

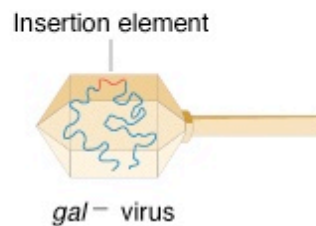
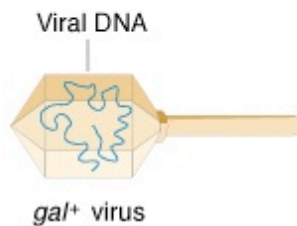
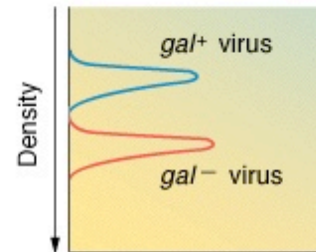
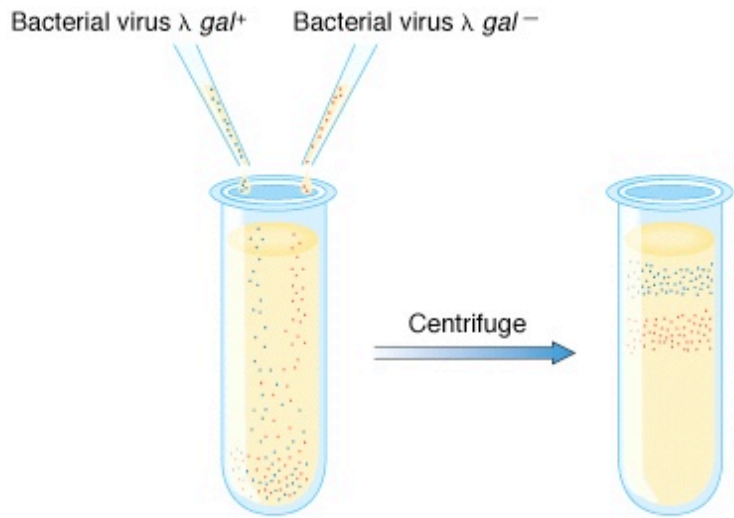
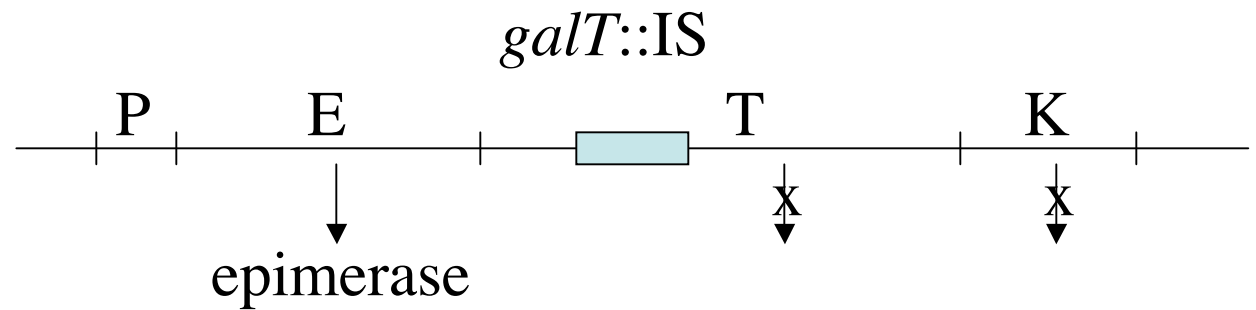
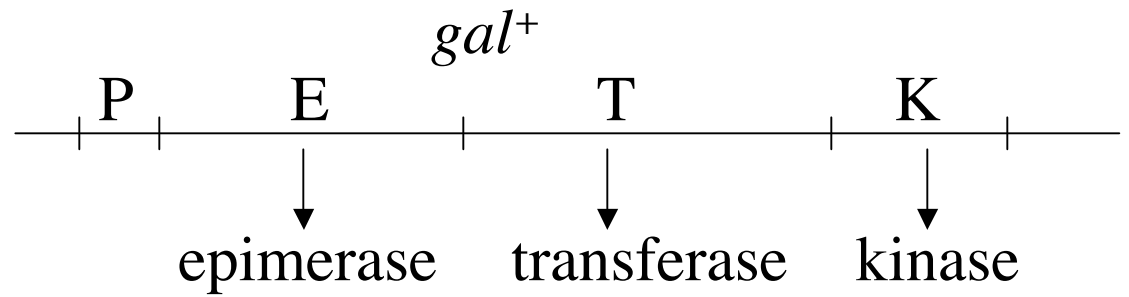
FOGA-III: HOW DOES GENETIC CHANGE HAPPEN? - NATURAL GENETIC ENGINEERING OF GENOME STRUCTURE

- Cells have a large toolbox of biochemical systems that carry out genome restructuring at all levels of complexity
- Sequenced genomes display structures and relationships that reveal the evolutionary importance of natural genetic engineering functions
- Natural genetic engineering functions are subject to cellular regulation and control

Outline

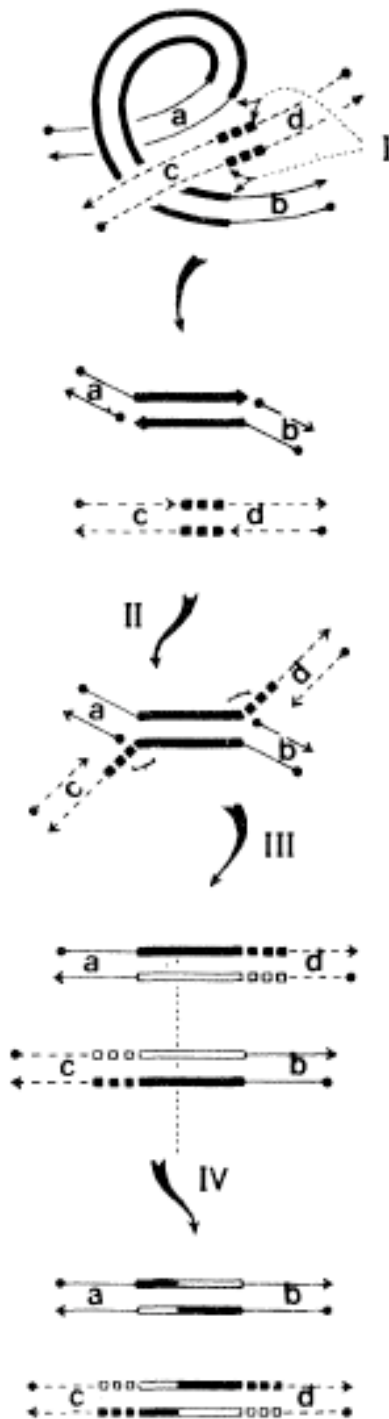
- Personal history with natural genetic engineering
- The mammalian immune system
- Natural genetic engineering in evolution
- Non-random features of natural genetic engineering
- Advantages of evolution by natural genetic engineering

Mobile DNA - IS elements

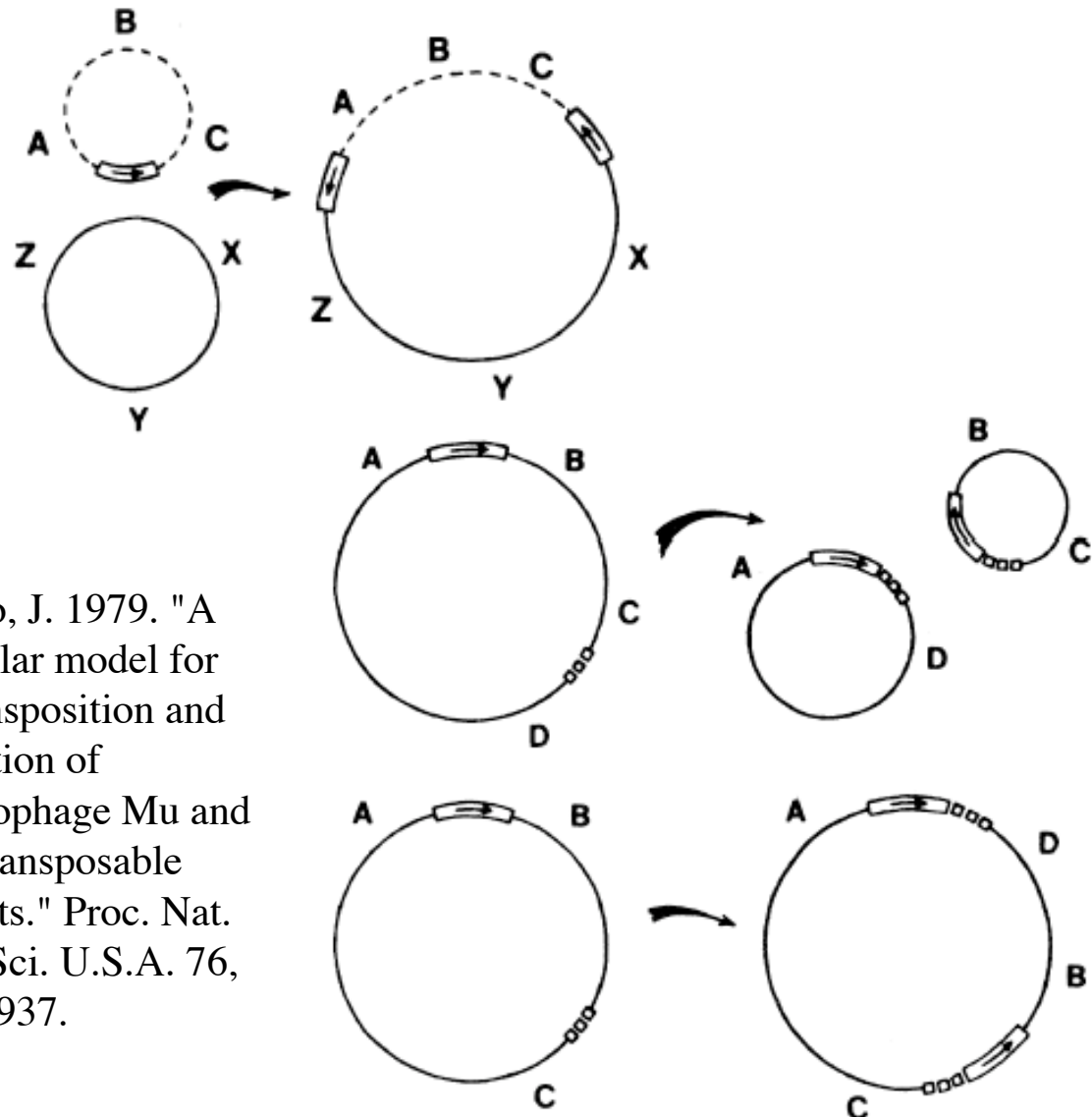


Shapiro JA. Mutations caused by the insertion of genetic material into the galactose operon of Escherichia coli. J Mol Biol. 1969 Feb 28;40(1):93-105.

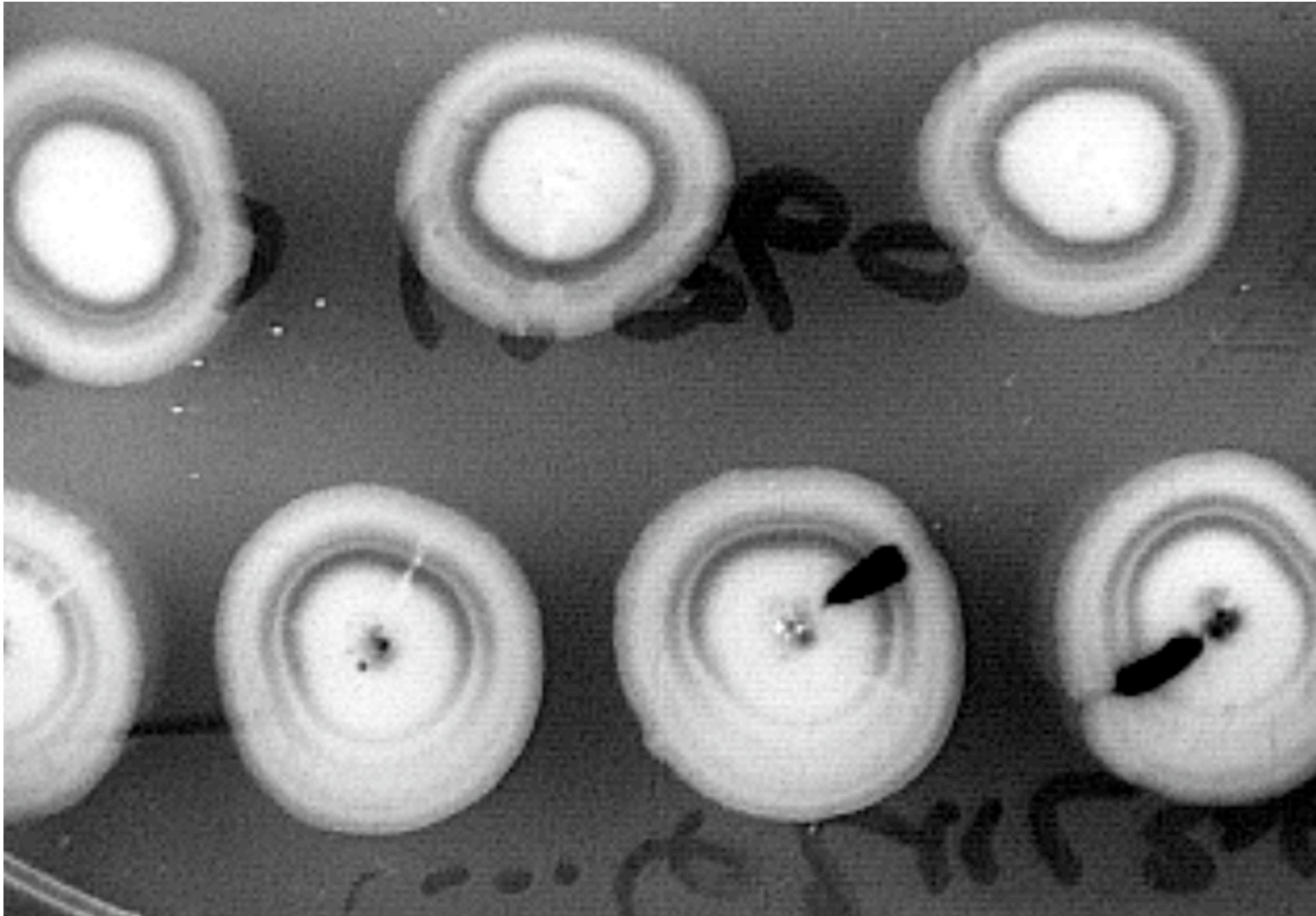
Replicative transposition and DNA rearrangements



Shapiro, J. 1979. "A molecular model for the transposition and replication of bacteriophage Mu and other transposable elements." *Proc. Nat. Acad. Sci. U.S.A.* 76, 1933-1937.

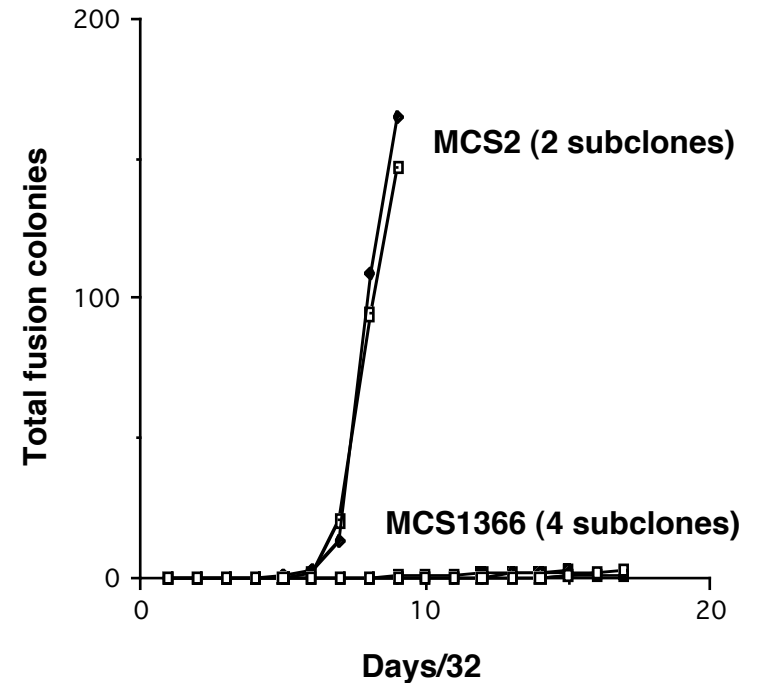
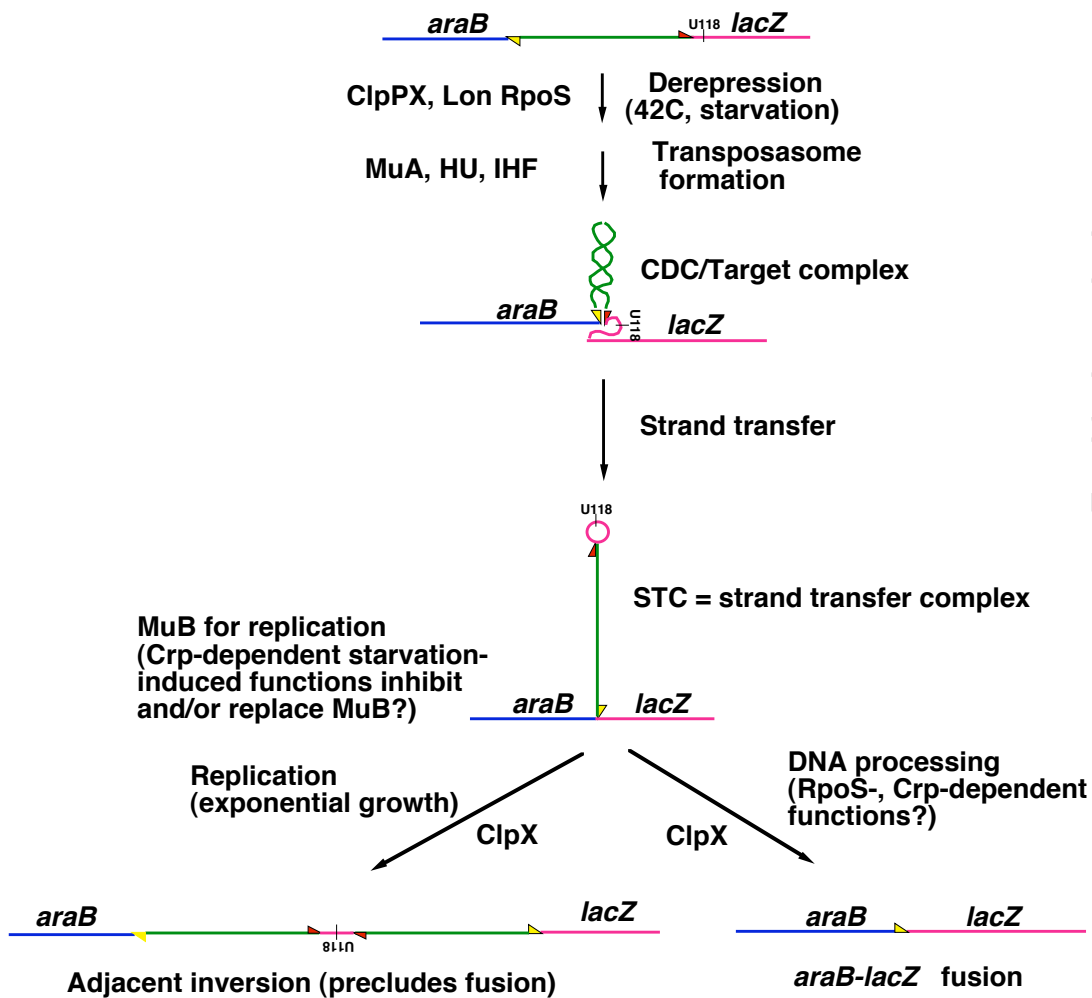


Differential Replicative Transposition of *Mudlac* in *E. coli* Colonies - Starvation Triggered



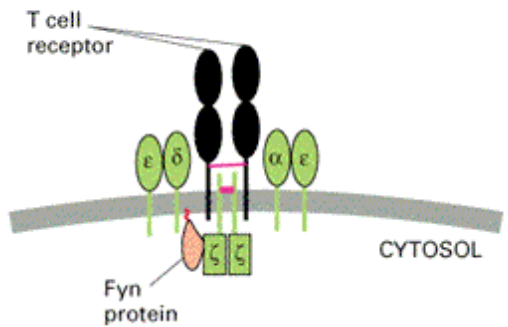
Shapiro, J.A. and N.P. Higgins. 1989. Differential activity of a transposable element in *E. coli* colonies. *J. Bacteriol.* **171**, 5975-5986.

Stress-induced *ara-lac* fusions and adaptive mutation

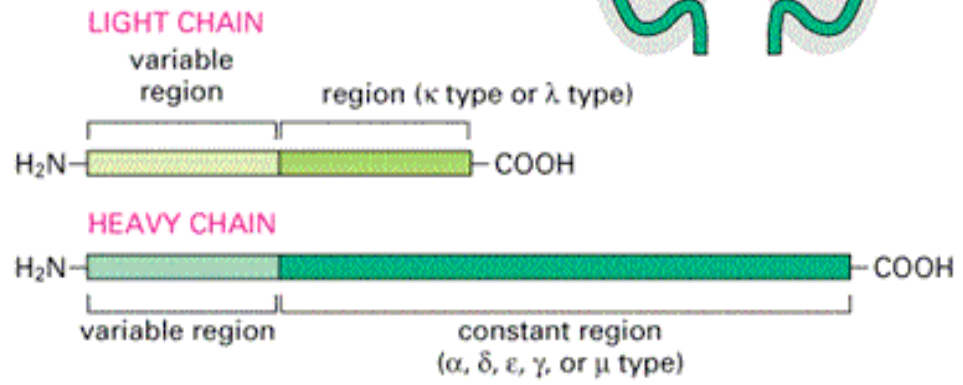
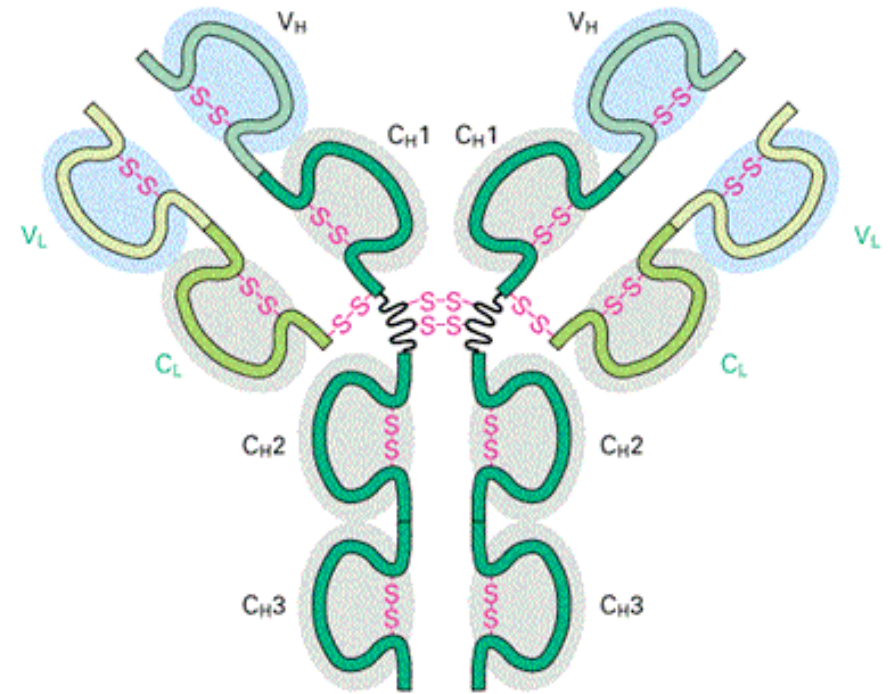
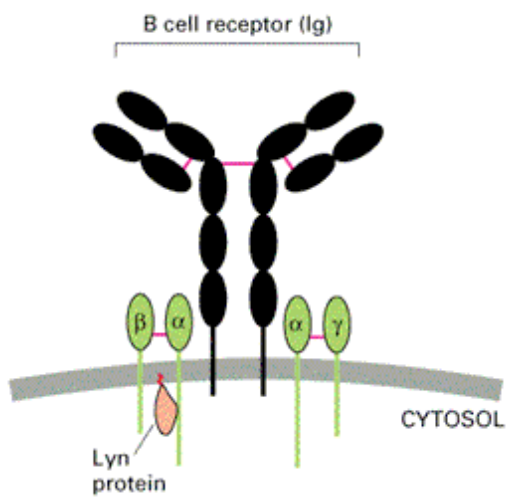


Immune Systems Receptors: How to generate virtually infinite diversity with finite coding capacity

(A) T cell receptor complex

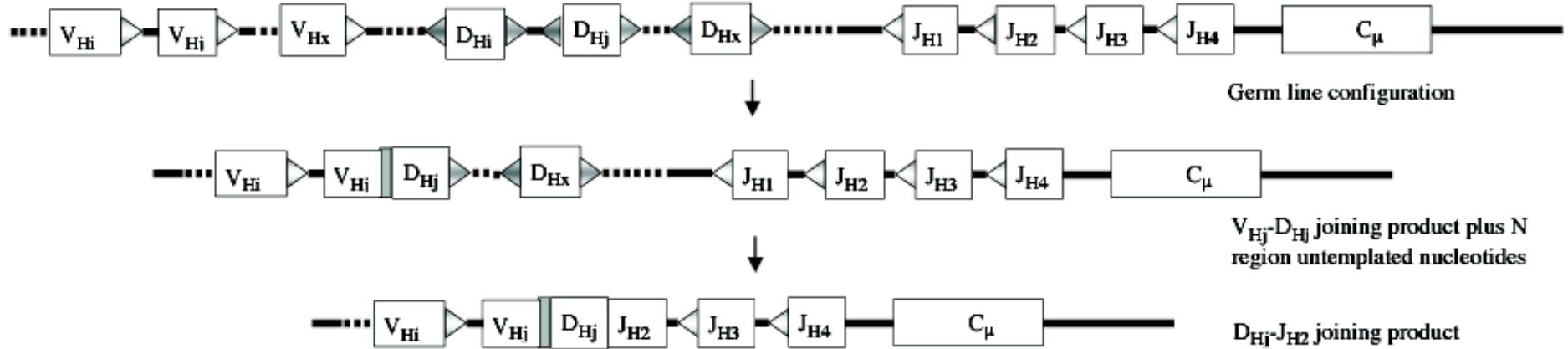


(B) B cell receptor complex

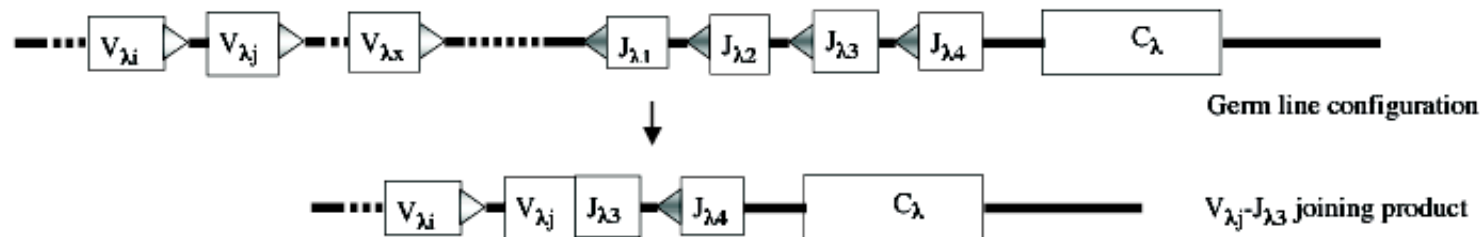


Combinatorial Diversity: assembling immunoglobulin coding sequences from cassettes

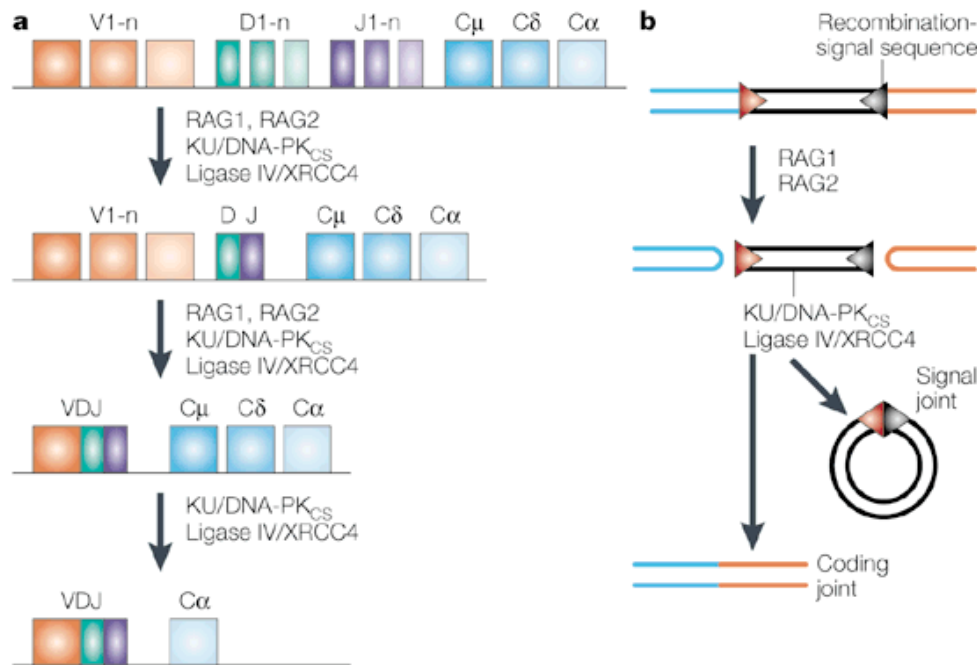
HEAVY CHAIN:



LIGHT CHAIN:

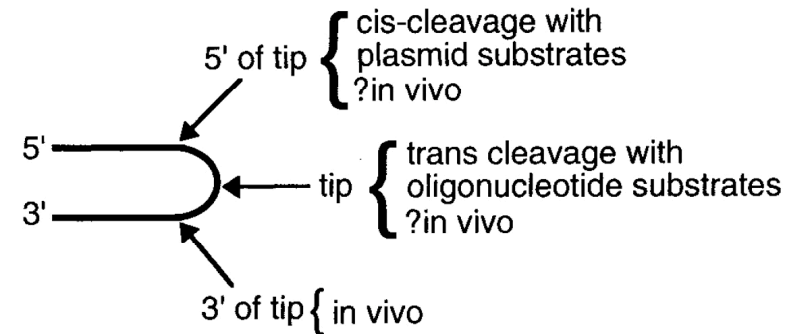


Junctional Flexibility: Augmenting Diversity



Nature Reviews | **Genetics**

A. Sites of Coding End Hairpin Nicking



B. Coding End Products Observed

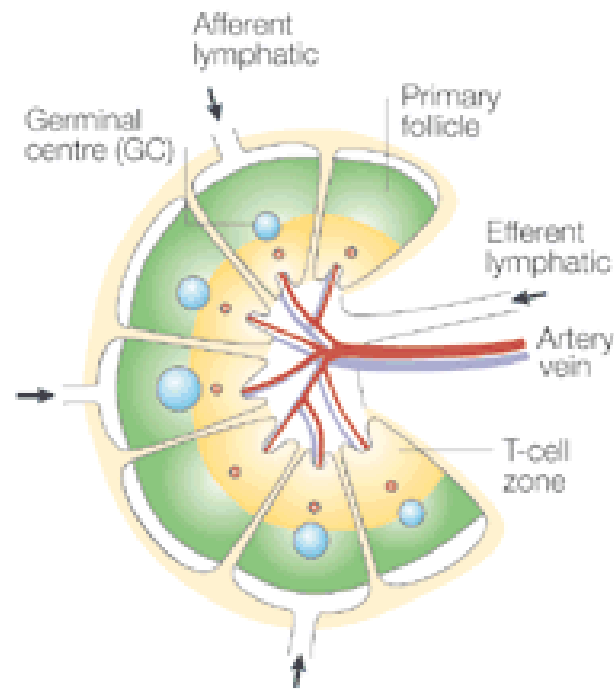
<u>in vitro</u>	<u>in vivo</u>
5' extensions	Deletions (3' overhangs)
Full length (blunt)	3' extensions
	Full length (?blunt)

D. C. van Gent, J. H. Hoeijmakers, R. Kanaar, Chromosomal Stability And The Dna Double-Stranded Break Connection Nature Rev. Genet. 2, 196 (2001)

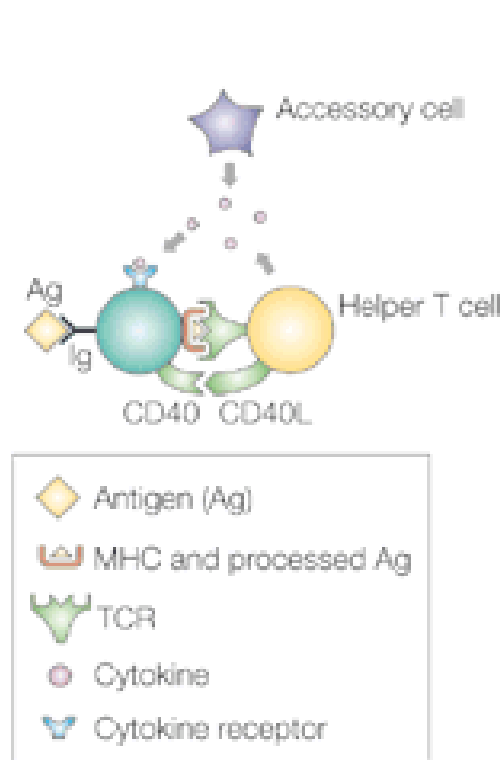
Fugmann et al. 2000. The RAG proteins and V(D)J recombination: complexes, ends and transposition. Annu Rev Immunol 18:495-527.

Antigen stimulation/selection: a rapid evolution system

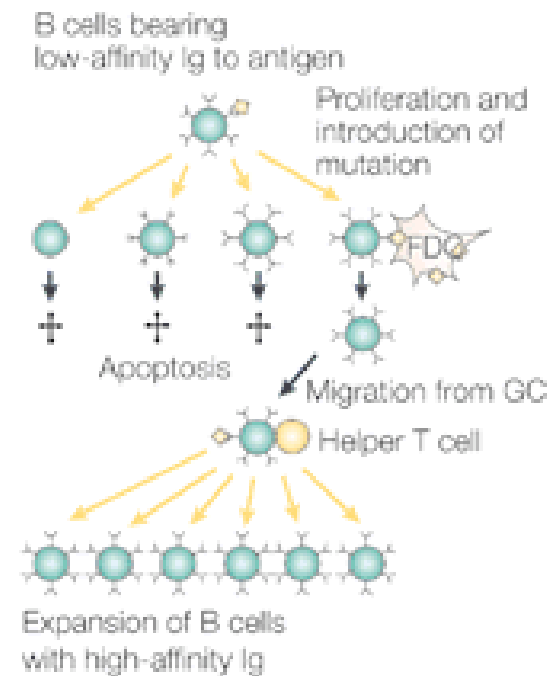
Lymph node



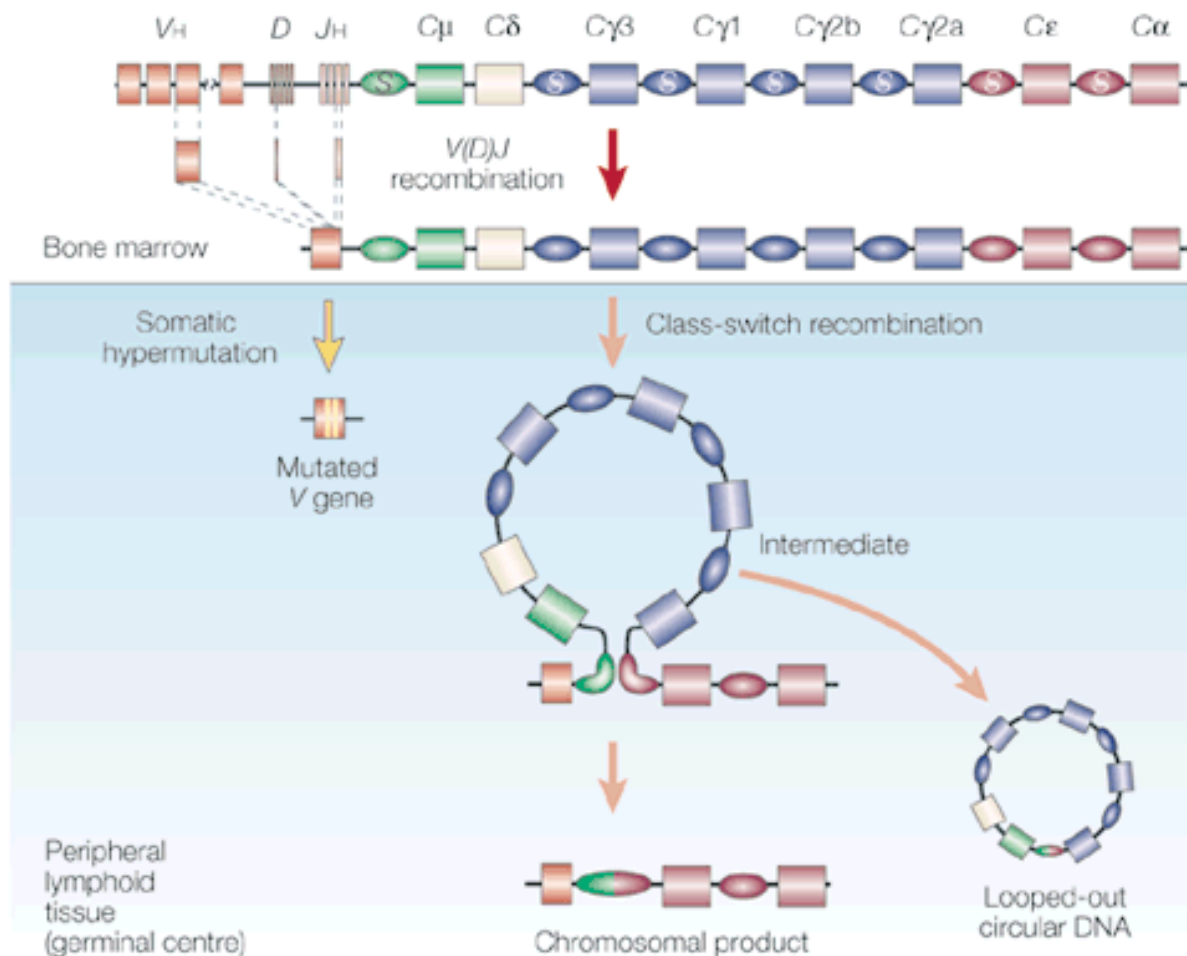
T-B cell interaction



Affinity maturation

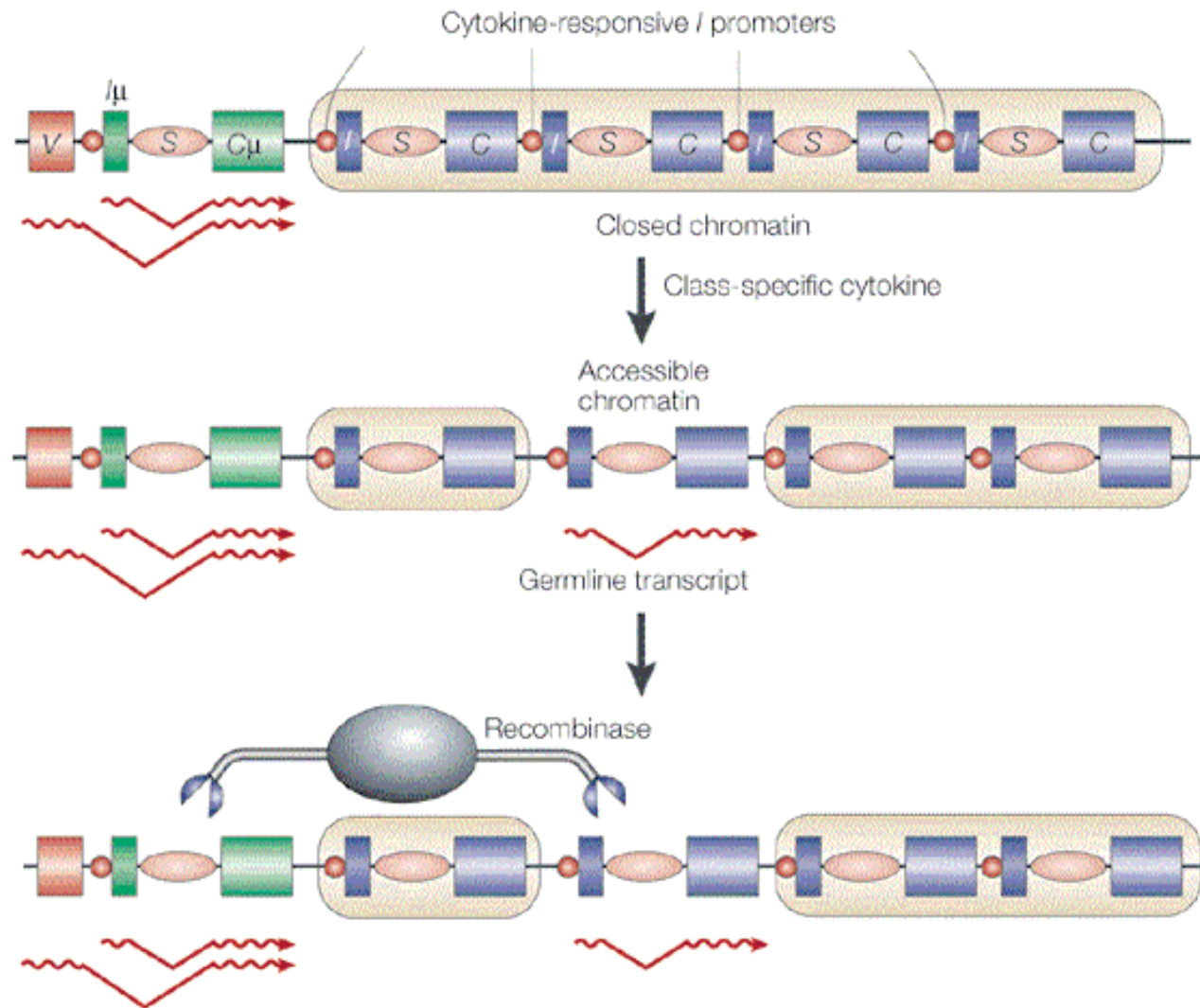


Post-selection (antigen stimulation): antibody improvement and functional diversification



Nature
Reviews
Molecular
Cell Biology
2; 493-503
(2001)
LINKING
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WITH
SOMATIC
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Transcriptional Targeting of Class Switch Recombination

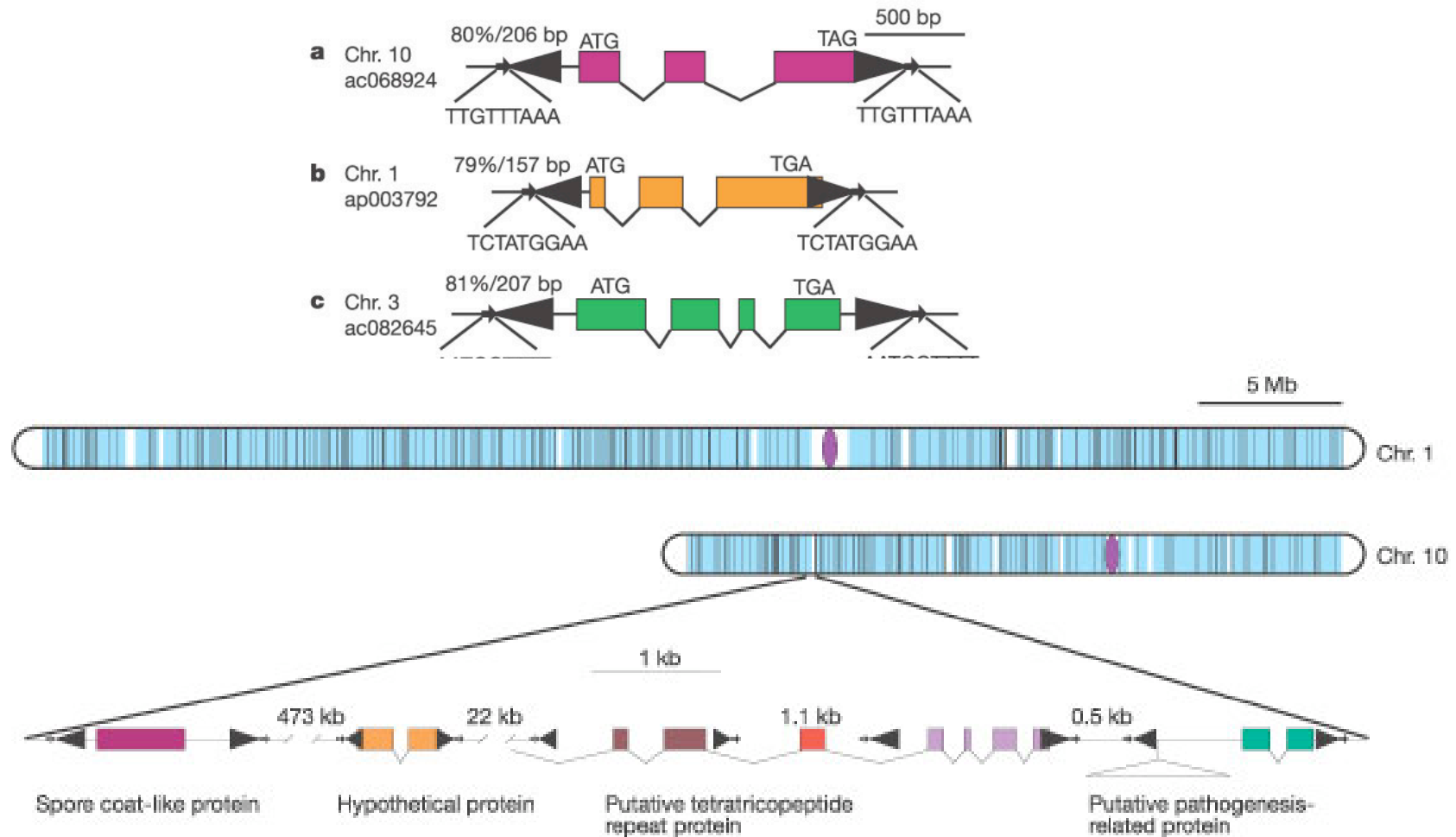


Nature
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SOMATIC
HYPERMUT
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Immune System Lessons: cellular capabilities for controlled but non- determined DNA restructuring

- Tight regulation of complex set of events as to cell type, sequence of particular DNA changes, and linkage to selection & cellular proliferation
- Capacity for multiple types of DNA changes, including ability to incorporate untemplated sequences
- Targeting of VDJ joining events to particular locations within coding regions while maintaining flexibility of novel sequences formed
- Transcriptional activation and targeting of somatic hypermutation (base changes) to V regions of Ig coding sequences
- Lymphokine-directed transcriptional activation and targeting of class switch recombination (breakage and rejoining)

Natural genetic engineering of sequenced genomes - Pack-MULEs



Ning Jiang, Zhirong Bao, Xiaoyu Zhang, Sean R. Eddy and Susan R. Wessler. 2004. Pack-MULE transposable elements mediate gene evolution in plants. *Nature* 431, 569–573.

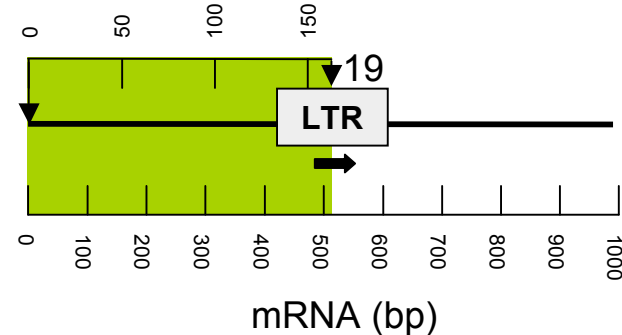
Natural Genetic Engineering Modalities

- Homology-dependent exchange & gene conversion:
 - DS break repair
 - Rearrangements by crossover at dispersed homologies
 - Cassette exchange, protein diversification
- Non-homologous end joining (NHEJ)
 - DS break repair
 - Targeted and untargeted rearrangements
- Mutator polymerases
- Terminal transferase - insertion of novel sequences
- Site-specific recombinases
 - Integration of horizontally transferred DNA
 - Regulation of protein synthesis, protein diversification
- DNA transposons (replicative, cut-&-paste, rolling circle helitrons)
 - Amplification and insertion of repeat elements
 - Large-scale rearrangements (in particular, duplications)
- Reverse transcription-dependent retrotransposons (retroviral-like, LINEs, SINEs)
 - Amplification and insertion of repeat elements
 - Integration of processed RNA cDNA copies
 - Small-scale movement of genomic segments (e.g. exon shuffling)
- Homing and retrohoming introns

Natural genetic engineering of sequenced genomes - protein coding sequences

a.

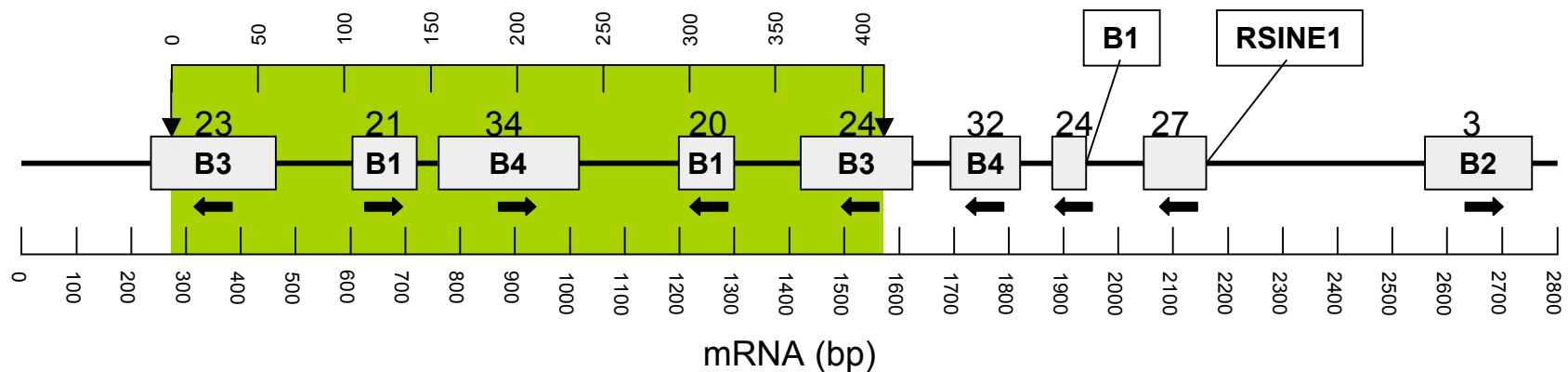
Coding region (codons)



Chemokine

b.

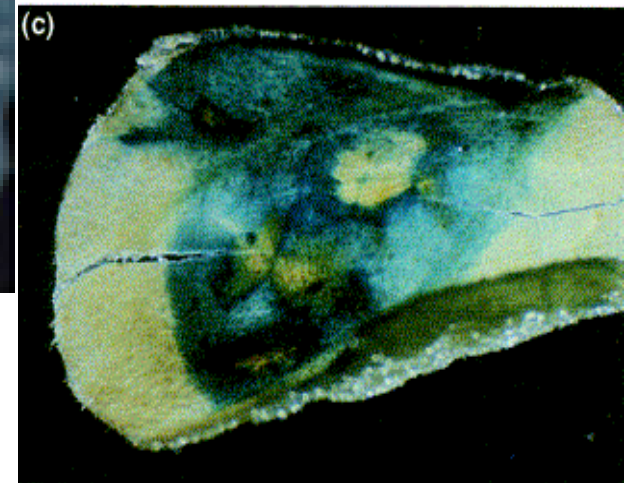
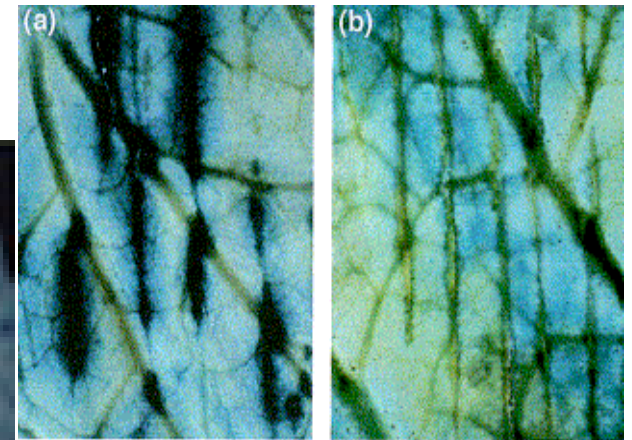
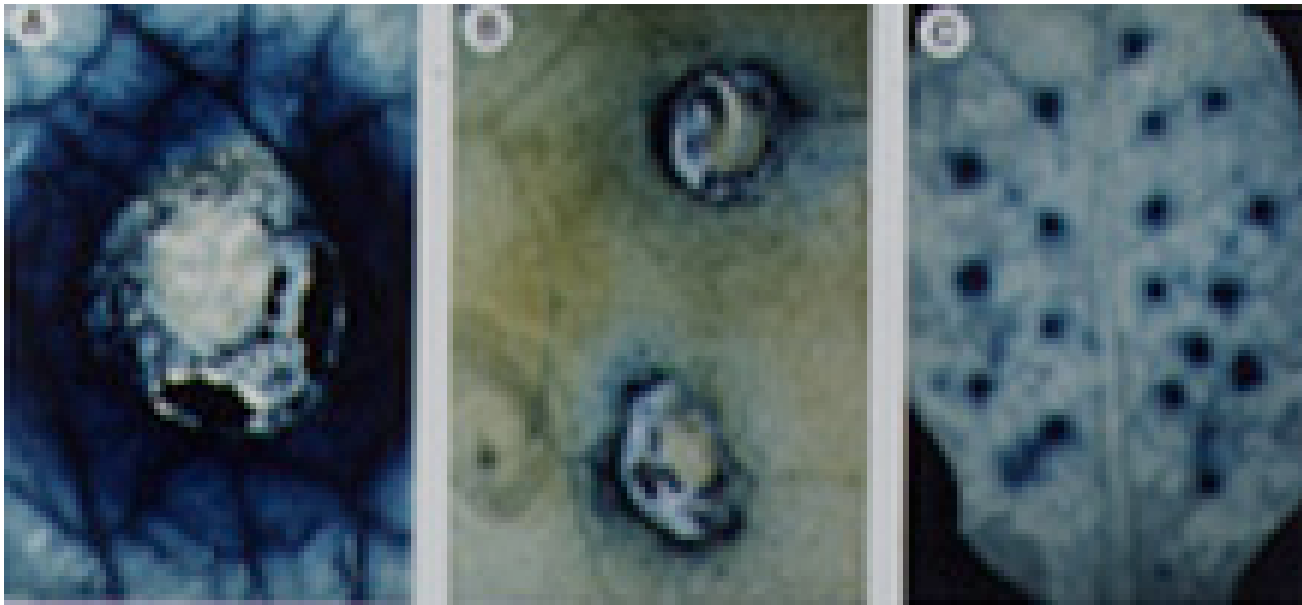
Coding region (codons)



Ion Channel

Nekrutenko, A. and W.-H. Li. 2001. Transposable elements are found in a large number of human protein coding regions. *Trends in Genetics* **17**: 619-625

Leaf wounding and retrotransposon transcription



<http://www-biocel.versailles.inra.fr/Anglais/03Transposon.html>

The expression of the tobacco Tnt1 retrotransposon is induced by wounding : the expression of the LTR-GUS construct is detected by a blue staining surrounding injury points in transgenic tomato (A), tobacco (B) and Arabidopsis (C) plants.

M.-A. Grandbastien et al. Stress activation and genomic impact of Tnt1 retrotransposons in Solanaceae. *Cytogenetic and Genome Research* 2005;110:229-241

Targeting of natural genetic engineering

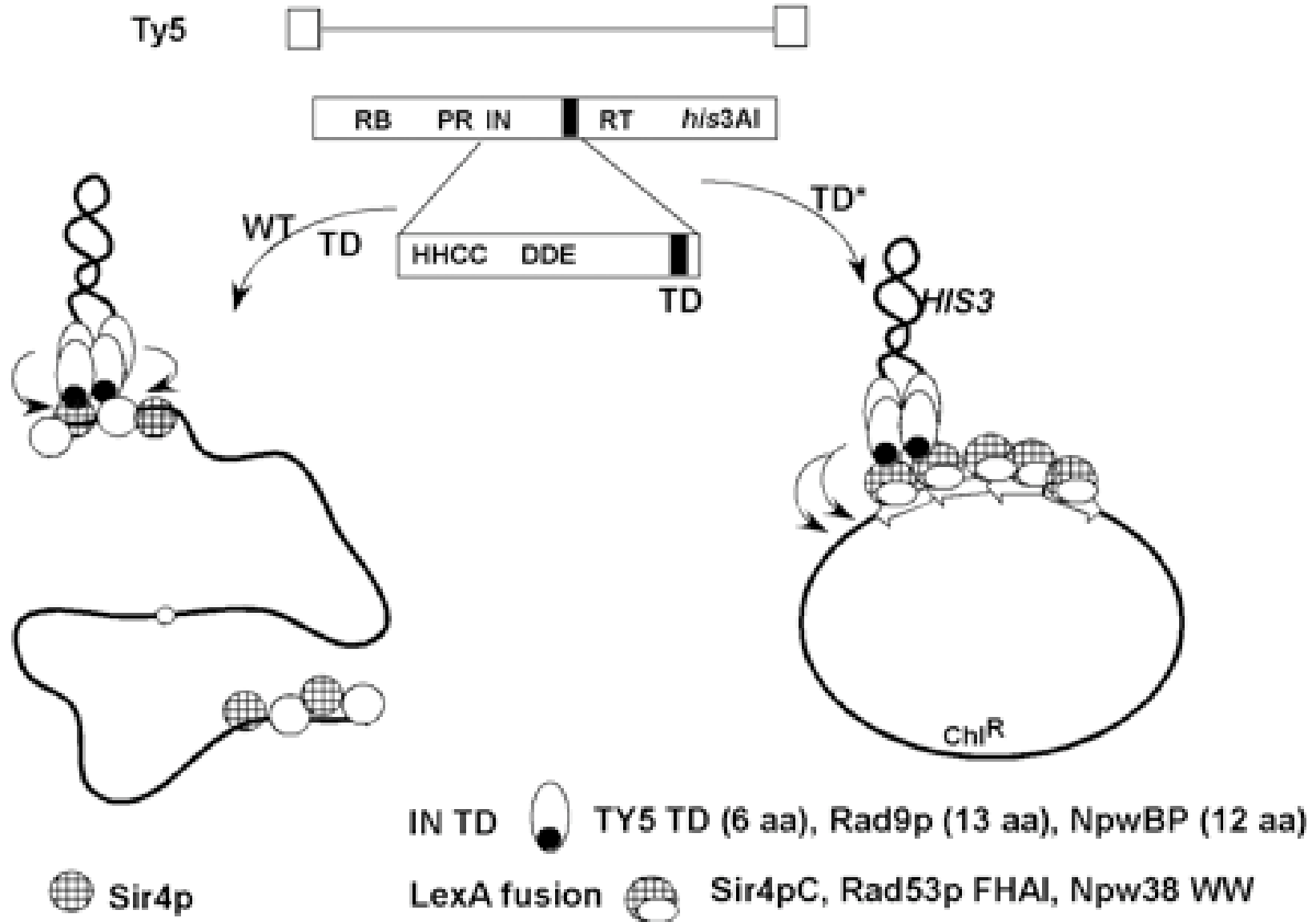
Known molecular mechanisms:

- Sequence recognition by proteins (yeast mating-type switching, ribosomal LINE elements, homing introns, VDJ joining);
- Protein-protein interaction with transcription factors or chromatin proteins (Ty retrotransposon targeting);
- Sequence recognition by RNA (reverse splicing of group II retrohoming introns);
- Transcriptional activation of target DNA (somatic hypermutation; class-switch recombination).

Unknown mechanisms:

- Telomere targeting of certain LINE elements in insects;
- HIV & MLV targeting upstream of transcribed regions;
- P factor homing directed by transcription, chromatin signals;
- P factor targeting to heat-shock promoters.

Yeast Ty5 targeting



S. Sandmeyer. Integration by design. PNAS, May 13, 2003; 100(10): 5586 - 5588.

Advantages of non-random searches of genome space at evolutionary crises

- Genome changes occur under stress or other conditions, when they are most likely to prove beneficial;
- Multiple related changes can occur when a particular natural genetic engineering system is activated;
- Rearrangement of proven genomic components increases the chance that novel combinations will be functional;
- Targeting can increase the probability of functional integration and reduce the risk of system damage (ensure syntactically correct changes in the program architecture, as in GP);
- Rearrangements followed by localized changes provide opportunities for fine tuning once novel function has been achieved.