

Study Guide- Exam I

(covers Classes 1.1 through 1.6)

Class 1.1---01/18/07: DNA Structure

Know the following terms:

Genome, chromosome, nucleotide, ribose, deoxyribose, purine, pyrimidine, guanine, cytosine, thymine, adenine, uracil, minor groove, major groove, negative supercoiling, positive supercoiling, DNA polymerase, RNA polymerase, reverse transcriptase, central dogma, replication, transcription, translation, transition, transversion, induced mutation, spontaneous mutation, insertion, deletion, back mutation, true reversion, second-site reversion, suppressor mutation.

Understand the Following Concepts:

1. Know the structure of the nucleotide (sugar, phosphate group, nitrogenous base) and how a ribonucleotide is different from a deoxy-ribonucleotide.
2. Know the difference between purine and pyrimidine nitrogenous bases.
3. Know how nucleotides are assembled into nucleic acid molecules.
4. Be familiar with the overall structure of double-stranded DNA: Know the concepts of antiparallel strands, 5' and 3' polarity, and major and minor grooves.
5. Understand the concept of supercoiling and how cells use it to help package and access DNA.
6. Know the three major types of polymerases and the types of molecules they produce.
7. Know the rules of complementary base pairing in DNA/DNA and DNA/RNA molecules.
8. Understand how nucleotide triphosphates build DNA and RNA from the 3' end.
9. Know what semiconservative replication means.
10. Understand how the concept of the central dogma has changed from its original inception.
11. Understand the concept of T_m and how it changes with AT content in DNA.
12. Know the difference between spontaneous and background levels of mutations.
13. Know the difference between transitions and transversion, and be able to recognize the difference from a DNA change.
14. Know the difference between a back mutation and a true reversion.
15. Know the difference between a true reversion and a second-site reversion.
16. Know the difference between a second-site reversion and a second-site suppressor.
17. Understand the concept of a hot spot and how it might relate to the concentration of Cs and DNA methylation.

Class 1.2---01/23/07: The Concept of the Gene

Terms:

Gene, locus, protein, polypeptide, phenotype, genotype, homozygote, heterozygote, pleiotropic, complementation, complementation group, loss-of-function, gain-of-function, null, hypomorphic, leaky, hypermorph, neomorph, allele, wildtype, polymorphism, meiosis, gametes, homologous chromosomes, DNA recombination, codon, open reading frame, message strand, template strand, genomic DNA, cDNA, hybridization, introns, exons, preRNA, mRNA, alternative promoter use, differential splicing, transcription unit, gene family, pseudogenes.

Concepts:

1. Know how the concept of the gene has changed over the last 100 years.
2. Know the difference between a protein and a polypeptide.
3. Know the relationship between the terms dominant and recessive and gain-of-function (GOF) and loss-of-function (LOF).
4. Understand how the complementation test is used to classify types of mutations as alleles of one gene or not.
5. Understand the difference between null and hypomorphic (leaky) LOF mutations.
6. Understand the difference between hypermorphic and neomorphic gain-of-function alleles.
7. Know how genetic tests are used to classify mutations.
9. Understand the concept of an allele and the potential for 1000s of alleles at any one gene locus.
9. Be familiar with the types of nomenclatures to represent alleles of a gene.
10. Understand the importance of context when classifying alleles as dominant or recessive.
11. Understand the concept of a wildtype and why it might be difficult to define.
12. Know that homologous chromosomes can physically recombine by crossing over.
13. Understand the concept of mapping linked genes based on recombination frequencies.
14. Understand the concept of the open reading frame and how it relates to the concept of the gene.
15. Be aware that mutations can occur in many different parts of a gene (not just the coding information).
16. Know the difference between a message and template strand of DNA. Be able predict the RNA produced from a template strand.
17. Know at least three differences between eukaryotic and prokaryotic genes.
18. Know the difference between preRNA and mRNA.
19. Know the types of experiments that demonstrate the presence of introns in eukaryotic genes.
20. Be aware of the splicing mechanisms that generate mRNAs.
21. Know that intron lengths and positions can be indicators of evolutionary relationships.
22. Know the 3 different ways of producing different polypeptides from the same gene.
23. Understand the concept of a transcription unit and how it relates to a modern definition of the gene.
24. Understand how genes and proteins can be grouped into family and superfamilies.
25. Understand some of the current theories to explain the presence of pseudogenes

Class 1.3---01/25/07: Genome Organization I

Terms:

Transcriptome, proteome, interactome, linkage maps, restriction maps, single nucleotide polymorphisms, restriction-fragment length polymorphisms, haplotype, C value, complexity, C-value paradox, non-repetitive DNA, moderately repetitive DNA, highly repetitive DNA, transposon, zoo blot, cDNA, non-mendelian inheritance, cytoplasmic inheritance, organelles, endosymbiosis, genome sequencing, archaea.

Concepts:

1. Know the relationship between genome, transcriptome, proteome, and interactome.
2. Understand how linkage maps are derived using classical transmission genetics.
3. Know how restriction and sequence maps are different from linkage maps in terms of resolution—the precise relationship between the map and physical distance on the chromosome.
4. Understand that most polymorphisms are found in DNA sequence outside of coding information.
5. Understand how gel electrophoresis is used to display DNA polymorphisms.
6. Understand how polymorphisms can be mapped and followed through a pedigree.
7. Understand how polymorphisms are used to map disease genes.
8. Understand the relationship between C value and complexity.
9. Be able to describe the C-value paradox in terms of a specific example.
10. Know the three types of repetitive sequences found in the eukaryotes.
11. Understand how the movement of transposable elements within an organisms can be a driving force for evolution and the creation of new species.
12. Understand the concept of the ORF and how it is used to evaluate genome organization.
13. Understand how a zoo blot may be an important analysis for identifying important genes within a genome.
14. Know how a genomic DNA/cDNA analysis (hybridization) can lead to the understanding of a gene structure (number and size of introns and exons).
15. Understand the relationship between cytoplasmic inheritance, non-Mendelian inheritance, and DNA found in organelles.
16. Have a basic understanding of the mitochondrial and chloroplast genomes and how they relate to bacterial genomes.
17. Know that not all proteins found in mitochondria and chloroplasts come from the DNA found in the organelles. Where do the other proteins found there come from, and how do they get into the organelles.
18. Understand the concept of endosymbiosis and how it relates to the possible origin of mitochondria and chloroplasts.
19. Have a basic understanding of the information that can currently be obtained from genomic sequencing.
20. Have a basic idea of the number of genes it takes to make a obligate parasite, free living bacteria, unicellular eukaryote, multicellular eukaryote, and an animal or plant with complex tissue/organ systems.
21. Know that in eukaryotic genomes there may not be a direct correlation between genome size and complexity.

22. Know that most genomes are represented in mega bases of DNA.

Class 1.4---01/30/07: Genome Organization II

Terms:

Model organisms, yeasts, *C. elegans*, *Drosophila*, *Arabidopsis*, desert regions in the genome, core proteome, ortholog, homolog, essential genes, genetic load, RNA abundance, SAGE, oligonucleotide arrays, tandem duplications, unequal crossing over, translocations, satellite DNA.

Concepts:

1. Have an idea of the comparative sizes of representative and model organisms' genomes (bacteria, yeast, *C. elegans*, *D. melanogaster*, mammals, *A. thaliana*).
2. Know the size of the human genome in Mb and in number of genes.
3. Understand how the human genome breaks down in terms of repetitive DNA, introns, exons, etc.
4. Understand the general trend relating genome size, number of gene families, and organism complexity.
5. Know the relative distribution of fractions of the proteome versus cellular compartments.
6. Know the difference between ortholog and homolog.
7. Understand why it would be important to understand the interactome—defining how proteins interact during different circumstances.
8. Know that as organisms trend toward complexity there is a dramatic increase in proteins with transmembrane and extracellular domains.
9. Understand the concept of essential genes and redundancy.
10. Know how one can test for redundancy in an essential function.
11. Understand the concept of expressed genes and the transcriptome.
12. Understand the relationship between abundance and RNA complexity.
13. Understand how a DNA microarray is performed to examine profiles of expressed genes under a defined set of circumstances.
14. Understand the relationship between tandem duplications and the generation of gene clusters.
15. Know two mechanisms in which tandemly duplicated genes can be moved to different chromosomes.
16. Understand how unequal crossing over can expand or shrink the number of genes in a cluster.
17. Understand the general organization of highly repetitive DNA.
18. Know how gene duplications can lead to the evolution of novel protein functions in an organism.
19. Know how globin genes are differentially expressed during development.
20. Know that not all tandem repeats will diverge: Understand the role of selection in the process.
21. Understand the types of satellite DNA in mammals and the concept of how it evolved from a short nucleotide sequence.

Class 1.5---02/01/07: Messenger RNA Structure/Function

Terms:

tRNA, acceptor arm, T ψ C arm, anticodon arm, D arm, extra arm, pseudouridine, dihydrouridine, 70S, 30S, 50S, 80S, 40S, 60S, polysome, leader, 5' UTR, trailer, 3' UTR, monocistronic message, polycistronic message, operon, 5' cap, 5'-5' triphosphate linkage, guanylyl transferase enzyme, Poly(A) tail, Poly(A) polymerase, Poly(A) binding protein, exonuclease, endonuclease, degradosome, RNase E, RNPase, helicase, ARE sequences, nonsense-mediated RNA decay, bicoid RNA, oskar RNA.

Concepts:

1. Know the 3 major types of RNA in cells.
2. Know the overall structure of tRNAs in terms of the arms (stem/loops).
3. Understand how tRNAs are numbered and modified after transcription.
4. Know how tRNAs are folded into a tertiary structure with placement of anticodon loop and acceptor arm.
5. Know the relationship between the codon and the anticodon.
6. Know that ribosomes are classified according to their sedimentation in a density gradient (S units)
7. Know the difference between the eukaryotic and prokaryotic ribosomes and subunits.
8. Know the basic differences between prokaryotic and eukaryotic mRNAs.
9. Know that transcription and translation are coupled in bacteria but not in eukaryotes.
10. Know the difference between a monocistronic and polycistronic message.
11. Understand how the GTP cap is added to the 5' end of eukaryotic messages.
12. Know how the 3' Poly(A) tail is added to eukaryotic messages.
13. Understand what PABP does.
14. Understand the function of the Poly(A) tail on message stability.
15. Know the difference between exonucleases and endonucleases.
16. Know the 3 components that make of the degradosome.
17. Understand the structure of ARE sequences and how they make a message more unstable.
18. Know the 3 major types of eukaryotic degradation pathways.
19. Know what the nonsense surveillance system is and how it works.
20. Know the importance of mRNA transport and localization in eukaryotes.
21. Know 3 mechanisms that localize eukaryotic mRNA.
22. Understand the importance of RNA localization in *Drosophila* development.

Class 1.6---02/06/07: Overview of Protein Synthesis

Terms:

Ribonucleoprotein particle, A site, P site, E site, aminoacyl-tRNA, peptidyl-tRNA, initiation, elongation, termination, ribosome binding site, initiation factors, IF-3, IF-2, IF-1, initiator codon, partial P site, AUG, GUG, UUG, tRNA_m, tRNA_f, tRNA_i, fMet-tRNA_f, Shine-Dalgarno sequence, AUG context, ribosome scanning, internal ribosome entry site, elongation factors, EF-Tu, ternary

complex (EF-Tu/aa-tRNA/GTP), binary complex, EF-T, eEF1 α , eEF1 $\beta\gamma$, peptidyl transferase, puromycin, ribosome translocation, hybrid state model, EF-G, stop codons, UAA, UAG, UGA, release factors, RF1, RF2, RF3, RRF.

Concepts:

1. Know the composition of the different types of ribosomes and ribosomal subunits in terms of rRNA species and r-proteins.
2. Know the general structure of the ribosome in terms of mRNA binding and tRNA binding to A, P, and E sites.
3. Understand the different forms of tRNA: deacylated, aminoacylated, peptidyl.
4. Know the 3 stages of protein synthesis.
5. Understand the initiation process in bacteria.
6. Know the 3 major types of initiation factors in bacteria and what role they each play in the process.
7. Know the 3 different types of initiator codons and their frequencies.
8. Understand the structure of the initiator tRNA and how it is different from tRNAs that code for internal methionine.
9. Understand how the initiator Met is modified to N-formyl Met in bacteria.
10. Know the position, sequence, and function of the Shine-Dalgarno sequence in bacteria.
11. Understand the role of IF-2 in delivering the fMet-tRNA_f.
12. Know how initiation in eukaryotes is different from initiation in bacteria: Shine-Dalgarno vs context scanning.
13. Know how IRES initiation is different from 5' scanning.
14. Understand how a ternary complex brings a charged amino acid to the A site of the ribosome.
- 15.. Know the different types of elongation factors and what they do.
16. Know how the 23S rRNA in the ribosome contains peptidyl transferase and catalyzes the transfer of the peptide bond from the peptidyl-tRNA to the incoming aminoacyl-tRNA.
17. Understand the mechanism by which puromycin acts as an antibiotic.
18. Understand the role of GTP in building the polypeptide chain.
19. Be familiar with the hybrid state model of ribosome translocation.
20. Know the 3 types of stop codons and their frequency of use.
21. Know the different types of release factors and how they function to release the polypeptide chain from the ribosome.
22. Know the 2 stages of termination
23. Know how RRF, EF-G, and IF-3 are involved in ribosome dissociation and mRNA release.