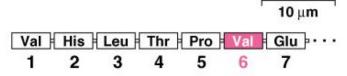
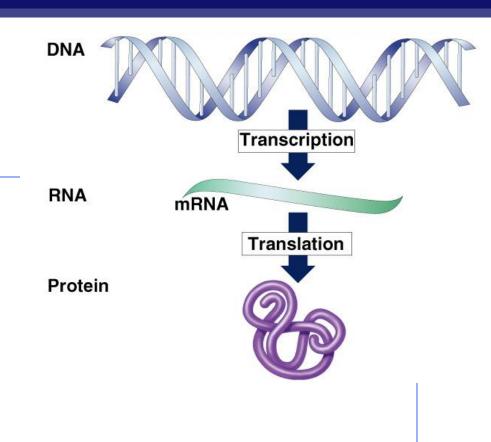
Chapter 17.





(b) Sickled red blood cells and the primary structure of sickle-cell hemoglobin

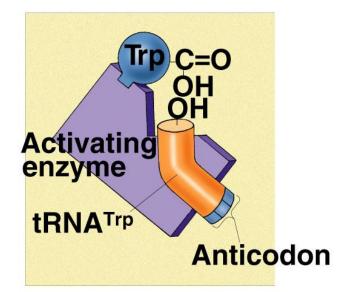


Mutations

Universal code

■ Code is redundant

- several codons for each amino acid
- "wobble" in the tRNA
- "wobble" in the aminoacyl-tRNA synthetase enzyme that loads the tRNA

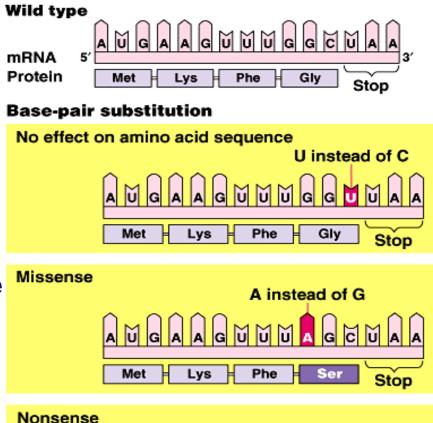


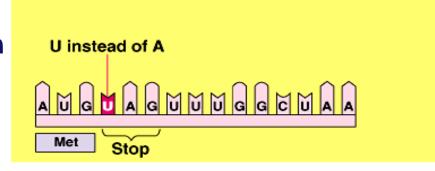
			Secon	d base		
		U	С	Α	G	
First base (5' end)	U	UUU Phe UUC Leu UUG Leu	UCU UCC UCA UCG	UAU Tyr UAC Stop UAG Stop	UGU Cys UGC Stop UGG Trp	U C A G
	С	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU His CAC GIn CAG	CGU CGC CGA CGG	D A G (3' end)
	A	AUU IIe AUA Met or	ACU ACC ACA ACG	AAU Asn AAC AAA AAA Lys	AGU Ser AGC AGA Arg	D V O C Third base
	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU Asp GAC GAA Glu	GGU GGC GGA GGG	U C A G

Mutations

- Point mutations
 - single base change
 - base-pair substitution
 - silent mutation
 - no amino acid change
 - redundancy in code
 - missense
 - change amino acid
 - nonsense
 - change to stop codon

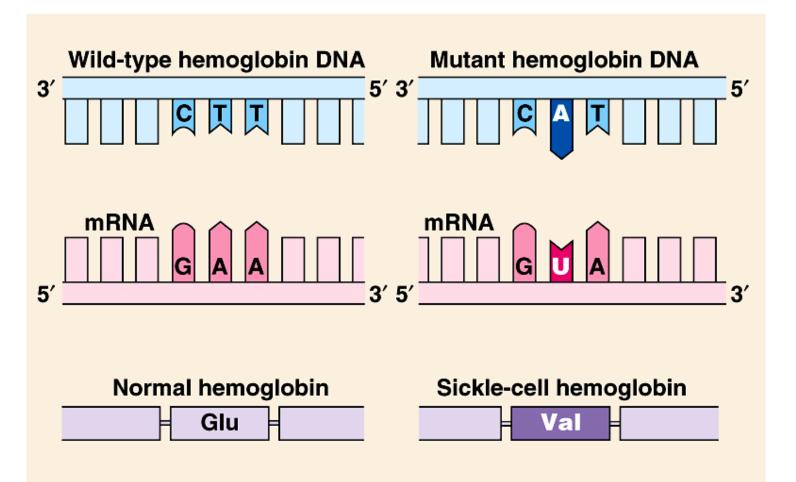
When do mutations affect the next generation?





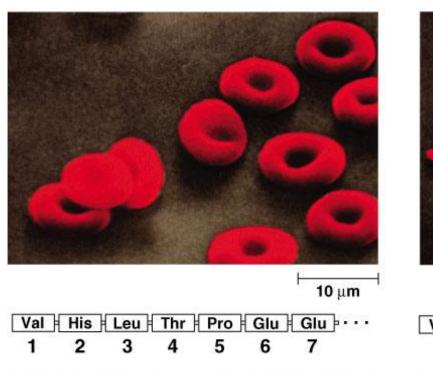
Point mutation leads to Sickle cell anemia

What kind of mutation?

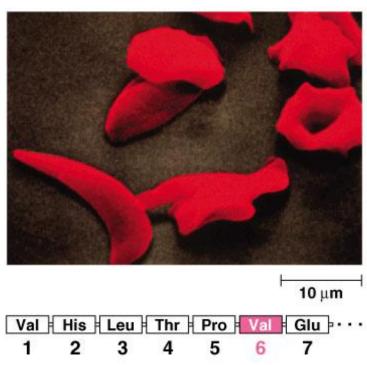


AP Biology 2005-2006

Sickle cell anemia



(a) Normal red blood cells and the primary structure of normal hemoglobin

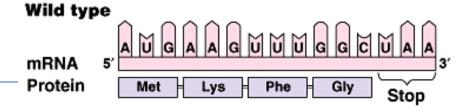


(b) Sickled red blood cells and the primary structure of sickle-cell hemoglobin

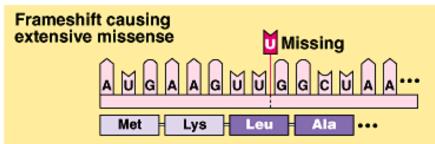
AP Biology 2005-2006

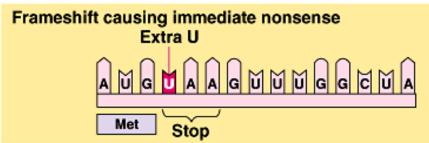
Mutations

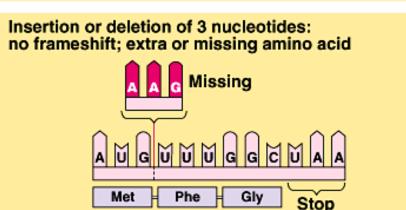
- Frameshift
 - shift in the reading frame
 - changes everything "downstream"
 - insertions
 - adding base(s)
 - deletions
 - losing base(s)



Base-pair insertion or deletion







Chapter 17.

G C A A 1 nm G C C (... G A T C (... G A T A T

RNA Processing

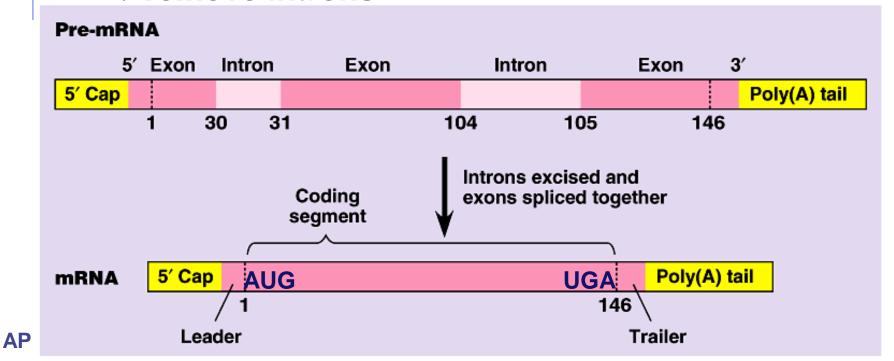
AP Biology 2005-2006

Transcription -- another look

- The process of transcription includes many points of control
 - when to start reading DNA
 - where to start reading DNA
 - where to stop reading DNA
 - editing the mRNA
 - protecting mRNA as it travels through cell

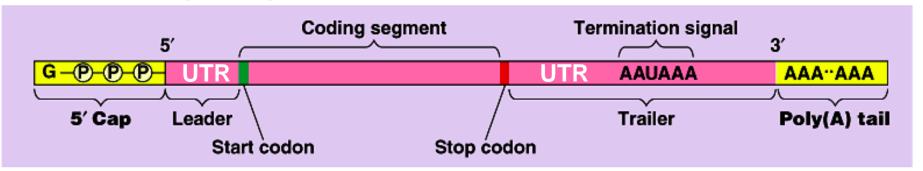
Primary transcript

- Processing mRNA
 - protecting RNA from RNase in cytoplasm
 - add 5' cap
 - add polyA tail
 - remove introns



Protecting RNA

- 5' cap added
 - ◆ G trinucleoside (G-P-P-P)
 - protects mRNA
 - from RNase (hydrolytic enzymes)
- 3' poly-A tail added
 - ◆ 50-250 A's
 - protects mRNA
 - from RNase (hydrolytic enzymes)
 - helps export of RNA from nucleus



Dicing & splicing mRNA

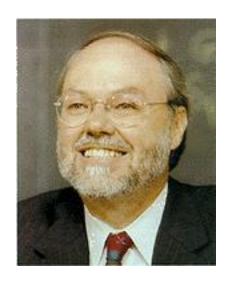
- Pre-mRNA → mRNA
 - edit out introns
 - intervening sequences
 - splice together exons
 - expressed sequences
 - In higher eukaryotes
 - 90% or more of gene can be intron
 - no one knows why...yet
 - there's a Nobel prize waiting...

1977 | 1993

Discovery of Split genes

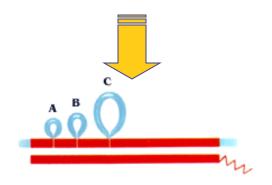


Richard Roberts
NE BioLabs



Philip Sharp MIT

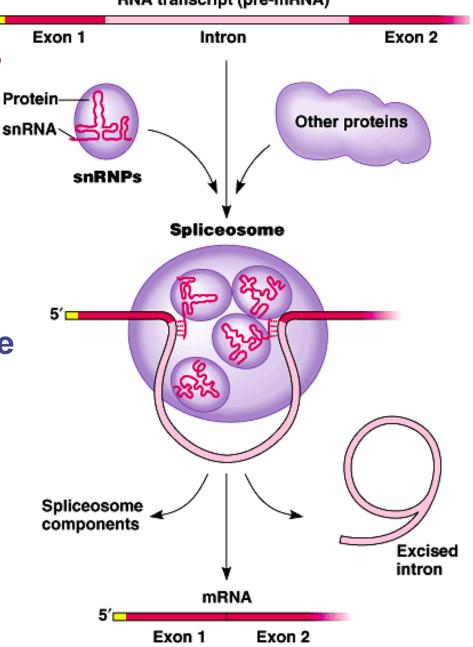




RNA transcript (pre-mRNA)

Splicing enzymes

- snRNPs
 - small nuclear RNA
 - RNA + proteins
- Spliceosome
 - several snRNPs
 - recognize splice site sequence
 - cut & paste
- RNA as <u>ribozyme</u>
 - some mRNA can splice itself
 - RNA as enzyme



1982 | 1989

Ribozyme

RNA as enzyme

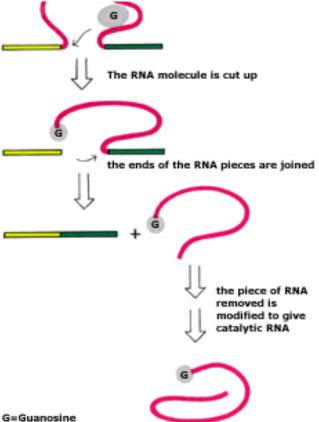




Sidney Altman Yale

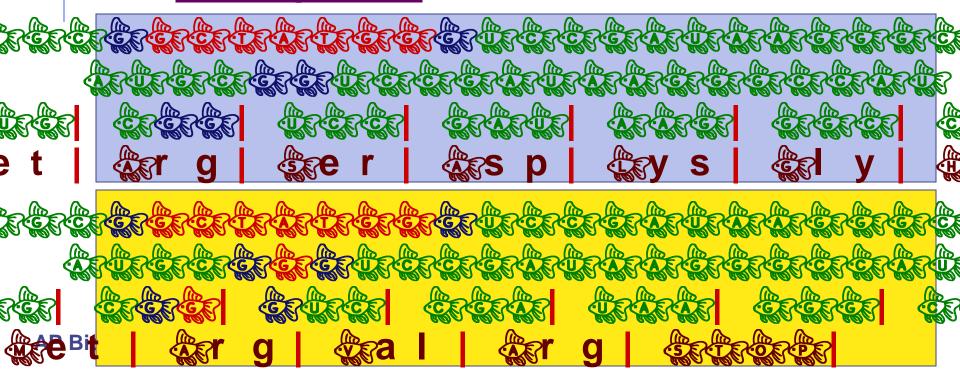


Thomas Cech U of Colorado



Splicing details

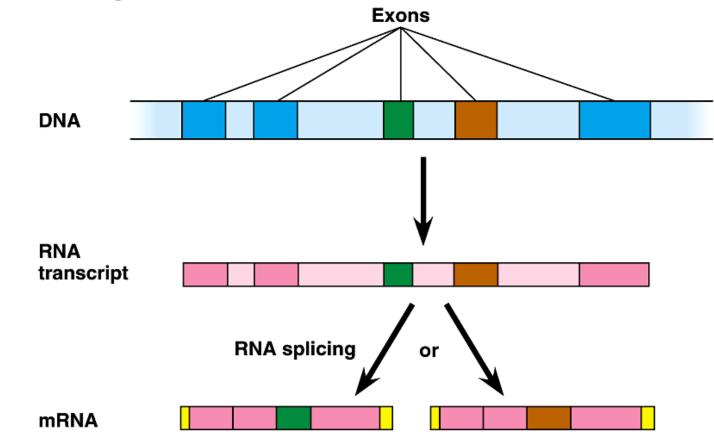
- No room for mistakes!
 - editing & splicing must be exactly accurate
 - a single base added or lost throws off the reading frame



Alternative splicing

AP Biology

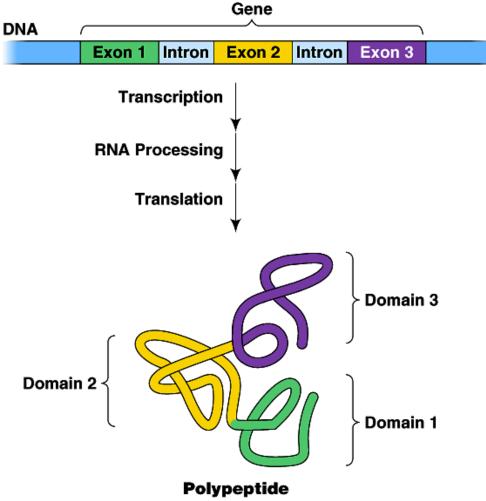
- Alternative mRNAs produced from same gene
 - when is an intron not an intron...
 - different segments treated as exons



Domains

Modular architecture of many proteins

- separate functional & structural regions
- coded by different exons in same "gene"



The Transcriptional unit (gene?)

