GREY

PART A (**Choose only one and the best answer among the choices given.**)

1. Which of the following enzymes is required in a Sanger's DNA sequencing reaction?

   a) RNA polymerase
   b) DNA polymerase
   c) Restriction endonuclease
   d) DNA ligase
   e) More than one of the above

2. After cutting DNA, which of the following enzymes is used to join the ends of two DNA fragments?

   a) restriction endonucleases
   b) RNA polymerase
   c) DNA gyrase
   d) DNA ligase
   e) Helicase

3. DNA molecules that are synthesized from an RNA template are known as:

   a) cDNA
   b) sDNA
   c) gDNA
   d) rDNA
   e) riDNA

4. Which of the following is a DNA palindrome?

   a) 5′-AATGCCGGCATT-3′
      3′-TTACGGCCGTAA-5′

   b) 5′-AATGCCCCGTAA-3′
      3′-TTACGGGGCATT-5′

   c) 5′-AATGCCAATGCC-3′
      3′-TTACGGTTACGG-5′

   d) 5′-AATGCCTTACGG-3′
      3′-TTACGGAATGCC-5′

   e) None of the above

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5. At which level is the gene expression of eukaryotes regulated?

a) Transcription
b) Alternative splicing of RNA
c) Post-transcription
d) Post-translation
e) All of the above

6. If gene expression is regulated at the transcriptional level, where in a eukaryotic cell does this regulation take place?

a) Nucleus
b) Mitochondria
c) Rough ER
d) Ribosome
e) Cytoplasm

7. Which of the following techniques is primarily used to detect the presence of a particular DNA sequence?

a) Southern Blotting
b) Northern Blotting
c) RT-PCR
d) ligation
e) More than one of the above

8. Which of the following is a common feature in all cloning vectors?

a) Sequences for protein purification
b) The ability to carry very large sequences
c) A centromere
d) A replication origin to enable autonomous dna replication
e) Shuttling sequences

9. miRNA stands for

a) mitochondria RNA
b) microsatellite RNA
c) mammalian interleukin RNA
d) microRNA
e) multiple interference RNA

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10. When using the DNA microarray technology for transcription profiling, one would

a) hybridize fluorescently labeled cDNA samples to DNA probes on the array
b) hybridize fluorescently labeled cDNA samples to RNA probes on the array
c) hybridize cDNA samples to fluorescently labeled DNA probes on the array
d) hybridize cDNA samples to fluorescently labeled RNA probes on the array
e) none of the above

11. Which of the following is a mechanism of dosage compensation?

a) Inactivation
b) Hyperactivation
c) Hypoactivation
d) Two of these are correct
e) All of these are correct

12. Which of the following can be used to construct a physical map of a chromosome?

a) Pedigree analysis
b) Linkage analysis
c) Northern blotting
d) Restriction mapping
e) None of the above

13. In transcribed DNA, nucleosomes are altered by multiprotein complexes that facilitate the binding of RNA polymerase in a process known as

a) chromosome reworking
b) chromatin remodeling
c) chromatin editing
d) chromosome altering
e) None of the above

14. Contigs are -

a) overlapping genomic DNA clones
b) overlapping cDNA clones
c) overlapping RNA clones
d) continuous tandem coding sequences
e) none of the above

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15. Gene imprinting is primarily caused by

a) DNA methylation
b) RNA methylation
c) RNA interference
d) X-linked genes
e) none of the above

16. The SNPs on a chromosome segment tend to be inherited together and define a genetic unit, which is called a:

a) phenotype
b) genotype
c) haplotype
d) maplotype
e) allotype

17. A gene that is introduced into the genome of an organism is known as a:

a) polygene
b) cisgene
c) transgene
d) xenogene
e) autogene

18. Which of the following statements about chimeras is correct? Chimeras are -

a) heterozygous transgenic animals
b) the animals that have two types of cells that have contributed to the formation of adult tissues
c) the animals whose germ line cells do not have a transgene
d) usually bred with other chimeras to produce true transgenic animals
e) none of the above
f)

19. Based on the sequencing data acquired from the Human Genome Project, approximately what percentage of the human genome is comprised of exons that code for proteins?

a) 1%
b) 25%
c) 50%
d) 75%
e) 99%

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P: where RNA poly + basal TFs bind
- control where T starts
- determine basal levels of T

E: where special TFs (activators or repressors) bind.
- assemble T activation complex + ↑ rate of T
- regulate inducible & tissue-specific gene expression

## PART B

20. a) [2 Marks] In eukaryotic transcriptional regulation, what is the function of a promoter and what is the function of an enhancer?

A promoter is the transcriptional start site (0.5) in DNA. An enhancer is a sequence that can either increase or repress transcription by causing certain proteins to bind. The promoter is the site where basal transcription factors and polymerase II bind (0.5) to complete transcription.

b) [2 Marks] Name two differences that can distinguish eukaryotic promoters from enhancers.

Promoters are position dependent (0.5), meaning that if it is moved, it will likely not function. Enhancers can be upstream, downstream or within introns, and ~~are~~ therefore position ~~de~~ independent (0.5). Promoters must also be close to the transcription initiation site (0.5) in order to function, while an enhancer can be many kbs (0.5) away from the initiation site and still function.

21. a) [2 Marks] What are VNTRs and STRs? What is the key difference between them?

VNTRs are variable number tandem repeats and are often ~10 – 100 ~~bps~~ nucleotides long. STRs are ~~small~~ short tandem repeats and are ~~only~~ only ~2-9 nucleotides long. VNTRs are also known as minisatellites and STRs are also called microsatellites.

3.5 (1.5)

- they are satellite (repetitive) dna which are highly polymorphic (variable) in the population due to the variability of the repeat numbers.

b) [2 Marks] What molecular genetic technique will you use to you detect VNTRs or STRs? Briefly describe your experimental strategy.

2 You can use a PCR technique to amplify a fragment of DNA that may contain a repeat. When testing for the STR of Huntington's, you can map the gene between ~~the~~ two RFLP sites, and amplify it. After this, a ~~gel~~ electrophoresis can be done, followed by a Southern Blot. When looking for the CAG repeat, you do a molecular hybridization with fluorescently labelled probes that will base pair to the CAG repeat. From this, you can count the number of repeats and find out whether the individual has Huntington's or not.

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22. a) [2 Mark] What is the origin of the Ti plasmid? What is the special property that makes it valuable in genetic engineering?

The Ti plasmid comes from a bacterial ~~genome.~~ (0.25) Plants are totipotent, which means any part of the plant can be taken to generate another plant. The Ti plasmid (tumour inducing) (0.5) creates a crown gall (plant tumour) near where the stem of the plant melts the dirt.

b) [2 Marks] Describe the major steps in creating a transgenic plant using the Ti plasmid?

1) Take plant genome + introduce transgene.

2) replicate plant with transgene; there are no chimeras in plants since they are totipotent.

22a) ① Ti (tumor-inducing) plasmid originates from Agrobacteria (soil bacteria) that causes tumors in plants

② Ti plasmid has a transposable elements (transposon) that can efficiently integrate into plant cellular genome; which can be exploited as a tool for making transgenic plants

b) ① clones transgene into Ti plasmid by replacing the original tumor gene.

② Transfect/insert the recombinant Ti plasmid into Agrobacteria

③ Agrobacteria infects plant cells (NOT embryonic or ES cells) & transgene in the recombinant Ti plasmid jumps/transfers to plant cell gene/chromosome.

④ Select for the correct transgenic cells & grow them into full size/adult plants

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23. The following sequence is the sense strand of genomic DNA of the Huntingtin gene. The CAG repeats are in lower case and in brackets. The underlined region is used to design 6-nucleotide PCR primers to amplify the CAG repeat region for diagnosis.

5′----------AAGTCC---**[cag]$_n$**---CAGCCG---------- 3′

3′ TTCTGG 5′ GTCGGC 5′

c) [1 marks] Write down the DNA sequences of the 6-nucleotide primers and label the 5' and 3' ends.

left primer 5′ AAGTCC 3′ ✓

right primer 5′ CGGCTG 3′ ✓

1

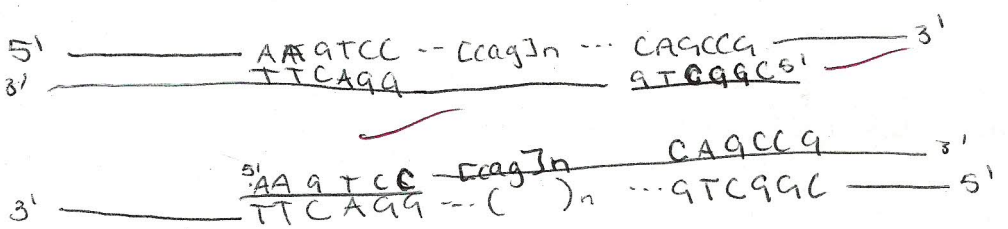
a) [3 marks] Use a diagram to illustrate the steps of two PCR cycles. Be sure to write down the nucleotide sequences of the primers and their targeting sequences, and label the ends of all DNAs.

Cycle 1:

Steps: 1) Denature ~~dsDNA~~ DNA at 95°C ✓

2) Anneal primers at 55°C ✓

3) Primer extension with Taq polymerase at 70°C ✓

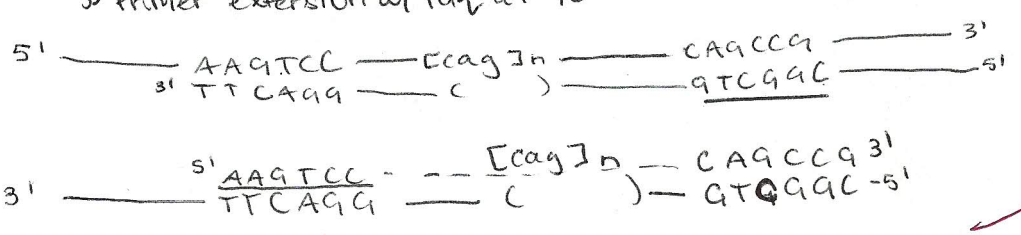



Cycle 2: 1) denature at 95°C

2) Anneal primers at 55°C

3) Primer extension w/ Taq at 70°C

3




✓