BE.440 15 September 2004 Essigmann

Loot day: sources of genetic error for evolution... through H-bonding W/C errors

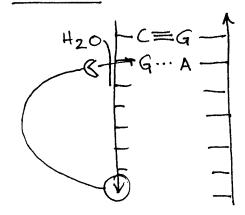
Polymerases: three activities

- 1. NT nucl. transferase
- 2. 3' -> 5' exonuclease kmetic proofreading
- 3. 5'-3' exonuclease nick transl. + Okazaki fragments

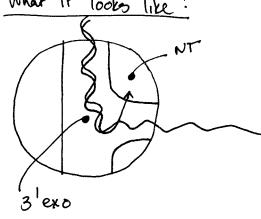
NT Admty:

&-X- bidentate complex

31 exo



What it looks like:



- Sites close together in 3D although 3.4 × 7 v 25 Å apart.
- Can hand off 3' exo'd chan to NT and start again.

5' exo: just mentioned Okazaki fragment maturation and DNA repair.

Back to Arkin: Replication

System protects against mutations to 10-11 to 10-12

10³⁻⁴ BP specif. In NT

10 3-4 31 exo

103-4 MMR

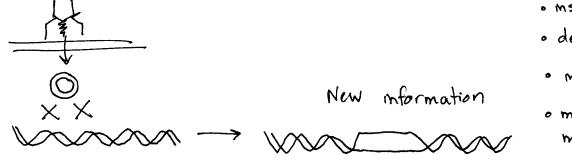
Horizontal Gene Transfer (Radman):

- 1. Vast pop. bact. some are MMRO
- 2. Environment changes -> many die.
- 3. B. sub / P. arugin / E. coli etc. all together
- 4. HGT m MMR € cells

genes are a mosaic - acquired from other species

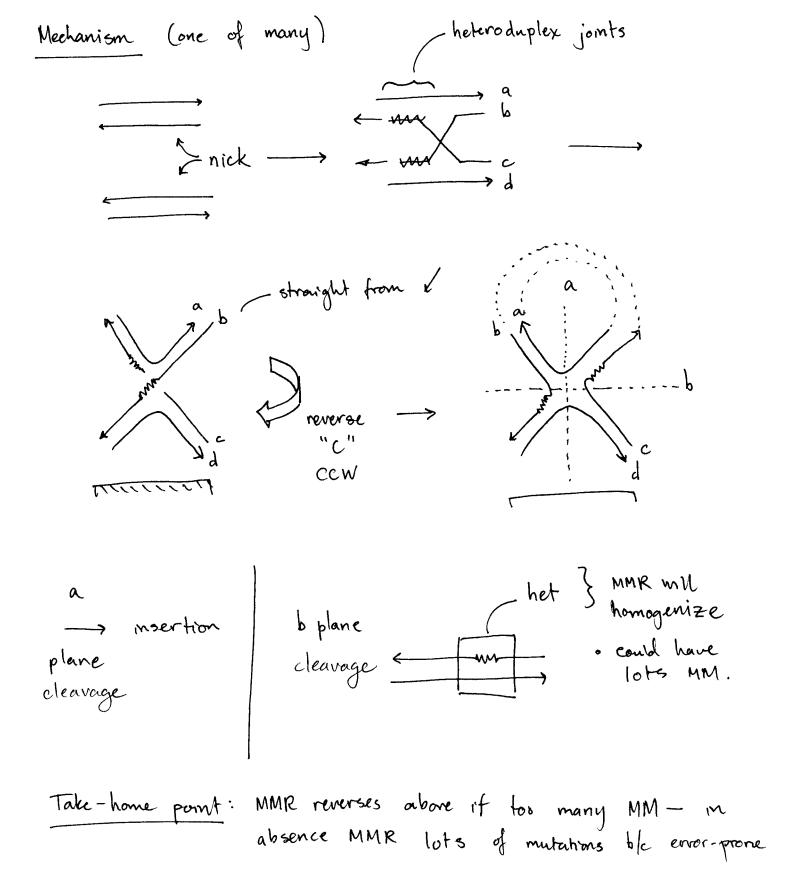
- 5. Pathways introduced
- 6. MMR € tweaks to ophnize for codon utilization
- 7. Acquire MMR gene from neighbor to re-aquire genetic stability

MMR prevents gene transcription from species to species:



- · msertion
- · deletion
- · mversion
- o multi-pont mutation

But: horizontal gene transfer gives vast opportunity for large-scale genetic change



General Features of Promoter Architecture.

Promoter = site where polymerase binds

Prokanyoles: "17 nucleotides

-35 -10

TTGACA TATAAT

pribnow +1

7 nucleotides | segments here cause | 103 x variation in promoter recognition by RNA Poll.

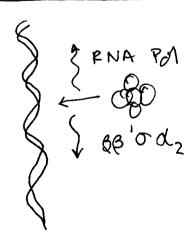
Eukanples:

-75 -25

V// TATA | +1

NOTE: there 103 x variations are for constitutive genes (one may to have different expression levels)... (not really regulation)

How does pol. find promoter?



p-dep and p-indep termination

