked to a QTL responsible for plant height in this population
16. Quantitative traits are:
	1. Controlled by many genes with small, additive effects that are sensitive to the effects of the environment
	2. The simplest targets for genetic engineering
	3. Controlled by one or few genes with large effects that are influenced by the environment
	4. Controlled by many genes with small, additive effects that are not influenced by the environment
17. A plant heterozygous for a deficiency is expected to be
	1. Semi-detached
	2. Fully fertile
	3. Completely sterile
	4. Semi-sterile
18. You compare two linkage maps. Each map is based on a different population of the same species. Population “A X B” is derived from “normal” parents. Population “C X D” is derived from parents homozygous for an inversion.
	1. Marker order will be the same in the two maps.
	2. Marker order will be the same but distances between markers will be would be different
	3. Marker order will be different between the two maps for the region involving the inversion.
	4. The “C X D” map will be shorter than the “A x B” map due to inversion loop.
19. Which of the following statements is correct?
	1. Partial sterility is expected when crossovers occur outside the inversion loops in inversion heterozygotes
	2. Partial sterility is expected when crossovers occur inside the inversion loops in inversion heterozygotes
	3. Partial sterility is expected in inversion homozygotes
	4. Inversions are defined by the breakage and reunion of chromosome segments from non-homologous chromosomes