What is a gene?

Accurate Replication	Proof-reading enzymes
General Stability	Double helix = prevents breaks and mutations
Information Storage	Nitrogen bases code for amino acids and proteins
Transmission Information	Transcription & Translation

History

1866; Gregor Mendel	Discovered factors (genes), come up with three laws of hereditary
1900; Corren, Tschermak, and Devries	Lead to the rediscovery of Mendel
1900; Robert Feulgen	Came up with DNA stain, "-feulgen stain" stains red
1902; Sutton and Boveri	Chromosomal theory of inheritance -> genes are located on chromosomes, narrowed down gene location
1925; Fred Griffith	Studied two type of bacteria. smooth (pathogenic) vs. rough (harmless), lead to the discovery of transformation (the ability of bacteria to pick up and use genetic material) which allows genetic engineering

History (cont)

1930s; Collection of Scientists	Eukaryotic chromosome is 80% protein (where most looked), and 20% DNA, prokaryotic DNA is 100% DNA
1944; Avery, Macleod, and McCarthy	Used enzymes to destroy different proteins and genetic material, concluded that DNA is the genetic material
1950s; Alfred Hershey and Martha Chase	Radioactively tagged DNA and proteins in bacterial phages, concluded that DNA can be transformed (confirmed Griffith)
1950s; Chargaff	Amount of A = Amount of T, Amount of C = Amount of G (Chargaff's Rule)
1953; Watson, Crick, Wilkins, and Franklin	Discovered the structure of DNA
1983; Barbara McClintock	Discovered transposons (jumping genes)
1992; W.F. Anderson	Human gene therapy with human growth hormones
1992; Kary Mullis	PCR (Polymerase chain reaction)

Crick's Discovery

Telomeres	"Cap" of DNA, keeps it from splitting
Double helix	Allows DNA to be stable
Distance between base pairs	.34 nm
Complete turn	3.4 nm, 10 base pairs

Crick's Discovery (cont)

Length of DNA molecules	2 meters
Width of DNA molecules	3 nm
Polymer	Made up of nucleotides
Nucleo-tides are made up of...	Ribose sugar (5C), a phosphate group, and a nitrogen base (A, T, G, C)
DNA is...	Antiparallel

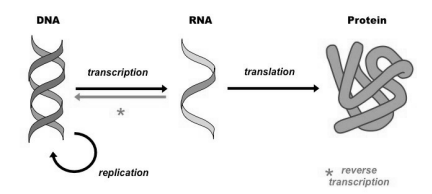
RNA Structure

- Single strand
- Ribose sugar (OH on 2')
- Nitrogen bases = A, U, C, G

Central Dogma

DNA -------> RNA ---------> Proteins

Central Dogma



3 Theories of DNA Replication

Conser-vative	1 completely new double helix, 1 completely new
Semi-C-onserv-ative	Double helixes are 1/2 new, 1/2 old
Dispersive	Different parts of the double helix are new and old
Meselson & Stahl	Proved DNA replication was semiconservative using bacteria cultures and nitrogen isotopes

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DNA Replication

Leading Strand	5' - 3'
Lagging Strand	3' - 5'
1) Topios-omerase	Relieves stress, DNA will not break
1) Helicase	Unzips/uncoils DNA, opens double helix into leading and lagging strand
2) Binding Proteins	Keeps the replication fork open
3) DNA Polymerase	Adds nucleotides to the leading strand 3' - 5'
4) Primase	Adds a RNA primer for nucleotide fragments (Okazaki fragments)
5) DNA Polymerase	Will connect to primase, adds nucleotides in 3' - 5'
6) DNA Ligase	Connects the new nucleo-tides from DNA polymerase to primer on 5' end, changes primer to DNA
7) Proof Reading Enzymes	Checks base pairs (A-T, C-G)

DNA Transcription

Making of a mRNA molecule (5' - 3') from a 3' to 5' DNA molecule

1) Transcription Factors (Proteins) attach to a regulatory gene (TATA box)

2) RNA Polymerase will bind to transcription factors, open up DNA

3) RNA Polymerase will add nucleotides of RNA to form a mRNA molecule, mRNA will hang off of the RNA polymerase

4) Once RNA reaches a stop codon on the DNA; 1) mRNA leaves 2) polymerase moves to the next gene 3) DNA closes

Introns	Junk DNA
Exons	Leaves nucleus

DNA Transcription (cont)

Poly-A Tail	3' end of mRNA, protects nucleotides

DNA Translation

Synthesize a protein using mRNA, rRNA, tRNA, and amino acids

1) First tRNA (amino acid) enters P sire, codon and anti codon are complementary

2) 2nd tRNA (amino acid) enters A site

3) Amino acid on P site forms a peptide bond with the amino acid in the A site

4) RIbosome moves down 1 codon, tRNA remains stationary

RNAi	Turning off a gene by using a complementary mRNA strand to block mRNA from translation

Genetic Code

4 bases x triplet code = 64 possible combin-ations

1 start code (AUG), 3 stop codons

Many codons equaling 1 amino acid buffers against mistakes

Characteristics of Genetic Code

Triple Code (Codons)

Commaless = no breaks inbetween

Non-Overlapping

Punctuation, stop and start codons

Degenerate = Some amino acids have more than one code

Unambiguous = Same genetic code can be used in different organisms

Types of Mutations

Deletion	Lose a base pair
Addition	Base pair is added
Substitution	Different base pair is added

Types of Mutations (cont)

Non-Disju-nction	Wrong chromosome number, occurs in cell division, caused when mitotic spindles break

Biotechnology

Northern Blotting	Electrophoresis of RNA
Southern Blotting	Electrophoresis of DNA
PCR (Polym-erase Chain Reaction)	1) Take DNA sample less than 2,000 pairs 2) Place in test tube with TAQ polymerase and nucleotides 3) Heat tube then cool, heat shock for 7-9 minutes, problem = no proof reading enzymes
Genetic Engineeri-ng/Rec-ombinant DNA	Need a target and a vector (usually bacterial plasmid)
Transgenic Animal	Introducing a gene from an animal into the genome of another species

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