PLNT2530 PLANT BIOTECHNOLOGY

MID-TERM EXAMINATION

11:30 am to 12:20 pm We

Wednesday, February 26, 2020

Answer any combination of questions totalling to <u>exactly</u> 100 points. If you answer questions totalling more than 100 points, answers will be discarded at random until the total points equal 100. The questions total to 120 points. This exam is worth 20% of the course grade.

Hand in these question sheets along with your exam book. Question sheets will be shredded.

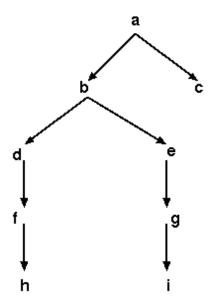
Ways to write a readable and concise answer:

- i. Just answer the question. Save time by specifically addressing what is asked. Don't give irrelevant background if it doesn't contribute to the question that was asked.
- ii. Avoid stream of consciousness. Plan your answer by organizing your key points, and then write a concise, coherent answer. Make your point once, clearly, rather than repeating the same thing several times with no new information.
- iii. Point form, diagrams, tables, bar graphs, figures are welcome. Often they get the point across more clearly than a long paragraph.
- iv. Your writing must be legible. If I can't read it, I can't give you any credit.
- 1. (15 points) In your exam booklet, re-write the table, using the terms below. Some terms may be used more than once. Some may not be used at all.

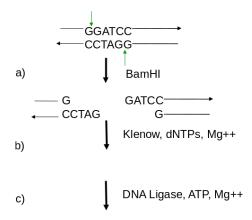
| | plastid | mitochondrion | nucleus |
|---------------------------|---------|---------------|---------|
| genome size (bp) | | | |
| copies of genome per cell | | | |
| chromosome topology | | | |
| number of genes | | | |
| inheritance | | | |

| maternal | | paternal | both parents | | |
|----------|---|----------|-----------------------------------|------------------|----------|
| 1 | 2 | <100 | > 100 | 50 - 200 | 10^{5} |
| > 104 | | | 10 ⁵ - 10 ⁶ | $10^7 - 10^{12}$ | |
| linear | | circular | branched | | |

- 2. (10 points) List two aspects of DNA structure that cause single-stranded DNA to spontaneously reanneal into double-stranded DNA.
- 3. (5 points) Which of the following would you expect to see in a cDNA library:
- a) exon
- b) intron
- c) TATA box
- d) promoter
- e) 3'UTR
- 4. (5 points) PCR primers used to amplify a single gene from total genomic DNA are typically around 20 nucleotides long. Why can't these primers be, for example, 10 nucleotides long? Hint: See the table of Restriction Site Frequencies on page 7.
- 5. (10 points) Describe the purpose of a laminar flow hood. Explain how it works. Drawing a diagram may make it easier to answer this question.
- 6. (10 points) Redraw the diagram showing the differentiation of the plant body plan. Replace each of the letters a i with one of the following terms: epicotyl, hypocotyl, embryo, cotyledon, root, shoot meristem, radicle, axis, root meristem



7. (15 points) In step a), the Bluescript vector was cut with BamHI, as illustrated in the accompanying figure. Redraw the figure, showing what the result would be after steps b and c.



The sequence of the region of the Bluescript vector that includes the BamHI site is shown below. This is the only BamHI site in the vector. We see that the BamHI site is within the protein coding region for the lacZ gene. Only the beginning of the protein coding region is shown.

| lacZ gene> | KpnI | XhoI |
|-------------------------------------------------------------|-------------------------------------|------|
| atg acc atg> 802 787 772 | 757 | 742 |
| ATG ACC ATG ATT ACG CCA AGC TCG AAA TTA ACC CTC ACT AAA GGG | AAC AAA AGC TGG GTA CCG GGC CCC CCC | TCG |
| TAC TGG TAC TAA TGC GGT TCG AGC TTT AAT TGG GAG TGA TTT CCC | TTG TTT TCG ACC CAT GGC CCG GGG GGG | AGC |
| MET Thr MET Ile Thr Pro Ser Ser Lys Leu Thr Leu Thr Lys Gly | Asn Lys Ser Trp Val Pro Gly Pro Pro | Ser |
| | | |
| | | |
| Salı Clai HindIII EcoRV EcoRI Psti Smai | • | |
| 727 712 697 | 682 | 667 |
| AGG TCG ACG GTA TCG ATA AGC TTG ATA TCG AAT TCC TGC AGC CCG | GGG GAT CCA CTA GTT CTA GAG CGG CCG | CCA |
| TCC AGC TGC CAT AGC TAT TCG AAC TAT AGC TTA AGG ACG TCG GGC | CCC CTA GGT GAT CAA GAT CTC GCC GGC | GGT |
| Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn Ser Cys Ser Pro | Gly Asp Pro Leu Val Leu Glu Arg Pro | Pro |
| SacII SacI | | |
| 652 637 622 | 607 | |
| CCG CGG TGG AGC TCC AAT TCG CCC TAT AGT GAG TCG TAT TAC AAT | TCA CTG GCC GTC GTT TTA CAA C | |
| GGC GCC ACC TCG AGG TTA AGC GGG ATA TCA CTC AGC ATA ATG TTA | AGT GAC CGG CAG CAA AAT GTT G | |
| Pro Arg Trp Ser Ser Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn | Ser Leu Ala Val Val Leu Gln | |

The Bluescript vector from step c was transformed into *E. coli*, and grown on media containing antibiotic and Xgal. The resultant colonies were all white.

Explain the result.

8. (5 points) Explain the distinction between transposons and retrotransposons.

- 9. (10 points) For the following macroelements found used in tissue culture media, match each element with the phrase that best describes its role in the cell. To answer the question, simply write a list a e, with the corresponding phrase. Only use each phrase once.
- a) Nitrogen (N)
- b) Potassium (K)
- c) Calcium (Ca)
- d) Magnesium (Mg)
- e) Phosphorus (P)
- i) nucleic acids, energy transfer, req'd in respiration and photosynthesis
- ii) enzyme cofactor, component in chlorophyll
- iii) proteins, nucleic acids
- iv) regulates osmotic potential, main inorganic cation
- v) cell wall structure, membrane function, signaling
- 10. (10 points) Consider the double-stranded duplexes shown below. Which duplex will be more stable, A or B? Which duplex will be more stable, C or D? In each case, explain your reasoning.

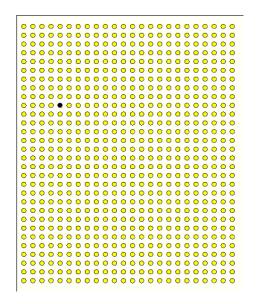
| A | | В |
|------|-------------------------------|------------------------------------------|
| 5' A | ACAATCGTAAG 3' | 5' AACTATCGTAAG 3' |
| 3' 1 | TGTTAGCATTC 5' | 3' TTGTTAGCATTG 5' |
| | | |
| C | | D |
| | _ | |
| 5' T | CTGCTAACTGA 3' | 5' CCACTGACCTGG 3' |
| | CTGCTAACTGA 3' GACGATTGACT 5' | 5' CCACTGACCTGG 3' 3' GGTGACTGGACC 5' |

11. (5 points) Based on the data in the table below, which species, do you expect to have longer chromosomes, Glycine max or Zea mays? Explain your reasoning.

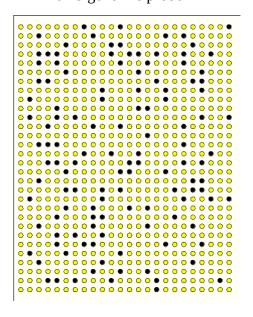
| Organism | Chromosome | | Gene No. |
|----------------------|------------|-------------------------|----------|
| | number (n) | (bp) | |
| Arabidopsis thaliana | 5 | 1.19 x 10 ⁸ | 25,400 |
| Frageria vesca | 7 | 2.80 x 10 ⁸ | 25,050 |
| Brassica rapa | 10 | 2.84 x 10° | 41,174 |
| Oryza sativa | 12 | 4.66 x 10 ⁸ | 58,000 |
| Glycine max | 20 | 1.10 x 10 ⁹ | 46,430 |
| Zea mays | 10 | 2.80 x 10 ⁹ | 63,000 |
| Triticum aestivum | 21 | 1.70 x 10 ¹⁰ | 41,910 |

12. (10 points) A BAC library from pea (Pisum sativum) was screened with two probes. The first probe was a cDNA clone for pea defense gene DRR206. An identical filter was also probed using as a probe a 6 kb genomic fragment containing the DRR206 gene. Hybridization results for the two experiments are shown below. What is the most likely explantaion for the different results? You can assume that trivial explanations such as probe contamination are not

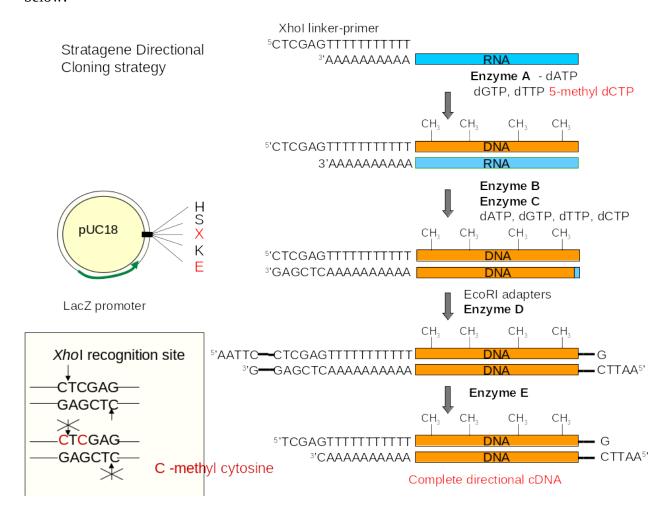
cDNA probe



6 kb genomic probe



13. (10 points) List the names of Enzymes A - E, used in the cDNA cloning protocol shown below.



Genetic code

| | | | | Secon | d base | | | | |
|--------------------|-----|--------|-----|-------|--------|-----|------|-----|------|
| | | U | | С | | Α | | G | |
| | | UUU | Phe | UCU | Ser | UAU | Tyr | UGU | Cys |
| | U | UUC | Phe | UCC | Ser | UAC | Tyr | UGC | Cys |
| | U | UUA | Leu | UCA | Ser | UAA | STOP | UGA | STOP |
| | | UUG | Leu | UCG | Ser | UAG | STOP | UGG | Trp |
| | | CUU | Leu | CCU | Pro | CAU | His | CGU | Arg |
| | С | CUC | Leu | CCC | Pro | CAC | His | CGC | Arg |
| First | 0 | CUA | Leu | CCA | Pro | CAA | Gln | CGA | Arg |
| base | | CUG | Leu | CCG | Pro | CAG | Gln | CGG | Arg |
| | | AUU | lle | ACU | Thr | AAU | Asn | AGU | Ser |
| | Α | AUC | lle | ACC | Thr | AAC | Asn | AGC | Ser |
| | , , | AUA | lle | ACA | Thr | AAA | Lys | AGA | Arg |
| | | AUG | Met | ACG | Thr | AAG | Lys | AGG | Arg |
| _ | | GUU | Val | GCU | Ala | GAU | Asp | GGU | Gly |
| Met | G | GUC | Val | GCC | Ala | GAC | Asp | GGC | Gly |
| Wet | | GUA | Val | GCA | Ala | GAA | Glu | GGA | Gly |
| | | GUG | Val | GCG | Ala | GAG | Glu | GGG | Gly |
| LRNA LLL UAC | | | | | | | | | |
| 5' AUG cod | on | — mRNA | | | | | | | |

Frequencies of Restriction Sites (or other oligonucleotides)

| | | | <u> </u> |
|-------------|----------------------------------------------|-------------------|----------|
| length n | frequency: occurs every 4 ⁿ | example | sequence |
| 1 | 4 | Single nucleotide | G |
| 2 | 16 | Di-nucleotide | GT |
| 3 | 64 | Codon | ATG |
| 4 | 256 | Taq I | TCGA |
| 5 | 1024 | Mboll | GAAGA |
| 6 | 4096 | Hind III | AAGCTT |
| 7 | 16384 | Abe I | CCTCAGC |
| 8 | 65536 | Not I | GCGGCCGC |