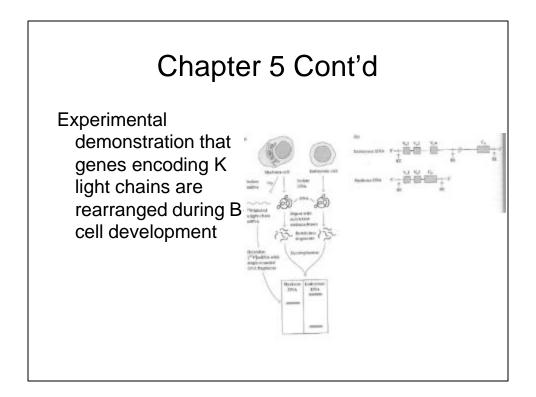
Chapter 5: Organization and Expression of Immunoglobulin Genes

- I. Genetic Model Compatible with Ig Structure
 - A. Two models for Ab structure diversity
 - 1. <u>Germ-line theory</u>: maintained that the genome contributed by the germ cells, egg and sperm, contains a large repertoire of immunoglobulin genes
 - 2. <u>Somatic-variation theory</u>: maintained that the genome contains a small number of immunoglobulin genes, from which a large number of Ab specificities are generated in the somatic cells by mutation or recombination

- B. The Two-Gene Model of Dreyer and Bennett
- said that two separate genes encode a single immunoglobulin heavy or light chain, one gene for the V region (variable region) and the other for the C region (constant region)
- these two genes must come together at the DNA level to form a continuous message that can be transcribed and translated into a single Ig heavy or light chain
- their theory was essentially proven correct in time

- C. Verification of the Dreyer and Bennett Hypothesis
- S. Tonegawa and N. Hozumi found that separate genes encode the V and C regions of Ig's and that the genes are rearranged in the course of B-cell differentiation
- experimental procedure and results are shown on the next slide
- results prove the two-gene model is correct: one gene encodes the V region and one encodes the C region



Chromosomal locations of Ig genes in mice and humans

TABLE 5	-1 CHRC	DMOSOMAL
LOCATIO	NS OF IM	MUNOGLOBULIN
GENES IN	HUMAN	AND MOUSE

	Chromosome		
Gene	Human	Mouse	
k Light chain	22	16	
κ Light chain	2	6	
Heavy chain	14	12	

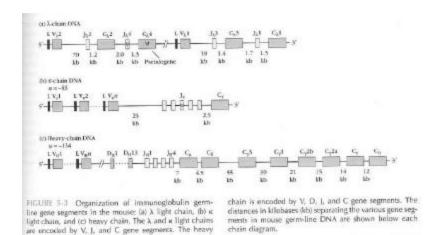
- II. Multigene Organization of Ig Genes
 - germ-line DNA contains several coding sequences, called gene segments, separated by noncoding regions
 - gene segments are rearranged during B cell maturation to form functional Ig genes
 - K and lambda light-chain families contain V, J, and C segments; the rearranged VJ segments encode the variable region of the light chains

- the heavy-chain family contains V, D, J, and C gene segments; the rearranged VDJ gene segments encode the variable region of the heavy chain
- each V gene segment is preceded at its 5' end by a signal or leader (L) peptide that guides the heavy or light chain through the endoplasmic reticulum
- signal peptide is cleaved from the nascent light and heavy chains before assembly of the final Ig molecule

Chapter 5 Cont'd

A. lambda-chain multigene family

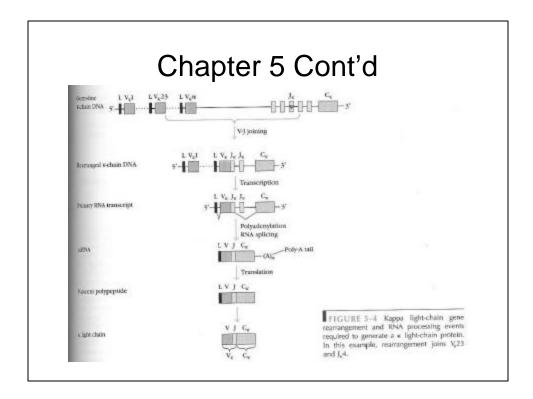
- functional lambda variable-region gene contains two coding segments – a 5' V segment and a 3' J segment – which are separated by a noncoding DNA sequence in unrearranged germ-line DNA
 - Mouse:
- has two V-lambda gene segments, four Jlambda gene segments, and four C-lambda gene segments
- J-lambda4 and C-lambda4 are pseudogenes, which are defective genes that are incapable of encoding protein



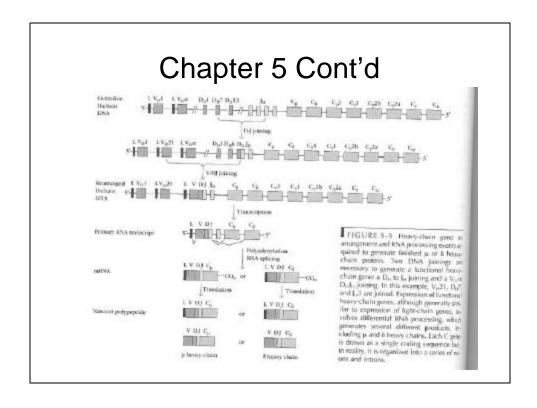
- B. K-chain Multigene Family
- in the mouse, the V-K and J-K gene segments encode the variable region of the K light chain, and the C-K gene segment encodes the constant region
- C. Heavy-chain Multigene Family
- see previous slide for heavy-chain structure

- III. Variable-Region Gene Rearrangements
 - this mechanism produces mature, immunocompetent B cells; each such cell is committed to produce antibody with a binding site encoded by the particular sequence of its rearranged V genes

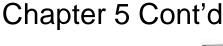
- A. V-J Rearrangements in Light-Chain DNA
- in humans, any of the functional V-lambda genes can combine with any of the four functional J-lambda-C-lambda combinations
- in human and mouse K light-chain DNA, any one of the V-K gene segments can be joined with any one of the functional J-K gene segments
- see next slide for Kappa light-chain gene rearrangement and RNA processing events required to generate a K light-chain protein



- B. V-D-J Rearrangements in Heavy-Chain DNA
- look at next slide for heavy-chain gene rearrangement and RNA processing events required to generate finished u or delta heavy chain protein



- IV. Mechanism of Variable-Region DNA Rearrangements
 - A. Recombination Signal Sequences
 - flank each germ-line V, D, and J gene segment
 - function as signals for the recombination process that rearranges the genes
 - see next slide



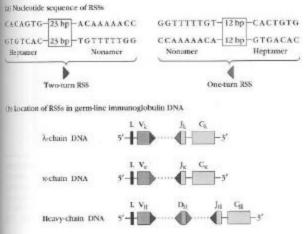
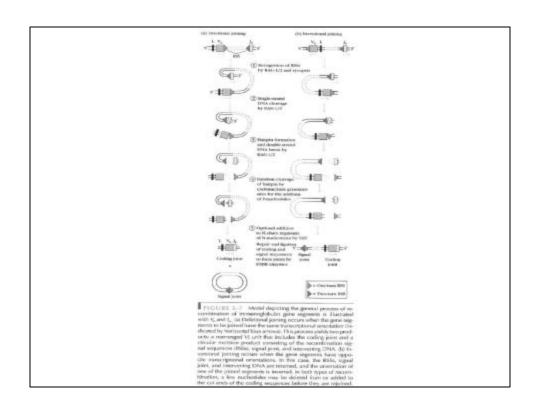


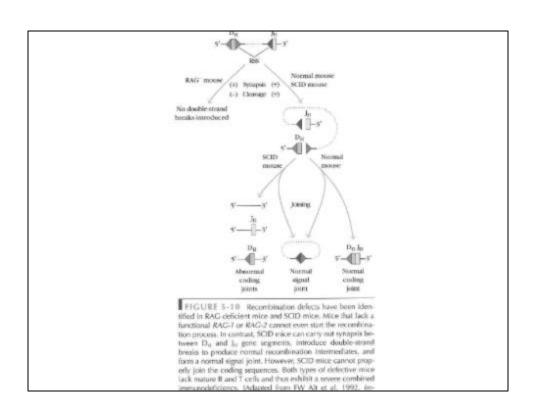
FIGURE 5-6 Two conserved sequences in light-chain and heavychain DNA function as recombina tion signal sequences (RSSs). (a) Both signal sequences consist of a conserved palindromic heptamer and conserved AT-rich nonamer; these are separated by nonconserved spacers of 12 or 23 base pairs. (b) The two types of RSS-designated one-turn RSS and two-turn RSS - have characteristic locations within A-chain, k-chain, and heavy-chain germ-line DNA. During DNA rearrangement, gene segments adjacent to the oneturn RSS can join only with segments adjacent to the two-turn RSS.

- B. Enzymatic Joining of Gene Segments
- V(D)J recombinase: catalyzes V-(D)-J recombination, which takes place at the junctions between RSSs and coding sequences
- recombination-activating genes (RAG-1 and RAG-2) encode for proteins that act synergistically to mediate V-(D)-J joining
- next slide shows that recombination of variable-region gene segments is a multistep process catalyzed by a system of recombinase enzymes



- C. Defects in Ig-Gene Rearrangements
- knockout mice lacking either RAG-1 or RAG-2 are unable to initiate the recombination process because they cannot introduce double-strand DNA breaks between the RSSs and coding sequences in germ-line immunoglobulin DNA
- result: V, D, and J gene segments remain unrearranged

- since both B and T cells utilize the same recombination machinery, the RAG-1- and RAG-2- knockout mice lack mature T and B cells and consequently exhibit a severe combined immunodeficiency (SCID)
- next slide demonstrates these two recombination defects

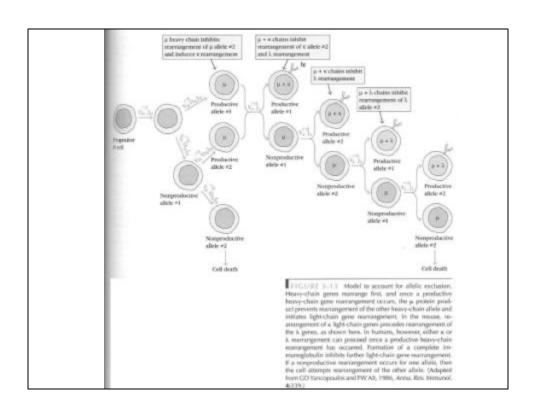


- D. Productive and Nonproductive Rearrangements
- <u>nonproductive rearrangement</u>: imprecise joining that results in gene segments that are joined out of phase, so that the triplet reading frame for translation is not preserved.
- resulting VJ or VDJ unit will contain numerous stop codons, which interrupt translation

- <u>Productive rearrangement</u>: the resulting VJ or VDJ unit can be translated in its entirety, which will yield a complete antibody
- these two type of rearrangements that occur produce only about 8% of pre-B cells in the bone marrow that undergo maturation and leave as mature, immunocompetent B cells

E. Allelic Exclusion

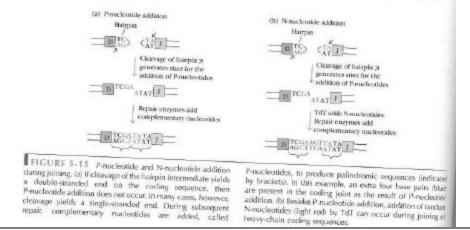
- even though a B cell is diploid, it expresses the rearranged heavy-chain genes from only one chromosome and the rearranged light-chain genes from only one chromosome. This is known as allelic exclusion
- this ensures that functional B cells never contain more than one VDJ from the heavy chain and one VJ unit from the light chain



- V. Generation of Antibody Diversity
 A. Multiple Germ-Line V, D, and J Gene Segments
 - contribute to the diversity of the antigenbinding sites in antibodies
 - B. Combinatorial V-J and V-D-J Joining
 - in humans, the ability of any of the 51 Vh gene segments to combine with any of the 27 Dh segments and any of the 6 Jh segments allows a considerable amount of heavy-chain gene diversity to be generated

- C. Junctional Flexibility
- increases the enormous diversity generated by means of V, D, and J combinations
- can lead to many nonproductive rearrangements, but it also generates several productive combinations that encode alternative amino acids at each coding joint, thereby increasing antibody diversity

- D. P-Addition
- E. N-Addition

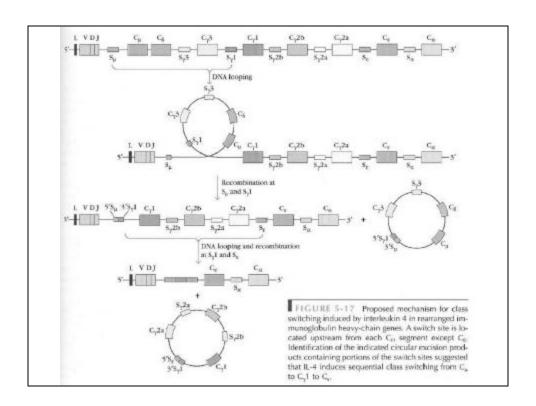


- F. Somatic Hypermutation
- results in additional antibody diversity that is generated in rearranged variableregion gene units
- also causes individual nucleotides in VJ or VDJ units to be replaced with alternatives, thus possibly altering the specificity of the encoded immunoglobulins

- usually occurs within germinal centers
- targeted to rearranged V-regions located within a DNA sequence containing about 1500 nucleotides, which includes the whole of the VJ or VDJ segment
 - largely random
- <u>affinity maturation</u>: following exposure to antigen, those B cells with higher affinity receptors will be selected for survival because of their greater ability to bind to the antigen
 - this takes place in germinal centers

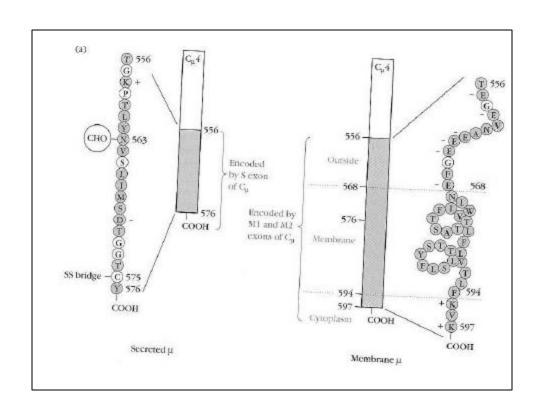
- G. Association of Heavy and Light Chains
 - combinational association of H and L chains also can generate antibody diversity
- VI. Class Switching Among Constant-Region Genes
 - <u>class switching</u>: after antigenic stimulation of a B cell the heavy chain DNA can undergo a further rearrangement in which the VhDhJh unit can combine with any Ch gene segment

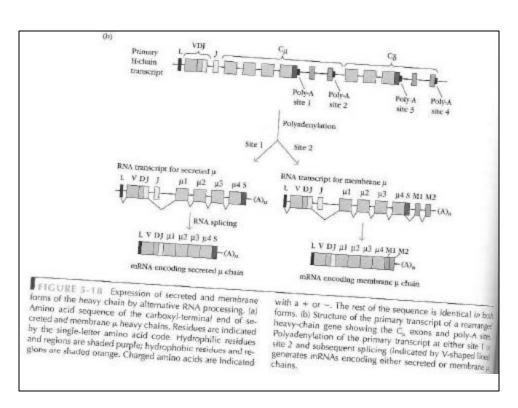
- <u>switch region</u>: DNA flanking sequences located 2-3 kb upstream from each Ch segment that are involved in class switching
- example of class switching on next slide



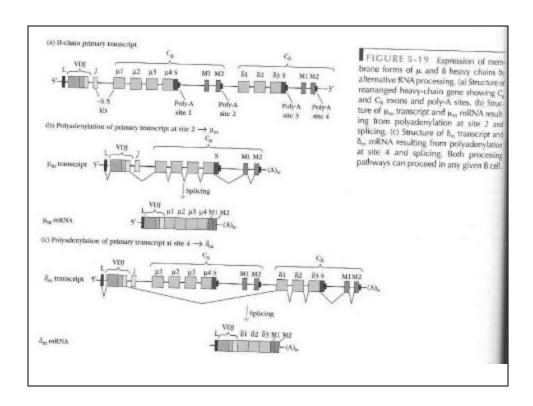
- VII. Expression of Ig Genes
 - A. Differential RNA Processing of Heavy-Chain Primary Transcripts
 - this can yield different mRNA's
 - this processing explains the production of secreted or membrane-bound forms of a particular immunoglobulin and the simultaneous expression of IgM and IgD by a single B cell

- 1. Expression of Membrane or Secreted Immunoglobulin
- difference depends on differential processing of a common primary transcript
- mature naïve B cells produce only membrane-bound antibody
- differentiated plasma cells produce secreted antibodies

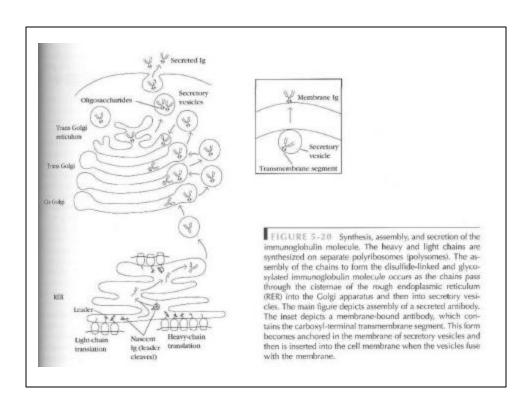




- 2. Simultaneous Expression of IgM and IgD
 - controlled by differential RNA processing
- if the heavy chain transcript is cleaved and polyadenylated at site 2 after the Cu exons, then the mRNA will encode the membrane form of the u heavy chain
- if polyadenylation is instead further downstream at site 4, after the C delta exons, then RNA splicing will remove the intervening Cu exons and produce mRNA encoding the membrane form of the delta heavy chain



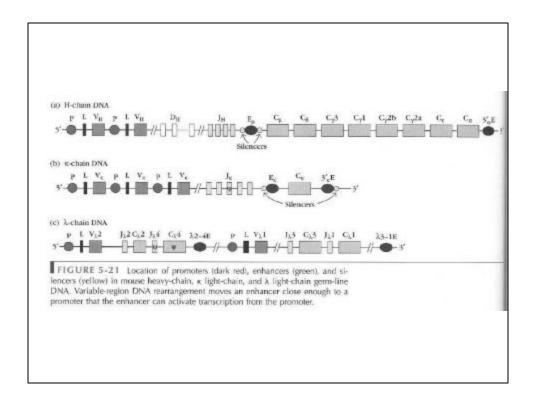
- B. Synthesis, Assembly, and Secretion of Immunoglobulin
- heavy and light chains are synthesized on separate polyribosomes of the rough ER
 - next slide shows this process



- VIII. Regulation of Ig-Gene Transcription
 - three regulatory sequences in DNA regulate transcription of immunoglobulin genes:
 - 1. promoters: promote initiation of RNA transcription in a specific direction
 - located about 200 bp upstream from transcription initiation site

- 2. Enhancers: nucleotide sequences located some distance upstream or downstream from a gene that activate transcription from the promoter sequence in an orientation-independent manner
- 3. Silencers: nucleotide sequences that down-regulate transcription, operating in both directions over a distance

- each Vh and VI gene segment has a promoter located just upstream from the leader sequence
- these promoters contain a TATA Box
- location of these regulatory sequences are shown on next slide



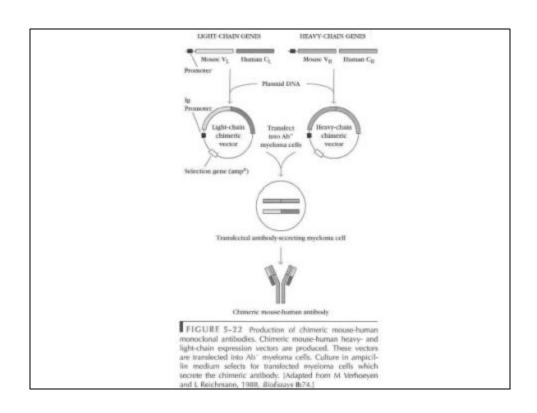
- A. Effect of DNA Rearrangement on Transcription
- rate of transcription of a rearranged VIJI or VhDhJh unit is as much as 10,000X the rate of transcription of unrearranged VI or Vh segments
- <u>oncogenes</u>: genes that promote cellular proliferation or prohibit cell death
- these can often translocate to the immunoglobulin heavy or light chain loci

- B. Inhibition of Ig-Gene Expression in T cells
- complete Ig-gene rearrangement of H and L chains occurs only in B cells
- complete TCR-gene rearrangement is limited to T cells

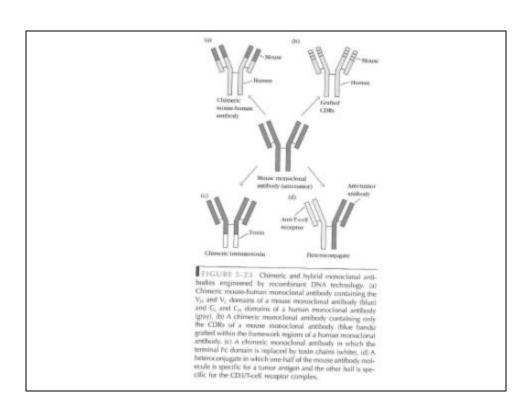
- IX. Antibody Genes and Antibody Engineering
 - possible to design and construct genes that encode immunoglobulin molecules in which the variable regions come from one species and the constant regions come from another

- A. Chimeric and Hybrid Monoclonal Antibodies
- to make an antibody one needs to clone recombinant DNA containing the promoter, leader, and variable-region sequences from a mouse antibody gene and the constant-region exons from a human antibody gene
- the Ab encoded by such a recombinant gene is a mouse-human <u>chimera</u>, also known as <u>humanized antibody</u>

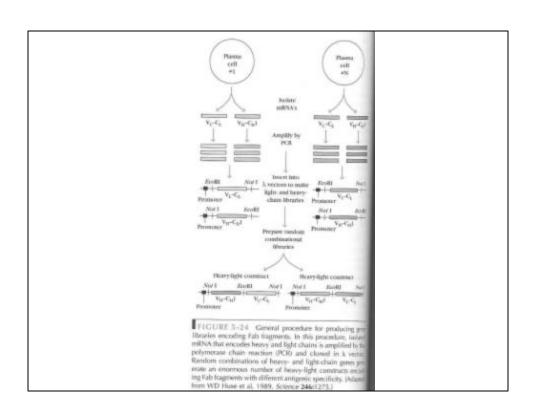
- its antigenic specificity is determined by the variable region and is derived from the mouse DNA
- its isotype is determined by the constant region and is derived from the human DNA
- the process is shown on the next slide



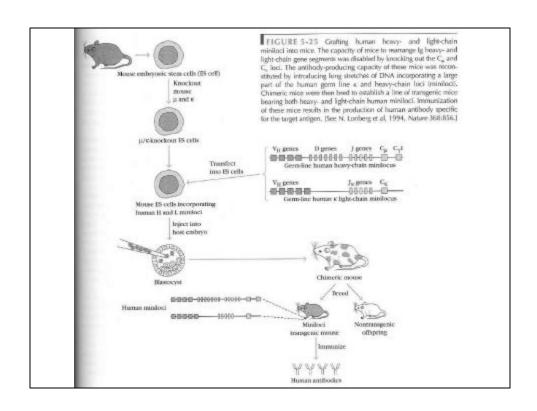
- heteroconjugates (or bispecific antibodies): hybrids of two different Ab molecules
- constructed by chemically crosslinking two different Ab's or synthesized in hybridomas consisting of two different monoclonal-Ab-producing cell lines that have been fused



- B. Monoclonal Antibodies Constructed from Ig-Gene Libraries
- use of PCR to amplify the DNA that encodes Ab heavy chain and light chain Fab fragments from hybridoma cells or plasma cells
 - process shown on next slide



- this procedure generates a diversity of Ab specificities; clones containing these random combinations of H + L chains can be rapidly screened for those secreting Ab to a particular Ag
- C. Mouse with Human Instead of Mouse Immunoglobulin Loci
- one can knockout the heavy and light chain immunoglobulin loci in mouse embryonic stem cells and introduce very large DNA sequences containing human heavy and light chain gene segments



- advantage of this process: completely human antibodies are made in cells of the mouse B-cell lineage, from which antibody-secreting hybridomas are readily derived by cell fusion
- therefore, this process offers a solution to the problem of producing human monoclonal Ab's of any specificity desired