**X-linked, Sex-linked traits, crosses**

**Okazaki fragments** – DNA fragments synthesized on the lagging strand. Primase creates primer on the lagging strand. Then, DNA Polymerase 3 synthesizes the DNA – Okazaki fragments. DNA Polymerase 1 erases the primer then fills the gap, finally ligase connecting Okazaki fragments.

**Leading Strand** – strand that is continous when DNA is being unwinded.

**Lagging Strand** – strand that is not continous when DNA is being unwinded.

**Where transcription/translation occurs in prokaryotes/eukaryotes?** In prokaryotes, transcription and translation are coupled, which means that it is happening together, simultaneously – translation beings while the mRNA is being synthesized as there is no nucleus. In eukaryotes, transcription and translation are separate, transcription happening nucleus, and translation happening in the ribosome.

**Three-Dimensional structure of RNA** tRNA can become a double-stranded structure (Cloverleaf model) based on intramlecular base-pairing. This structure is then flded in space to form an L-shaped molecule that has two functional ends - the acceptor stem (3' end of the molecule, which always ends in 5' CCA 3, amino acid atached to this end), and the anticodon loop(can base-pair with codons in mRNA).

**Difference of transcription factors in prokaryotes/eukaryotes?**

Prokaryotes:-10, -35 promoters, upstream elements, Eukaryotes: TATA box, initiator elements, downstream core promoter element, CAAT box, and the GC box. RNA Polymerase I (transcribes rRNA), RNA Polymerase 2 (transcribes mRNA), and RNA Polymerase 3 (transcribes tRNA and some other small RNAs).

**Why is control of gene expression different in eukaryotes than in prokaryotes?** Eukaryote gene structure and function differ from prokaryote gene structure and function in several important ways. Eukaryotes generally have many more genes and these genes are spread across multiple chromosomes. Prokaryotes have fewer genes and these genes are all located on one chromosome. Groups of genes producing proteins with related functions are often organized into operons in prokaryotes but not in eukaryotes. Eukaryotes also have mRNA that must have its introns excised and the mRNA transported out of the nucleus to the ribosomes. The greater complexity of the eukaryote genome means that a greater variety and complexity of control mechanisms is necessary. There are also more steps in the transcription and translation process at which control of expression can occur in eukaryotes.

**How is mRNA mature in prokaryotes?** Little to no post-RNA processing. No need to cut away introns, which are done so in eukaryotic mRNA.

**Alternative splicing** makes it possible to run all the functions of a human body, with all its function and abilities, with only 25,000 – 30,000 genes. During RNA splicing event, different combinations of exons can be joined together to create a diverse array of mRNAs from a single pre-mRNA. When these are translated, they produced different proteins which do different things.

Book: A single primary transcript can be spliced into different mRNAs by the inclusion of different sets of exons.

**Junk DNA** – noncoding DNA, components of an organism’s DNA sequences that do not encode for protein sequences. In many eukaryotes, large percentage of organism’s total genome size is noncoding DNA.

**ENCODE project –** Encyclopedia of DNA Elements, goal to identify all functional elements in the human genome sequence. 80% of genome has a “biochemical” function.

**Different types of RNA**

* Messenger RNA, mRNA – Bring information from DNA from the eukaryotic nucleus to the cytoplasm for ribosomal processing to make proteins. Distinguished from other RNAs through presence of poly-A tail (string of adenine nucleotides), used as a primer site for reverse transcription
* Ribosomal RNA, rRNA – Critical to the function of ribosomes
* Transfer RNA, tRNA – Have amino acids covalently attached to one end and an anticodon that can base-pair with an mRNA codon at the other. The tRNAs act to interpret information in mRNA and to help position the amino acids on the ribosome.
* Small nuclear RNAs, snRNAS – part of the machinery that is involved in nuclear processing of eukaryotic “pre-mRNA”
* SRP RNA - Mediates protein synthesizing on the rough endoplasmic reticulum
* Small RNAs – includes both micro-RNA (miRNA) and small interfering RNA (siRNA). Involved in the control of gene expression

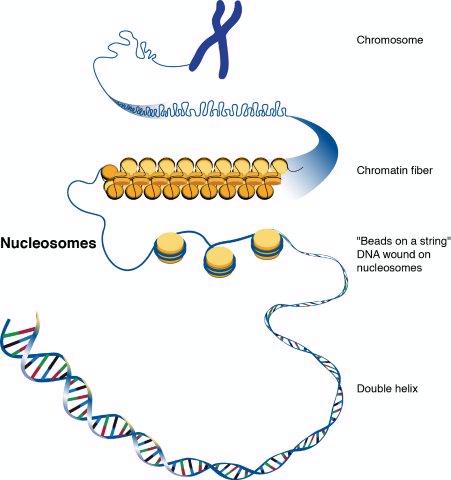
**cRNA** – Complementary RNA. Synthethic RNA produced by transcription from a specific DNA template.

**Telomeres** – Specialized structures found on the ends of eukaryotic chromosomes. Protects the ends of the chromosomes from nucleases and maintain the integrity of linear chromosomes. Composed of specific DNA sequences, made with repeating sequences of DNA, made by an enzyme called telomerase, which uses an internal RNA as a template.

**Operon** – Grouping of functionally related genes. A single transcription unit that encodes multiple enzymes necessary for a biochemical pathway. Prokaryotes only.

**How spliceosome works** – snRNA forms base pairs with 5’ end of intron, and at a branch site. These snRNA associate with other factors to form spliceosome. 5’ end is removed and forms bond at the branch site. 3’ end of intron is cut, forming a lariat – excised intron.

**What is a nucleosome** – Nucleosome is any repeating subunit of chromatin, consisting of a DNA chain coiled around a core of histones.



**Mutations**

Substitution – mutation that exchanges one base for another (switching Adenine to Guanine). Could cause:

* + Change to a codon that encodes a different amino acid, causing a small change in a produced protein
  + Change to a codon that encodes the same amino acid, causing no change in protein – aka silent mutations
  + Changing an amino-acid-coding codon to a single “stop” codon, causing an incomplete protein.



Substitution

Frameshift – since protein-coding DNA is divided into codons three bases long, insertions and deletions can alter a gene so that is message is no long correctly parse.



* + - Insertion **–** mutations in which extra base pairs are inserted into a new place in the DNA



* + - Deletion – mutations in which a section of DNA is lost, or deleted



Point mutation - single nucleotide mutation. Missense and nonsense mutations are types of point mutations

* + Missense mutation - changes a single nucleotide so that the codon results in a different amino acid.
  + Nonsense mutation - changes a single nucleotide so that the resulting codon codes for a stop codon.

Chromosomal mutations – change the structure of a chromosom, more extensive changes than point:

1. Deletions – part of chromosome is lost
2. Duplication – part of chromosome is copied
3. Inversion – part of chromosome in reverse order
4. Translocation – part of chromosome is moved to a new location.

**cDNA Library –** made by first isolating mRNA from genes being expressed and then using reverse transcriptase enzyme to make cDNA from the mRNA. The cDNA is then used to make a library, as mentioned earlier. These cDNA libraries are commonly made to represent the genes expressed in many different tissues or cells.

**DNA Library** – a collection of DNAs in a vector that taken together, represent the complex mixture of DNA.

**Transformation** - transfer of virulence from one cell to another, termed by Griffith, experimenting with bacterial cells/DNA and mice. Avery, Macleod, and McCarty identify the principle of transformation. Hershey and Chase, proves phage genetic material is DNA.

**Restriction Enzymes** - Three types of restriction enzymes.

* Type II cleaves at precise locations. Enable creation of recombination molecules. These enzymes recognize a specific DNA sequence, ranging from 4 bases to 12 bases, and cleave the DNA at a specific base within this sequence. Recognition sites for most type 2 enzymes are palindromes.
* Type 1 and 3 cleave with less precision and are not often used in cloning and manipulating DNA.

**Gel electrophoresis** - Restriction endonucleases cut DNA into fragments of different sizes. Separating the fragments based on size makes it possible to select the DNA sequence of interest. The most common separation technique used is **Gel electrophoresis.** This technique takes advantage of the negative charge on DNA molecules by using an electrical field to provide the force necessary to separate DNA molecules based on size.

**Vectors** - Something to carry the recombinant DNA molecule (DNA molecule made from two different sources), required so that DNA can be propagated into the host cell, that can replicate in the host when it has been introduced.

**Restriction maps** - Map of known restriction sites within a sequence of DNA. Requires the use of restriction enzymes. Provides crucial data for identifying and working with DNA molecules.

**DNA Sequencing** – Determination of actual base sequence of DNA. Basic idea is nested fragments. Each begin with the same sequence and end in a specific base. By starting with the shortest fragment, one can then read the sequence by moving up the ladder.

**PCR –** Polymerase Chain Reaction (PCR) enables researchers to produce millions of copies of a specific DNA sequence in approximately 2 hours. This automated process bypasses the need to use bacteria for amplifying DNA. Hot, Cold, Hot. First heating application – DNA denaturation. Cooling application – allow for priming. Second heating application – optimal temperature for taq DNA polymerases to extend primers.

**Transgenic organisms** – A transformed cell can also be used to form all or part of a multicellular, eukaryotic organism.

**Hybridization** – process of combining two complementary single-stranded DNA or RNA molecules and allowing them to form a single double-stranded molecule through base pairing. In a reversal of this process, a double-stranded DNA (or RNA, or DNA/RNA) molecule can be heated to break the base-pairing and separate the two strands.

**Fingertypes**

Fingerprint types - <http://ridgesandfurrows.homestead.com/fingerprint_patterns.html> and Bio Lab

**Karyotypes**

The particular array of chromosomes an individual organism possesses.

**Lack Operon**

Encodes the proteins necessary for utilization of lactose, and proteins necessary for the synthesis of tryptophan are encoded by the trp operon.

**Homeostasis** – maintenance of a constant internal environment – hallmark of multicellular organisms. Cells in such organisms respond to signals in their immediate environment (such as growth factors and hormones) by altering gene expression, and in doing so they participate in regulating the body as a whole.

**Blotting techniques**

* Southern blot – DNA from the sample is cleaved into fragments with a restriction endonuclease, and the fragments are separated by gel electrophoresis.
* Northern blot – When mRNA is separated by electrophoresis. Methodology same as Southern blot, but uses mRNA instead of DNA, and no denaturation step is required.
* Western blot – Proteins can also be separated by electrophoresis and blotted by a procedure

**Why don’t we have as many genes as polypeptides?**

Because of alternative splicing - one gene can code for many polypeptides because pre-mRNA can be processed by post transcriptional methods - splicing, etc.

**DNA -> RNA -> transferRNA -> polypeptide**

**Stop/Start codons**

Stop - UAA, UAG, UGA

Start - AUG

**Wobble**

There are fewer tRNAs than codons. The pairing between the 3' base of the codon and the 5' base of the anticodon is less stringent than normal. In some tRNAs, presence of modified bases with less accurate pairing in the 5' position of the anticodon enhances this flexibility. This effect is referred to as wobble pairing because these tRNAs can "wobble" a bit on the mRNA, so that a single tRNA can "read" more than one codon in the mRNA.

**RNA from DNA (Transcripting RNA)**

**Central Dogma**

DNA -> RNA -> Protein. Reverse Transcriptase can go against this - RNA -> DNA

**Jumping genes**

Transposable elements, also termed transposons and mobile genetic elements, are bits of DNA that ae able to move from one location on a chromosome to another. Discovered by Barbara McClintock.Human chromosomes contain 4 sorts of transposable elements

* Long Intersped Elements (LINEs)
* Short Intersped Elements (SINEs)
* Long terminal repeats (LTRs).
* Dead transposons

**2 Dark Fly Questions**

Pedigree - http://faculty.clintoncc.suny.edu/faculty/michael.gregory/files/bio%20101/Bio%20101%20Laboratory/Pedigree%20Analysis/Pedigree%20analysis%20self-study%20exercise.pdf