# DNA REPAIR AND CANCER

DR SITARAM SWAIN

### DNA REPAIR IN CANCER

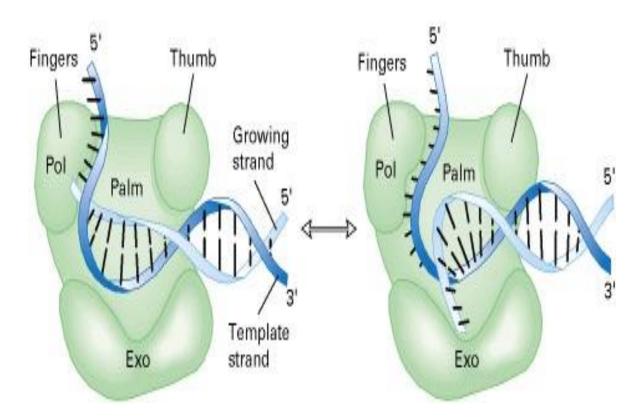
- The DNA sequence can be changed as the result of copying errors introduced by DNA polymerases during replication and by environmental agents such as mutagenic chemicals and certain types of radiation.
- If DNA sequence changes, whatever their cause, are left uncorrected, both somatic cells and germ cells might accumulate so many mutations that they could no longer function.
- Thus the correction of DNA sequence errors in all types of cells is important for survival.

### TYPES OF REPAIR

- PROOFREADING
- MISMATCH REPAIR
- BASE EXCISION REPAIR
- NUCLEOTIDE EXCISION REPAIR
- DOUBLE-STRANDED BREAK REPAIR

# PROOFREADING BY DNA POLYMERASE CORRECTS COPYING ERRORS

- Because the specificity of <u>nucleotide</u> addition by <u>DNA</u> polymerases is determined by <u>Watson-Crick base</u> pairing, a wrong base (e.g., A instead of G) occasionally is inserted during DNA synthesis.
- *E. coli* <u>DNA polymerase</u> III introduces about 1 incorrect base in 10<sup>4</sup> internucleotide linkages during replication and would cause a potentially harmful <u>mutation</u> during each replication
- DNA polymerase I can remove a mismatched <u>base</u> at the 3' growing end of a <u>primer-template</u> complex.



<u>DNA</u> polymerases add the correct nucleotides are added to the 3' end of the growing strand. Incorporation of an incorrect <u>base</u> at the 3' end causes a melting of the end of the duplex.

As a result, the polymerase pauses and the 3' end of the growing strand is transferred to the  $3' \rightarrow 5'$  exonuclease site (Exo) where the mispaired base and probably other bases are removed. Subsequently, the 3' end flips back into the polymerase site and elongation resumes.

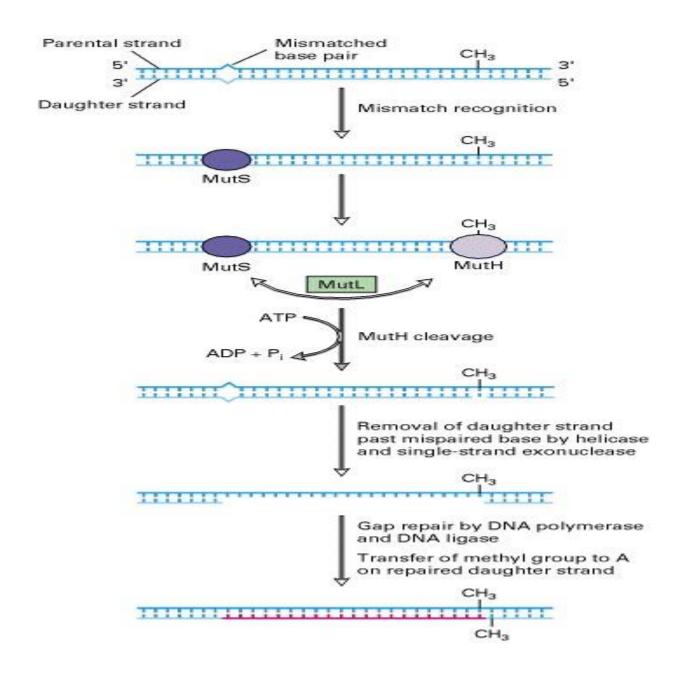
## MISMATCH REPAIR

- Bacterial and eukaryotic cells have a mismatch-repair system that recognizes and repairs all single-base mispairs except C'C, as well as small insertions and deletions.
- The conceptual problem with mismatch repair is determining which is the normal and which is the mutant <u>DNA</u> strand,
- In *E. coli* DNA, adenine residues in a GATC sequence are methylated at the 6 position. Since DNA polymerases incorporate adenine, not methyl-adenine, into DNA,
- methylated only on the parental strand. methylated by a specific <u>enzyme</u>, called *Dam methyltransferase*, only after a lag of several minutes.
- During this lag period, the newly replicated DNA contains hemimethylated GATC sequences.

$$CH_3$$
  
 $5'-G-A-T-C-3'$  Parental strand  
 $3'-C-T-A-G-5'$  Daughter strand

#### **MODEL OF MISMATCH REPAIR**

- This repair system operates soon after incorporation of a wrong base, before the newly synthesized daughter strand becomes methylated.
- MutH binds specifically to a hemimethylated GATC sequence, and MutS binds to the site of a mismatch.
- Binding of MutL protein simultaneously to MutS and to a nearby MutH activates the endonuclease activity of MutH, which then cuts the unmethylated (daughter) strand in the GATC sequence.
- A stretch of the daughter strand containing the mispaired base is excised
- Then gap repair and ligation and then methylation of the daughter strand.(DNA ligase and polymerase)

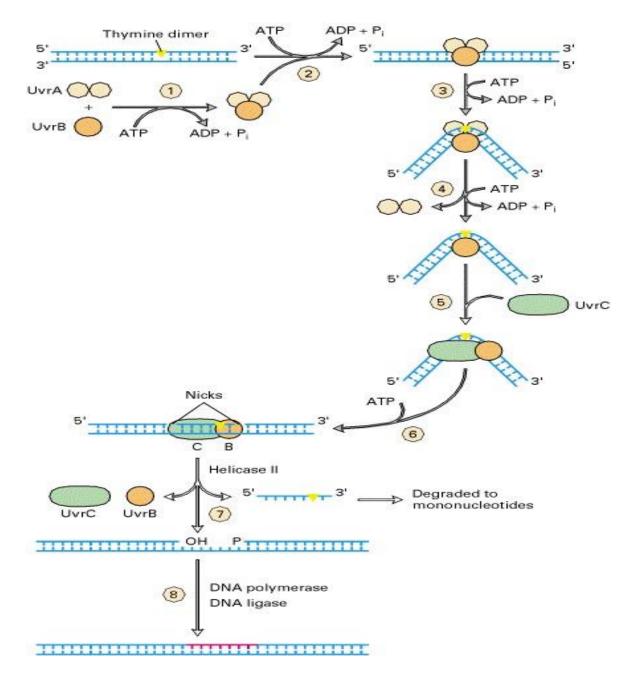


#### **EXCISION REPAIR**

- Two molecules of UvrA and one of UvrB form a complex that moves randomly along <u>DNA</u> (steps 1 and 2).
- Once the complex encounters a lesion, conformational changes in DNA, powered by ATP <a href="hydrolysis">hydrolysis</a>, cause the helix to become locally denatured and kinked by 130° (step 3).
- After the UvrA dimer dissociates (step 4), the UvrC endonuclease binds and cuts the damaged strand at two sites separated by 12 or 13 bases (steps 5 and 6). UvrB and UvrC then dissociate, and <a href="helicase">helicase</a> II unwinds the damaged region (step 7).
- Releasing the single-stranded fragment with the lesion, which is degraded to mononucleotides.
- The gap is filled by <u>DNA polymerase</u> I, and the remaining nick is sealed by DNA <u>ligase</u>.

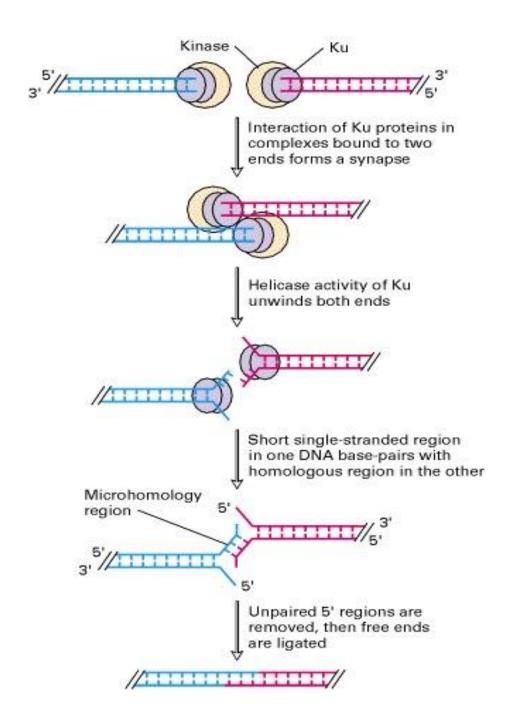
#### **EXCISION REPAIR**

- Cells use excision repair to fix <u>DNA</u> regions containing chemically modified bases, often called *chemical* adducts, that distort the normal shape of DNA locally.
- It has the ability of certain proteins to slide along the surface of a double-stranded DNA molecule looking for bulges or other irregularities in the shape of the double helix.
- For example, this mechanism repairs thymine-thymine dimers, the most common type of damage caused by UV light and these dimers interfere with both replication and transcription of DNA. Excision repair also can correct DNA regions containing bases.carcinogens such as benzo(a)pyrene



# Repair of double-strand breaks by end-joining of nonhomologous DNAs. DNAs with dissimilar sequences at their ends

- These DNAs could be cut fragments from a single gene, or DNAs cut from different chromosomes.
- A complex of two proteins, Ku and DNA dependant protein kinase, binds to the ends of a double-strand break.
- After formation of synapse in which the broken ends overlap, Ku unwinds the ends, by chance revealing short homologous sequences in the two DNAs, which base-pair to yield a region of microhomology.
- The unpaired single-stranded 5' ends are removed
- The two double-stranded molecules ligated together.
   As a result, the double-strand break is repaired.



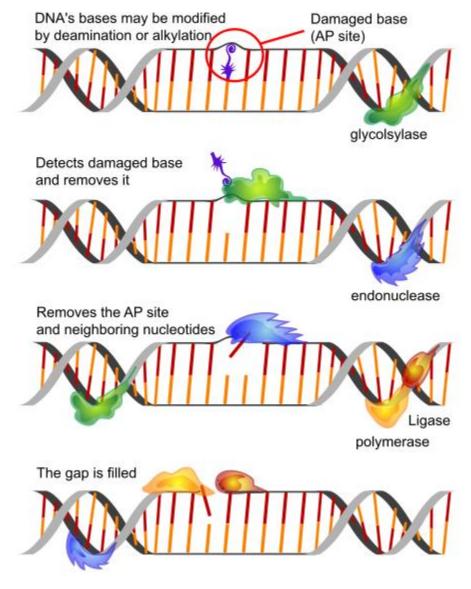
A cell that has suffered a particular doublestrand break usually contains other breaks; such breaks can be repaired by joining the free DNA ends.

The joining of broken ends from different chromosomes, however, leads to translocation of pieces of DNA from one chromosome to another.

Double-strand breaks are caused by ionizing radiation and by anticancer drugs, such as bleomycin, which is why these drugs are used to kill rapidly growing cells.

#### **BASE-EXCISION REPAIR**

- Every cell has a class of enzymes called **DNA glycosylases** that recognize particularly common DNA lesions and remove the affected base by cleaving the *N*-glycosyl bond. This cleavage creates an **AP site** or **abasic site**.
- DNA glycosylases recognize and remove a variety of damaged bases, including formamidopyrimidine and 8-hydroxyguanine (both arising from purine oxidation), hypoxanthine (arising from adenine deamination), and alkylated bases such as 3-methyladenine and 7methylguanine.
- Glycosylases that recognize other lesions, including pyrimidine dimers, have also been identified in some classes of organisms.
- Once an AP site has formed, another group of enzymes must repair it. This process begins with AP endonucleases, enzymes that cut the DNA strand containing the AP site.
- A segment of DNA including the AP site is then removed, DNA polymerase I replaces the DNA, and DNA ligase seals the remaining nick. In eukaryotes, nucleotide replacement is carried out by specialized polymerases.



**BASE-EXCISION REPAIR** 

 Cellular DNA-repair processes have been implicated both in protecting against and contributing to the <u>development</u> of cancer.

# THANK YOU