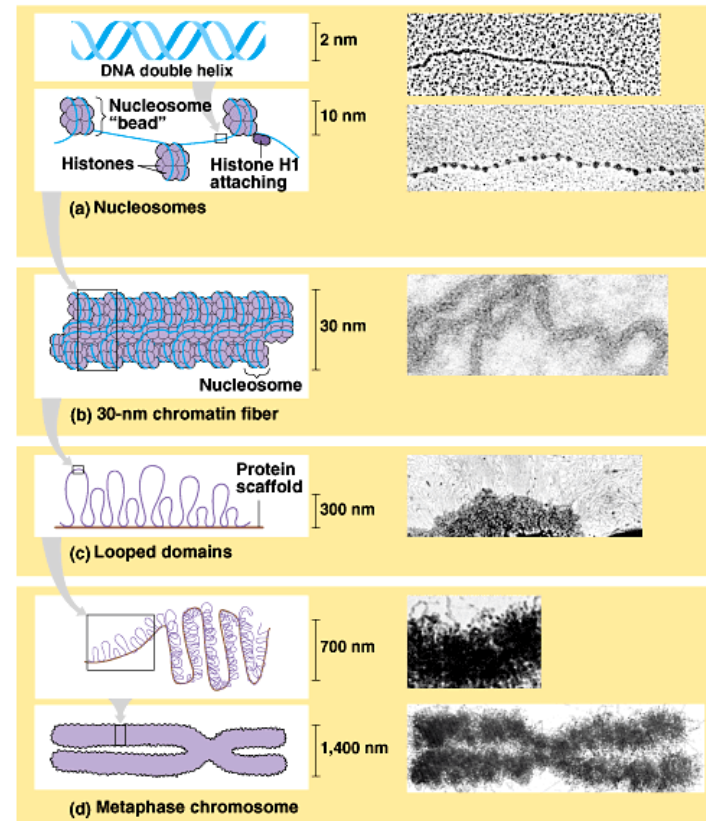


BI107 CHAP 19

Organization & Control of Eukaryotic Genomes

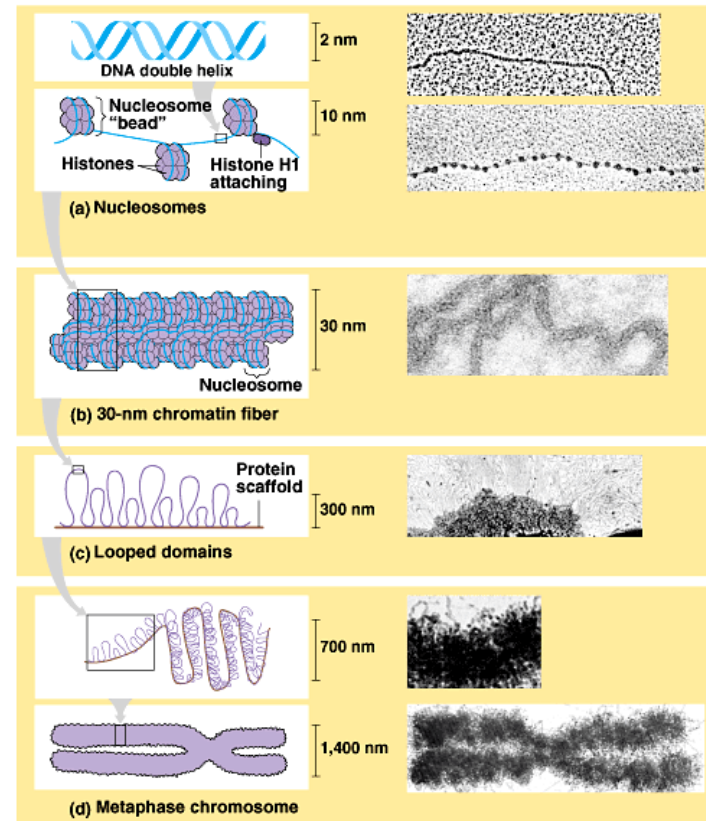
Chromatin Structure

- DNA is associated with proteins called histones giving 1st level of DNA packing
- Leads to ‘beads on a string’ model called nucleosomes containing 2 molecules of each of 4 histones (H2A, H2B, H3, H4) & the 5th histone H1 is near the bead in the ‘linker’ region



Chromatin Structure cont.

- Higher levels of chromatin structure exist
- 30-nm chromatin fiber forms looped domains which appear to be attached to nuclear scaffold
- Heterochromatin – compact chromatin & euchromatin – less compact chromatin seen in light microscope



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Genome Level Organization of DNA

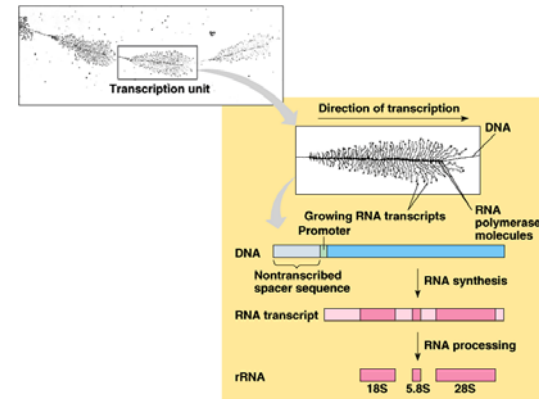
- Eukaryotic genomes have 90% or more sequences which do not code for proteins
- Many sequences are repetitive sequences & come in different types
- Tandemly repetitive DNA – about 10%-15% of DNA in mammals is called satellite DNA due to repeat sequence which gives it a different density

Genome Organization cont.

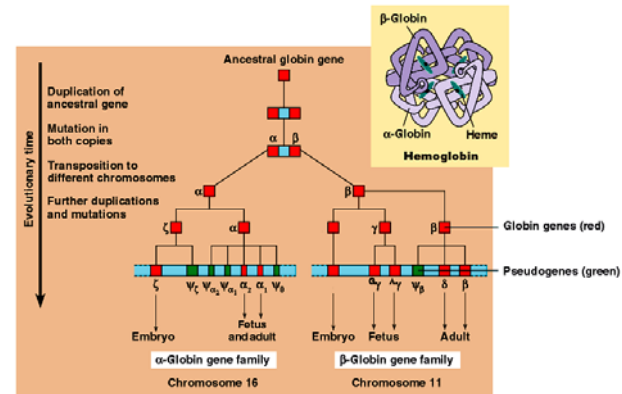
- Satellite DNA comes in 3 types – regular (100,000 or more repeats) mini - & micro- satellite DNA
- Human diseases called fragile X syndrome & Huntington's disease due to changes in number of repeats of 3 nucleotide sequences all of triplet repeat diseases identified affect nervous system
- Much of regular satellite DNA is located at telomeres & centromeres suggesting a structural role
- Interspersed repetitive DNA are interspersed in the genome 20%-40% of many genomes with an Alu sequence about 300 nucleotide bases making up 5% of total & it is transcribed into RNA

Genome Organization cont.

- Gene families are present – called multigene families & may be clustered or dispersed
- Some are identical – ribosomal genes - & some are similar – hemoglobin gene family



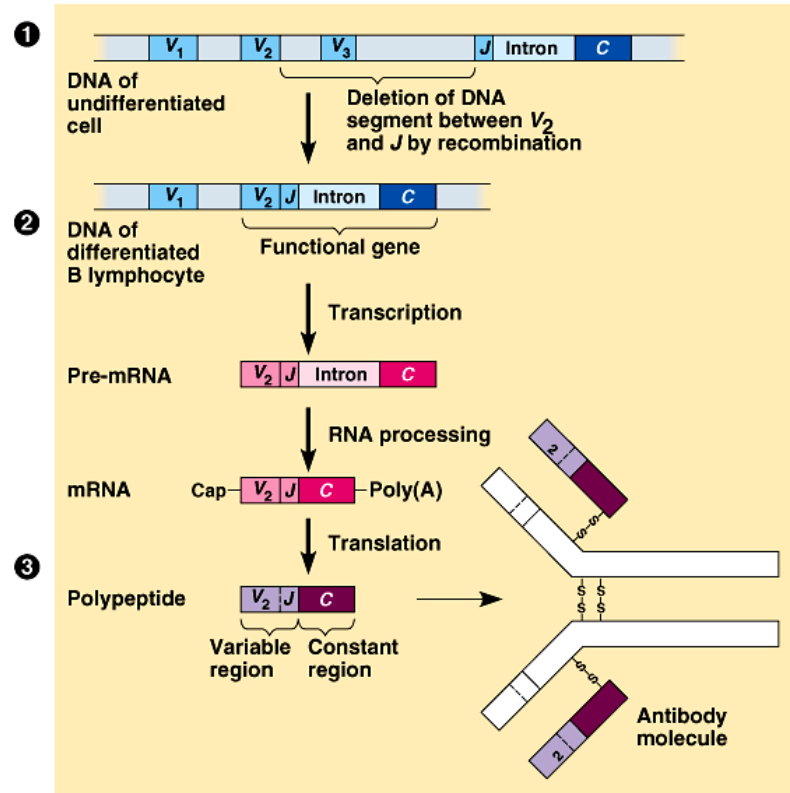
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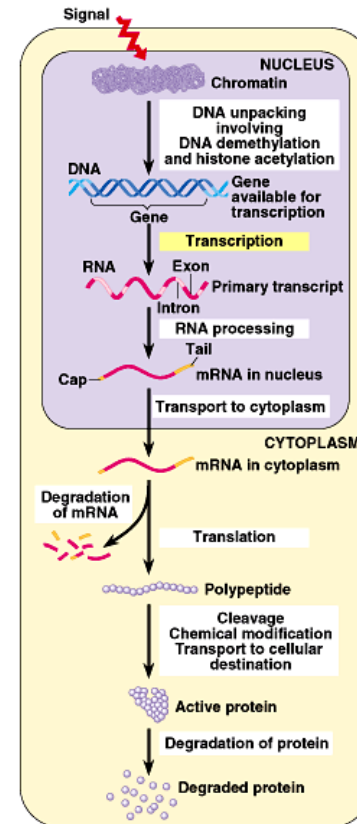
Genome Organization cont.

- DNA can be amplified (rRNA genes in frog development) or rearranged (immunoglobulin genes) (transposons & retrotransposons – move in DNA by means of RNA intermediate)



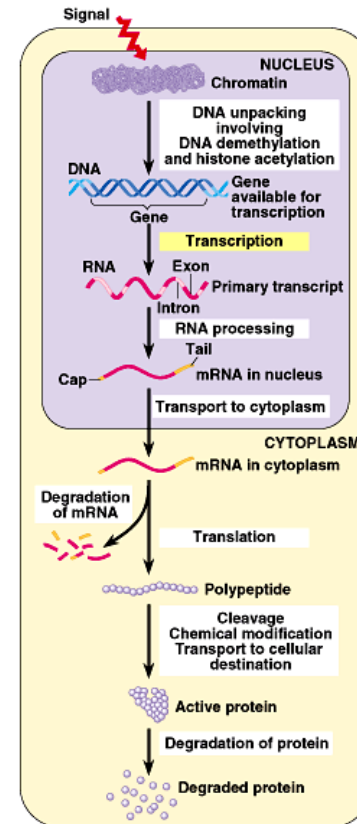
Control of Gene Expression

- In cellular differentiation only a subset of all genes are expressed in an individual cell
- Control can occur at any point in path from gene to functional protein



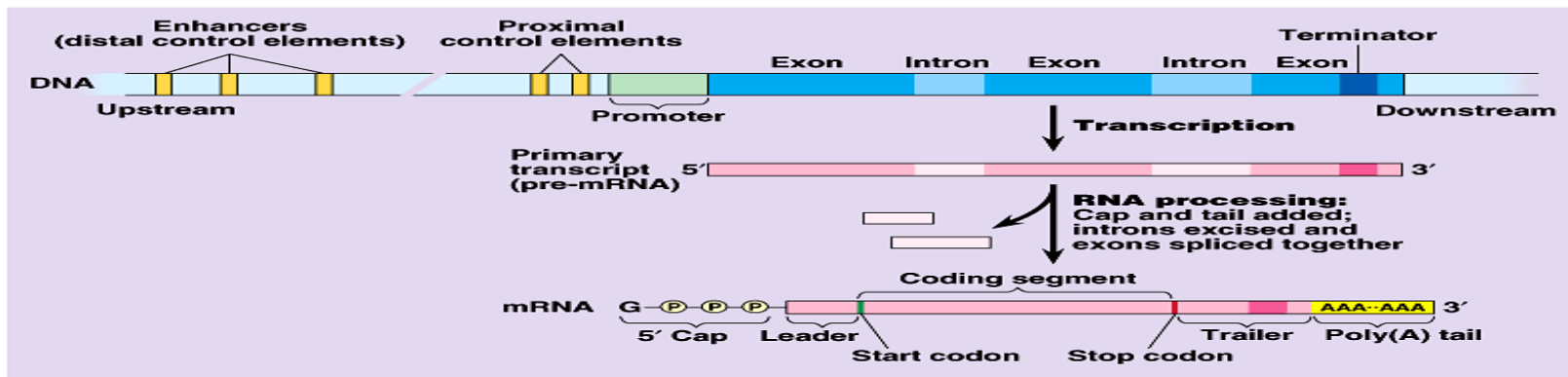
Control of Gene Expression cont.

- Chromatin modifications – 2 types
- DNA methylation esp. to cytosine residues seems to lead to inactivation of genes
- Histone acetylation – acetylated histones bind DNA less tightly & so DNA sequences are more available for transcription



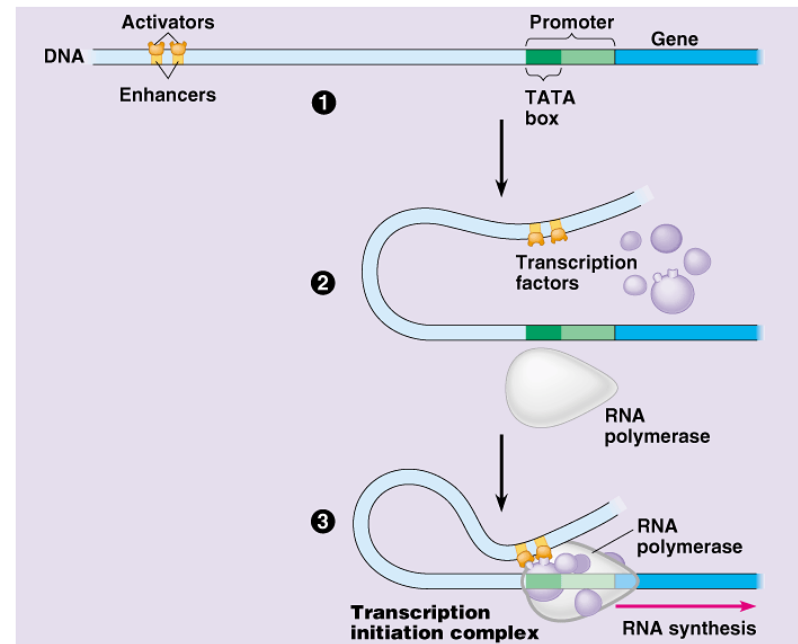
Control of Gene Expression cont.

- Transcription initiation controlled by proteins that interact with DNA & each other – called transcription factors
- Control elements are noncoding DNA sequences that regulate by binding transcription factors



Control of Gene Expression cont.

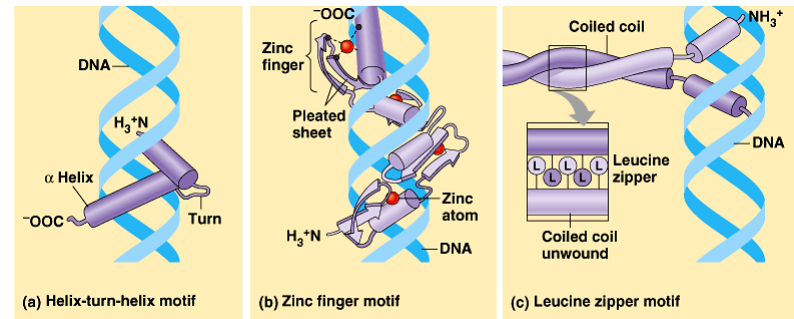
- Distal control elements called enhancers bind activators & can affect activity of proximal control elements called promoters with the TATA box



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Control of Gene Expression cont.

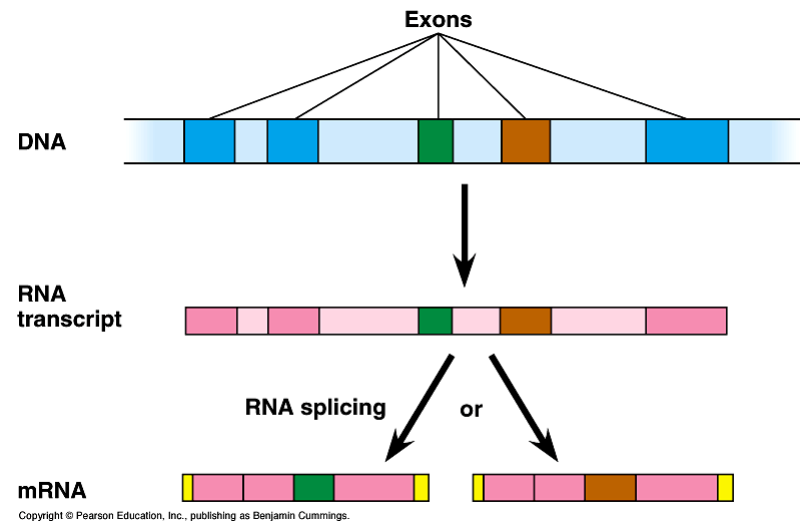
- Control of transcription due to proteins that bind to DNA – all put into 1 of several categories based on presence of DNA binding domains
- Zinc finger, leucine zipper, helix to helix are DNA binding domains in transcription factors



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Control of Gene Expression cont.

- Post-transcriptional mechanisms – alternative RNA splicing where different splice sites in introns are used to generate a mature mRNA



Control of Gene Expression cont.

- Regulation of mRNA degradation – mRNA can be present in cytoplasm for minutes to days
- Translation can be blocked at initiation stage of protein synthesis because initiation factors can be modified
- Protein degradation is controlled by proteasomes which act in conjunction with ubiquitin to target proteins for removal

