**Exam 2 PBG430-530, 2017**

**Online - The exam is available for 60 minutes.**

**Please no open notes, texts, online search, or sharing of information with other students**

**Linkage:**

1. Non-sister chromatid exchange
	1. Leads to significant addition and losses of genetic information
	2. Is one the principal causes of genome expansion (the C-value paradox)
	3. Does not lead to the loss or addition of chromatin
	4. Occurs in both mitosis and meiosis
2. If you calculate a recombination value of 30% between two loci and convert this value to centiMorgans (Haldane or Kosambi)
	1. The cM value will be larger than the % recombination value
	2. The cM value will be smaller than the % recombination value
	3. The cM value will be the same as the % recombination value
3. Significant segregation distortion, as describe in the assigned reading by Cistue et al., would lead you to:
	1. Reject a chi square hypothesis of 1:1 segregation of alleles at a locus in a doubled haploid population
	2. Under-estimate the coefficient of coincidence
	3. Give up on trying to make a linkage map
	4. Conclude that the phenotype controlled by these alleles show quantitative rather than qualitative inheritance
4. Which of the following are the best examples of utility of linkage maps for plant geneticists?
	1. Gene discovery
	2. Measuring transcription rates of specific genes
	3. Understanding synteny
	4. Measuring DNA replication rates during the S phase
	5. All of the above
	6. None of the above
	7. A and C
5. Molecular marker linkage maps are often sufficiently dense (e.g. <10% recombination) that the usual assumption is complete interference.
	1. T
	2. F
6. Assume you have a plant that is completely homozygous. Assume that there is no mutation and that the crossover event does not involve loss or addition of chromatin. If a crossover occurs between two loci in this plant, will the crossover be detectable as a new combination of alleles at the two loci?
	1. Yes
	2. No
	3. No way to know
7. If there is 14% recombination between the N locus and the L locus; there is 39% recombination between the W locus and the N locus; and there is 48% recombination between the W and L loci, what is the most likely order of these loci in a linkage map?
	1. NLW
	2. LWN
	3. WNL
	4. No way to know
8. Double crossovers can complicate genetic analysis because they lead to incorrect estimates of the correct % recombination between two adjacent loci. Consider the case of two loci and the possible types of double crossovers between them (3-strand and 4-strand).
	1. Both types of double crossovers will give the same ratios of parental: non-parental combinations of alleles at the two loci.
	2. Three strand doubled crossovers will give different ratios of parental: non-parental combinations of alleles than the 4-strand double crossovers
9. You have two different linkage mapping populations in the common bean. Which of the following is most likely (assuming that your data are excellent for both populations)?
	1. The loci in the two maps will be in different orders for a given linkage group
	2. The loci in the two maps will be in the same order for a given linkage group but distances between loci may vary
10. In the following map, locus 392 and locus 177 are in the same linkage group. If you measured recombination between just those two loci you would expect to see:
	1. 0% recombination
	2. independent assortment
	3. 101% recombination



1. Mutation is the source of new alleles and recombination is the source of new combinations of alleles
	1. T
	2. F
2. You are offered a job breed a new variety of tomato with great flavor and long shelf life. Experience and data confirm that poor flavor and long shelf life are associated. Which of the following genetic phenomenon would offer you the greatest chance of success in your new job?
	1. Flavor and shelf life are the pleiotropic effects of the same gene
	2. Flavor and shelf life are controlled by two tightly linked genes
3. Knowing the Haldane cM distance between two loci in an ancestral diploid species and polyploid relative is most useful for potentially understanding which of the following?
	1. Homoeology and syntney
	2. Orthology and systematics
	3. Orthology and ornithology

**DNA structure and function**

1. One of the features of DNA that makes it an ideal genetic material is that it is capable of change. Which of the following terms best describes the “capability for change”
	1. Semiconservative replication
	2. Information content
	3. Mutation
	4. None of the above
2. In a double helix of DNA, there are hydrogen bonds
	1. Between the phosphate groups of contiguous nucleotides
	2. Between the paired bases
	3. Between the histone proteins and the free 3’ OH group of each nucleotide
	4. All of the above
3. Which of the following is **not** essential for DNA synthesis?
	1. A promoter
	2. dNTPs
	3. Template DNA
	4. DNA polymerase
4. A polymerase with exonuclease activity will most likely cleave
	1. an unpaired nucleotide from the 3’OH end of the developing strand
	2. an unpaired nucleotide from the 5’OH end of the developing strand
	3. between nucleotides in the parental template strand
5. Which of the following is most likely to prevent a mutation from occurring during DNA replication?
	1. Removal of the RNA primer that initiated replication
	2. Removal of an unpaired nucleotide from the 3’OH end of the developing strand
	3. Endonuclease activity leading the removal of an exon
6. Where do you expect Okazaki fragments?
	1. Leading strands
	2. Lagging strands
	3. At the replication fork, where they stabilize the open DNA helix
7. What 3 factors would lead you to deduce that there must be multiple origins of DNA replication in a plant genome?
	1. The length of the G2 phase, the length of the telomere, and the length of the centromere
	2. The size of the plant, the rooting volume of the plant, and the average yield per acre of the plant
	3. The size of the genome, the rate of DNA synthesis, and the length of the S phase
8. After DNA replication in mitosis, one of the mature daughter chromosomes will consist of a mosaic of RNA and DNA due to the need for RNA primers to initiate DNA replication
	1. T
	2. F
9. Telomere shortening, if it is going to occur in mitosis, will occur
	1. On the leading strand
	2. On the lagging strand
	3. On both the leading and lagging strands
10. Mutations are rare and usually deleterious. However, genetic analysis requires abundant DNA polymorphisms. Where would you most likely expect to find abundant polymorphisms that do not lead to major effects on phenotype?
	1. UTRs
	2. Exons
	3. Promoters

**DNA to protein**

1. The sequence of the promoter can be found in a mRNA sequence.
	1. T
	2. F
2. mRNA processing in eukaryotes refers to
	1. 5’ caps, 3’ tails, and intron removal.
	2. 3’ caps, 5’ tails, and exon removal.
	3. transport of the mRNA to the cytoplasm.
	4. coupling of the ribosomal subunits.
3. A diagnostic sequence always found in 5’ UTRs is the ATG start codon.
	1. T
	2. F
4. Exons are always longer than introns.
	1. T
	2. F
5. One of the explanations for the fact that in eukaryotes ~ 30,000 genes can specify ~ 100,000 proteins is
	1. alterative 5’ capping.
	2. alternative removal of introns and splicing of exons.
	3. alternative use of 3’ and 5’ promoters.
	4. each gene is transcribed 5’ to 3’ and 3’ to 5’ on leading and lagging strands.
6. Transfer RNAs (tRNAs)
	1. very generic, with each tRNA able to carry any of a number of amino acids.
	2. are coded for by sequences in introns.
	3. are very specialized, with each tRNA able to carry a specified amino acid.
	4. consists of 15S and 35S subunits.
7. The components of ribosomes are
	1. specific to each type of mRNA.
	2. coded for by nuclear genes.
	3. formed by exon shuffling.
	4. double stranded RNA molecules.
8. The mechanism by which a stop codon stops translation is that
	1. tRNAs with affinity to the stop codon always bring methionine.
	2. polymerases have exonuclease activity.
	3. there are no tRNAs with anticodons matching the stop codon.
	4. the ribosomes pinch off the completed sequence of amino acids.
9. The DNA code is degenerate because
	1. the same codons specify different amino acids in different organisms.
	2. start and stop codons are reversed in prokaryotes and eukaryotes.
	3. the same amino acid can be specified by more than one codon.
	4. the same codon can specify different amino acids.
10. Given the following DNA sense strand – 5’ ATG GCC TGG ACT TCA 3’, what is the corresponding mRNA?
	1. 5’ UAC CGG ACC UGA AGU 3’
	2. 5’ AUG GCC UGG ACU UCA 3’
	3. 3’ UAC CGG ACC UGA AGU 5’
	4. 3’ AUG GCC UGG ACU UCA 5’
11. Given the following DNA sense strand – 5’ ATG GCC TGG ACT TCA 3’, what the correct translation?
	1. Tyr Arg Thr Stop Ser
	2. Met Ala Trp Thr Ser
	3. Ser Thr Trp Ala Met
	4. Thr Ser Gly Pro Val



1. If you know the primary structure of a protein you can deduce the exact DNA code of the corresponding gene.
	1. T
	2. F
2. 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
	1. a premature stop codon in the aromatic allele due to a SNP.
	2. a premature stop codon in the aromatic allele due to a frameshift mutation.
	3. a premature stop codon in the non-aromatic allele due to a frameshift mutation.
	4. post-translational modifications of the betaine aldehyde dehydrogenase gene product.
3. 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:
	1. failure of transcription of the gene to a mRNA.
	2. failure to add a 3’ tail to the mRNA corresponding to this gene.
	3. failure of translation of the mRNA corresponding to this gene.
	4. failure of the protein to assume its three-dimensional configuration.
4. The HvCBF2 gene used as an example in class is different from many other plant genes because it does not have
	1. Exons
	2. Introns
	3. A start codon
	4. A stop codon
5. In both the replication of DNA and the transcription of DNA
	1. Okazaki fragments are formed.
	2. Promoters are the binding site for RNA and DNA polymerases.
	3. Synthesis of new strands proceeds 5’ to 3’, with nucleotides added to the ends of developing strands.

**Gene to phenotype**

1. In the case of complete dominance, what is the simplest and most likely explanation for the lack of a recessive allele?
	1. Loss of function due to a premature stop codon
	2. Silent mutation
	3. Gene deletion
	4. A and b
	5. A and c
2. In the case of complete dominance, the homozygous recessive condition always leads to less of a phenotype (e.g. less color, less aroma, fewer fertile florets per rachis node)
	1. T
	2. F
3. In the case of incomplete dominance, where one parent has red flowers, the other parent has white flowers and the F1 has pink flowers what will be the expected ratio of flower color in doubled haploids derived from the F1?
	1. 3 red: 1 white
	2. 1 red: 2 pink:1 white
	3. 1 red: 1 white
	4. 1 red: 0 white
4. In the case of codominance, heterozygous F2 plants can be distinguished from homozygous F2 plants.
	1. T
	2. F
5. There are two classical theories for the genetic basis of hybrid vigor. These are:
	1. Epistasis and codominance
	2. Overdominance and dispersed dominant genes
	3. Obligate and facultative apomixis
	4. Monoecy and dioecy
6. The two classical theories of heterosis are mutually exclusive in that according to one of the theories the F1 will always be superior to the parents and according to the other theory it is theoretically possible to accumulate all possible favorable alleles in a single homozygous plant
	1. T
	2. F
7. According to the assigned reading on the molecular basis of heterosis, the majority of genes differentially expressed between the parents will be
	1. Expressed at the high parent level in the F1
	2. Expressed at the mid-parent level in the F1
	3. Expressed ad the low parent level in the F1
8. Epistasis can be observed when considering alleles at just one locus
	1. T
	2. F
9. In the vernalization example given in class there are three loci involved in vernalization. Which of the following is most correct?
	1. In a set of homozygous progeny derived by selfing a plant heterozygous at all three loci, vernalization sensitivity will occur at a high frequency because it can result from 7/8 possible combinations of alleles at the three loci.
	2. In a set of homozygous progeny derived by selfing a plant heterozygous at all three loci, vernalization sensitivity will occur at a low frequency because it can result from only 1/8 combinations of alleles at the three loci.
	3. Vernalization is strictly due to epigenetics and does not involve allelic variation at the DNA level.
10. Which of the following genetic scenarios relates to *VRN-H1* (the meristem identity gene)?
	1. Alternative functional alleles
	2. Gene deletion
	3. Chromatin remodeling
	4. A and b
	5. A and c
11. The VRN isogenic lines of barley, reported by Takahashi and Yasuda in 1971, were developed by
	1. CRISPR
	2. RNAi
	3. Doubled haploidy
	4. Backcrossing