

**Dr. H. N. Sinha Arts and Commerce
College, Patur**

DNA Mutation and Repair

Presented by- Pallavi S. Nikhade

What is a mutation?

- Substitution, deletion, or insertion of a base pair.
- Chromosomal deletion, insertion, or rearrangement.

Somatic mutations - occur in somatic cells and only affect the individual in which the mutation arises.

Germ-line mutations - alter gametes and passed to the next generation.

Mutations are quantified in two ways:

1. Mutation rate = probability of a particular type of mutation per unit time (or generation).
2. Mutation frequency = number of times a particular mutation occurs in a population of cells or individuals.

Two types of point mutations:

1. Base pair substitutions.

1. Transitions

- Convert a purine-pyrimidine to the other purine-pyrimidine.
- 4 types of transitions; $A \leftrightarrow G$ and $T \leftrightarrow C$
- Most transitions results in synonymous substitution because of the degeneracy of the genetic code.

1. Transversions

- Convert a purine-pyrimidine to a pyrimidine-purine.
- 8 types of transversions; $A \leftrightarrow T$, $G \leftrightarrow C$, $A \leftrightarrow C$, & $G \leftrightarrow T$
- Transversions are more likely to result in nonsynonymous substitution.

2. Base pair deletions and insertions

Missense mutation :

Base pair substitution results in substitution of a different amino acid.

Nonsense mutation:

Base pair substitution results in a stop codon (and shorter polypeptide).

Neutral mutation:

Base pair substitution results in substitution of an amino acid with similar chemical properties (protein function is not altered).

Silent mutation:

Base pair substitution results in the same amino acid.

Frameshift mutations:

Deletions or insertions (not divisible by 3) result in translation of incorrect amino acids, stops codons (shorter polypeptides), or read-through of stop codons (longer polypeptides).

Types of base pair substitutions and mutations

Sequence of part of a normal gene

Sequence of mutated gene

a) Transition mutation (AT to GC in this example)

5' TCTCAA **AA**ATTTACG 3'
3' AGAGTT **TT**TAAATGC 5'

5' TCTCAAG **A**AATTTACG 3'
3' AGAGTT **C**TTAAATGC 5'

b) Transversion mutation (CG to GC in this example)

5' TCT **C**AAAAATTTACG 3'
3' AGA **G**TTTTTAAATGC 5'

5' TCT **G**AAAAATTTACG 3'
3' AGA **C**TTTTTAAATGC 5'

c) Missense mutation (change from one amino acid to another; here a transition mutation from AT to GC changes the codon from lysine to glutamic acid)

5' TCTCAA **AA**ATTTACG 3'
3' AGAGTT **TT**TAAATGC 5'

... Ser Gln **Lys** Phe Thr ...

5' TCTCAAG **A**AATTTACG 3'
3' AGAGTT **C**TTAAATGC 5'

... Ser Gln **Glu** Phe Thr ...

d) Nonsense mutation (change from an amino acid to a stop codon; here a transversion mutation from AT to TA changes the codon from lysine to UAA stop codon)

5' TCTCAA **AA**ATTTACG 3'
3' AGAGTT **TT**TAAATGC 5'

... Ser Gln **Lys** Phe Thr ...

5' TCTCAAT **A**AATTTACG 3'
3' AGAGTT **AT**TAAATGC 5'

... Ser Gln **Stop** ...

Types of base pair substitutions and mutations

Sequence of part of a normal gene

Sequence of mutated gene

- e) Neutral mutation (change from an amino acid to another amino acid with similar chemical properties; here an AT to GC transition mutation changes the codon from lysine to arginine)



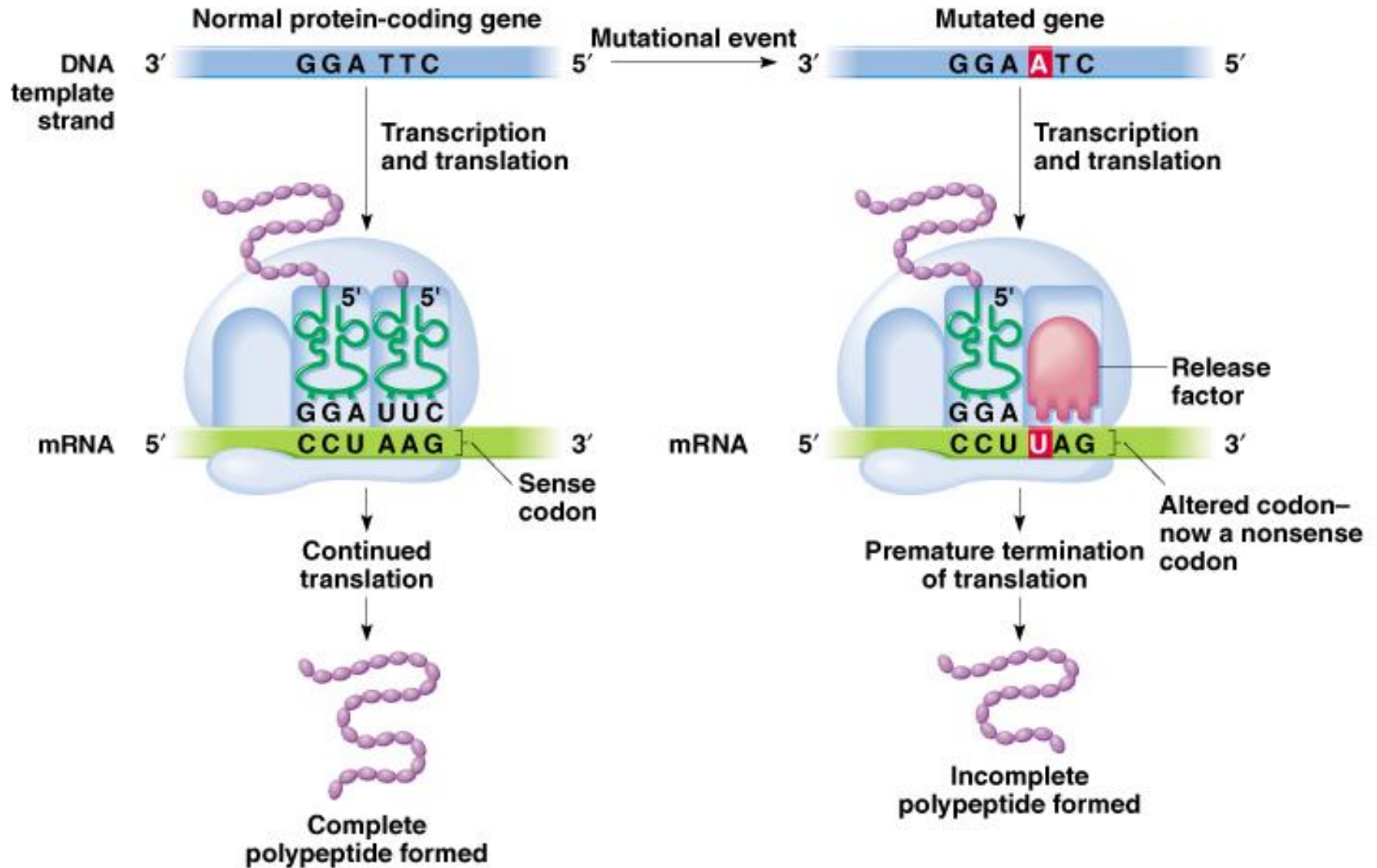
- f) Silent mutation (change in codon such that the same amino acid is specified; here an AT-to-GC transition in the third position of the codon gives a codon that still encodes lysine)



- g) Frameshift mutation (addition or deletion of one or a few base pairs leads to a change in reading frame; here the insertion of a GC base pair scrambles the message after glutamine)



Effect of a nonsense mutation on translation



Reverse mutations and suppressor mutations:

Forward mutation

Mutation changes wild type (ancestral) to mutant (derived).

Reverse mutation (back mutation)

Mutation changes mutant (derived) to wild type (ancestral).

- Reversion to the wild type amino acid restores function.
- Reversion to another amino acid partly or fully restores function.

Suppressor mutation

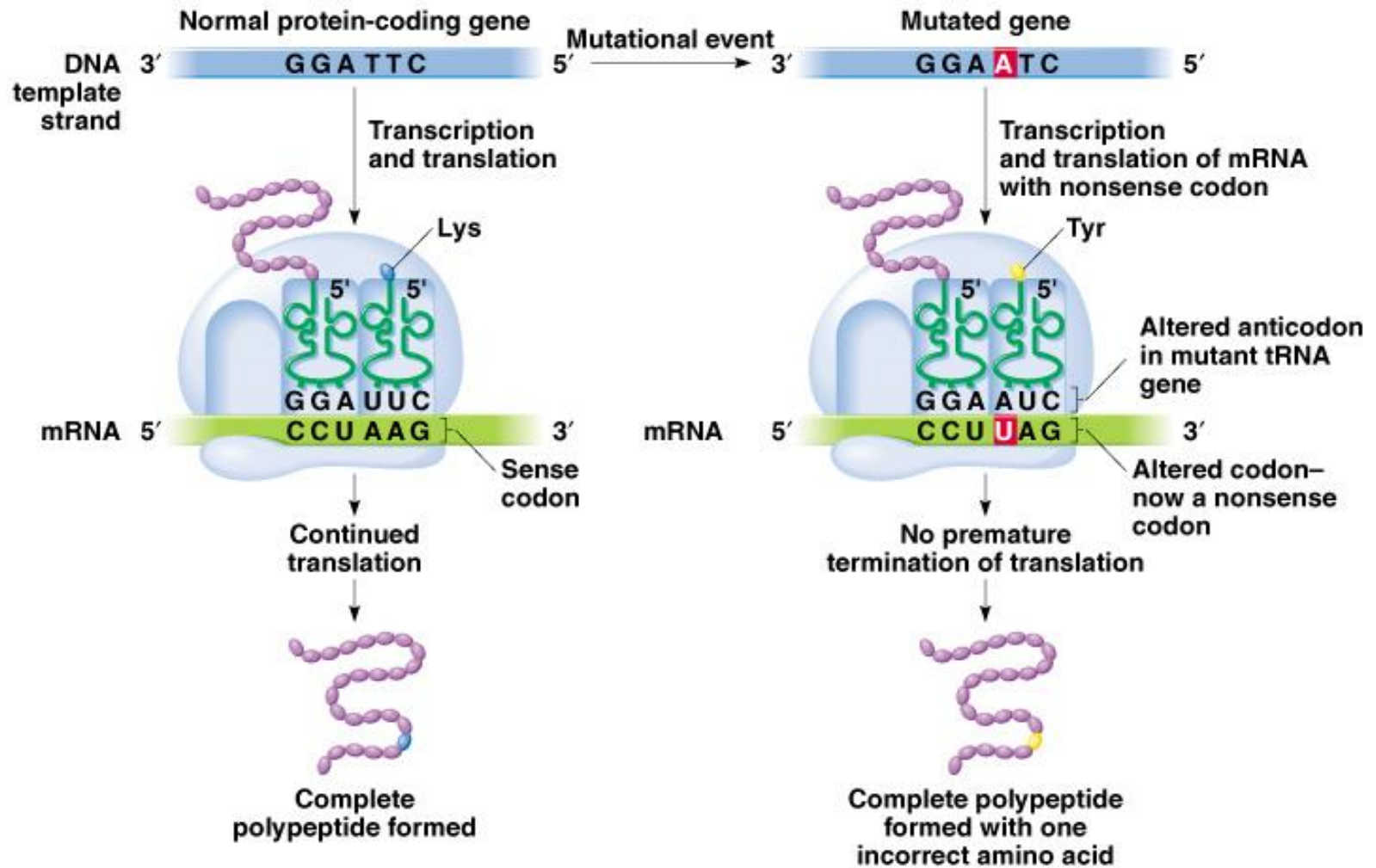
Occur at sites different from the original mutation and mask or compensate for the initial mutation without reversing it.

- Intragenic suppressors occur on the same codon;
e.g., nearby addition restores a deletion
- Intergenic suppressors occur on a different gene.

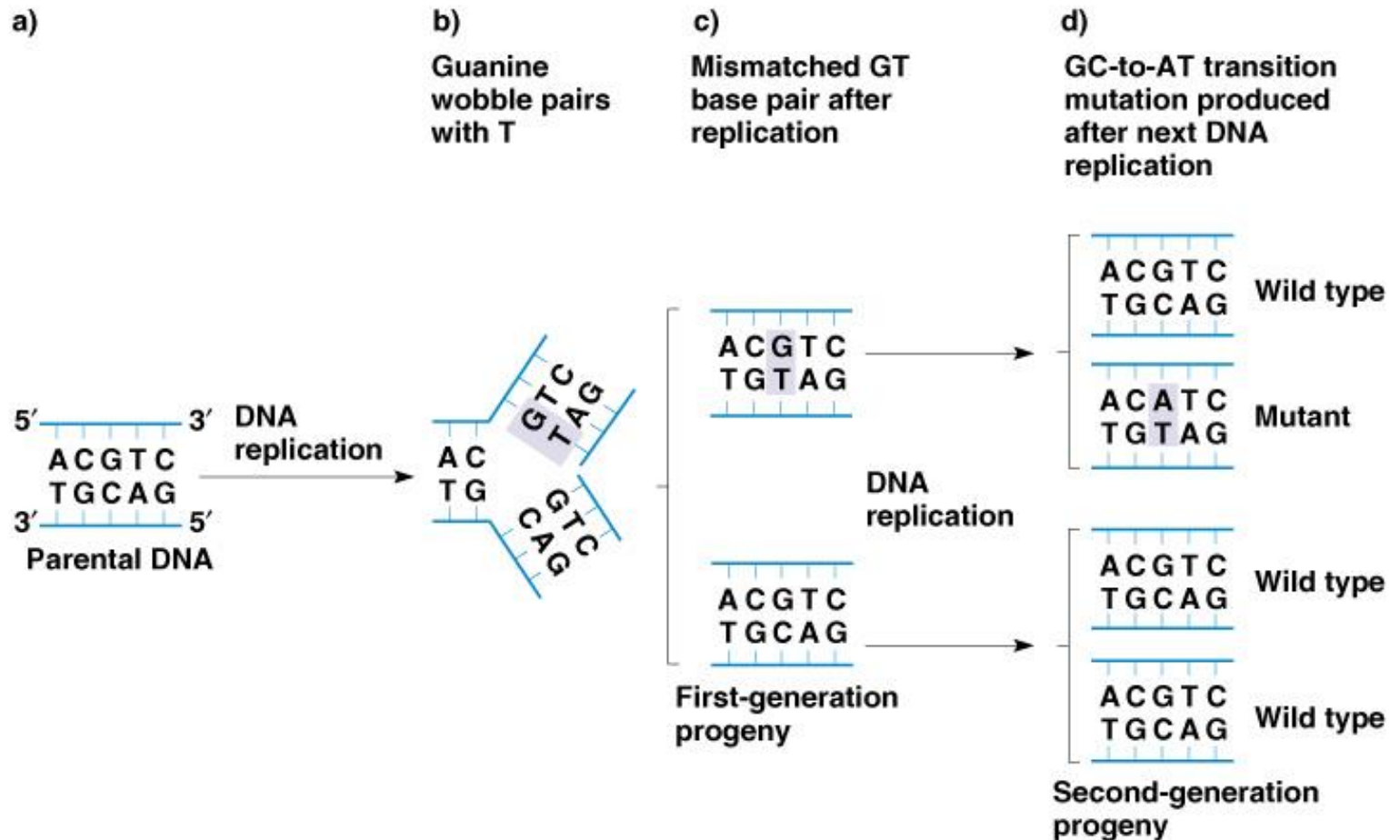
Intergenic suppressor genes:

- Many function in mRNA translation.
- Each suppressor gene works on only one type of nonsense, missense, or frameshift mutation.
- Suppressor genes often encode tRNAs, which possess anti-codons that recognize stop codons and insert an amino acid.
- Three classes of tRNA nonsense suppressors, one for each stop codon (UAG, UAA, UGA).
- tRNA suppressor genes coexist with wild type tRNAs.
- tRNA suppressors compete with release factors, which are important for proper amino acid chain termination.
- Small number of read-through polypeptides are produced; tandem stop codons (UAGUAG) are required to result in correct translation termination.

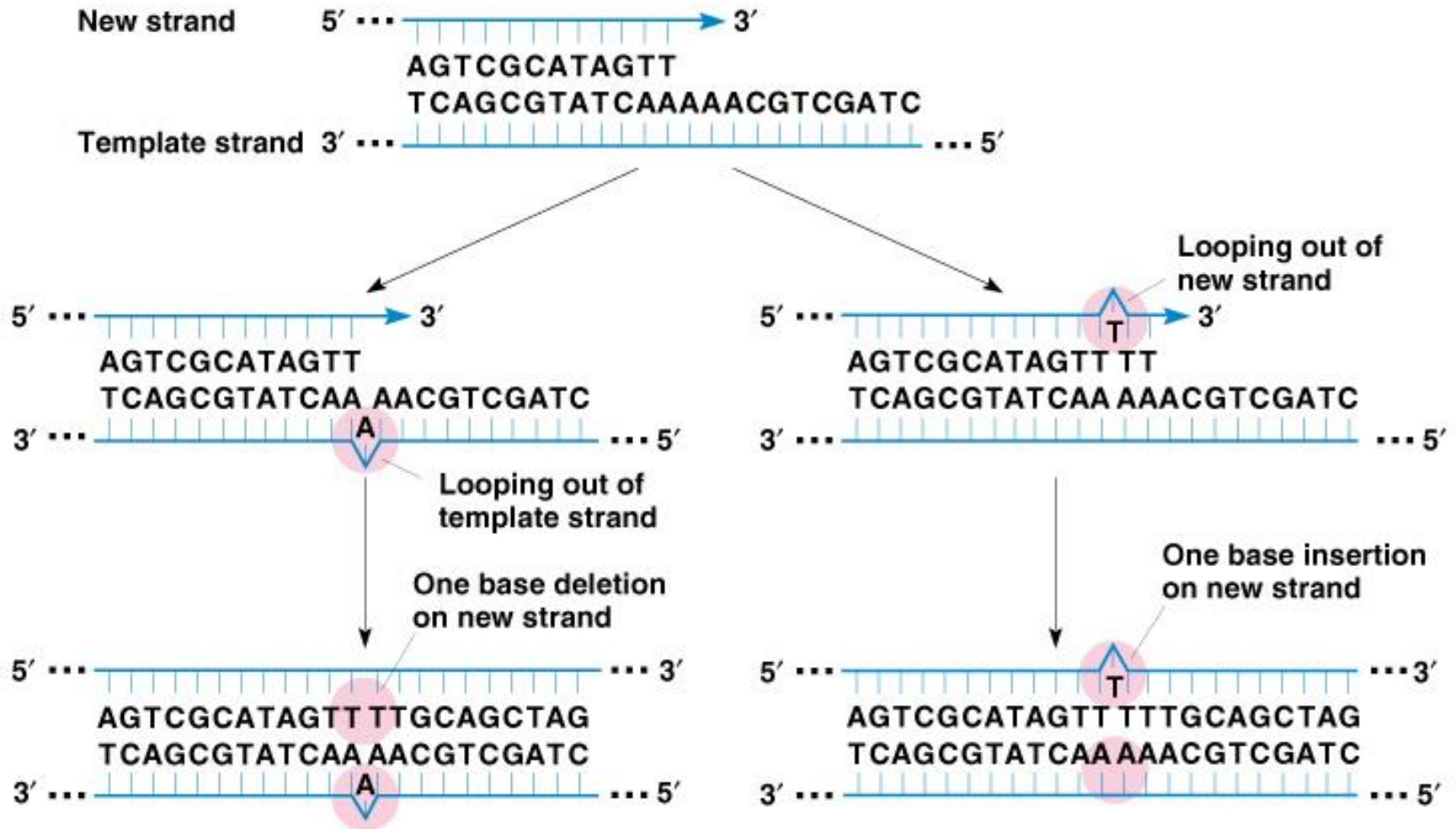
tRNA suppressor gene mechanism for nonsense mutation



Mutation caused by mismatch wobble base pairing



Addition and deletion by DNA looping-out.



Spontaneous mutations:

Depurination

Common; A or G are removed and replaced with a random base.

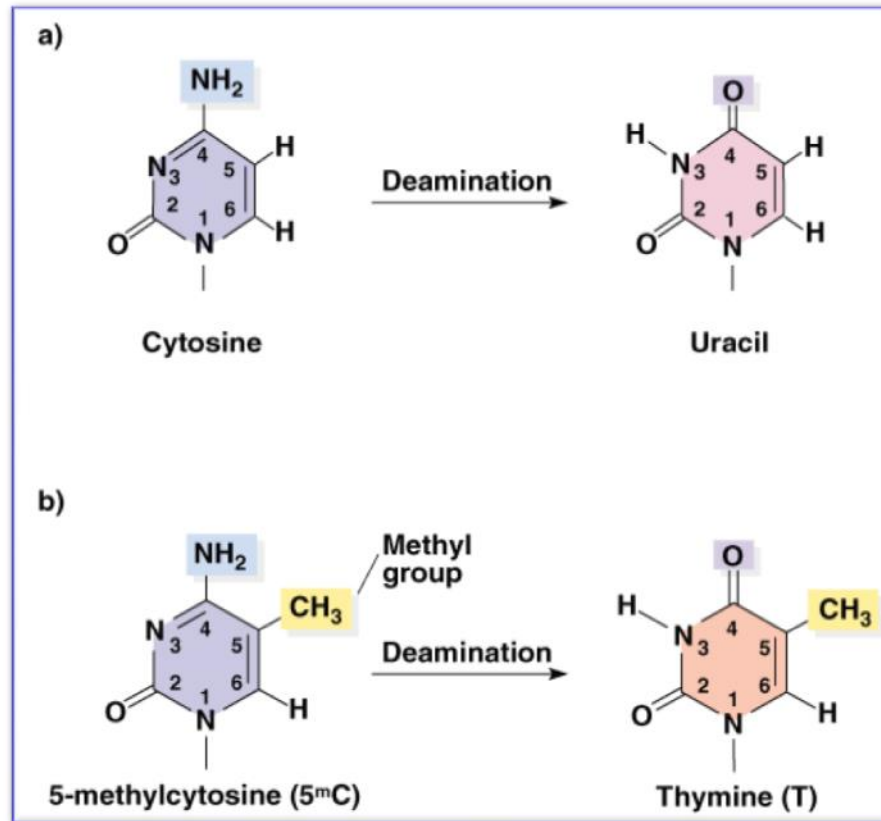
Deamination

Amino group is removed from a base ($C \rightarrow U$); if not replaced U pairs with A in next round of replication ($CG \rightarrow TA$).

Prokaryote DNA contains small amounts of $5^M C$; deamination of $5^M C$ produces T ($CG \rightarrow TA$).

Regions with high levels of $5^M C$ are mutation hot spots.

Deamination



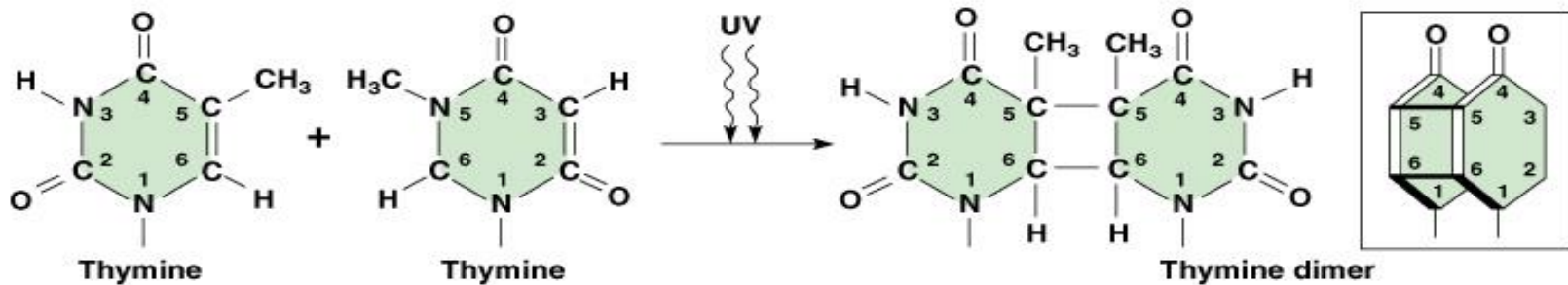
Induced mutations

Radiation (e.g., X-rays, UV)

Ionizing radiation breaks covalent bonds including those in DNA and is the leading cause of chromosome mutations.

Ionizing radiation has a cumulative effect and kills cells at high doses.

UV (254-260 nm) causes purines and pyrimidines to form abnormal dimer bonds and bulges in the DNA strands.



Thymine dimers induced by UV light.

Induced mutations:

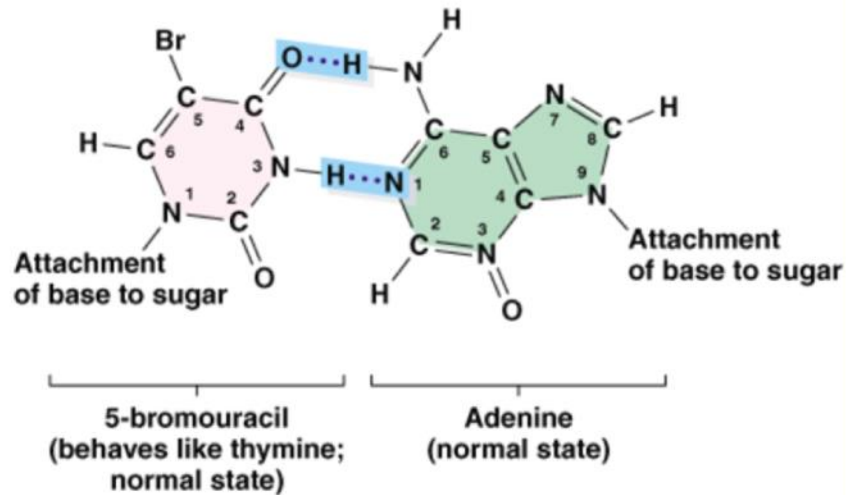
Chemical mutagens

Base analogs

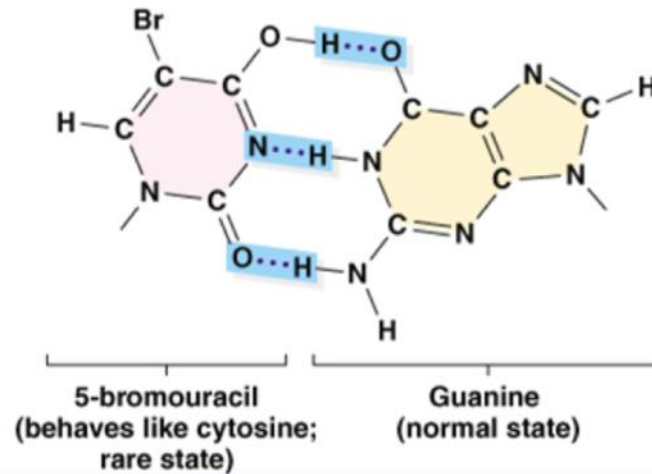
- Similar to normal bases, incorporated into DNA during replication.
- Some cause mis-pairing (e.g., 5-bromouracil).
- Not all are mutagenic.

Mutagenic effects of 5-bromouracil

a) Base-pairing of 5-bromouracil in its normal state

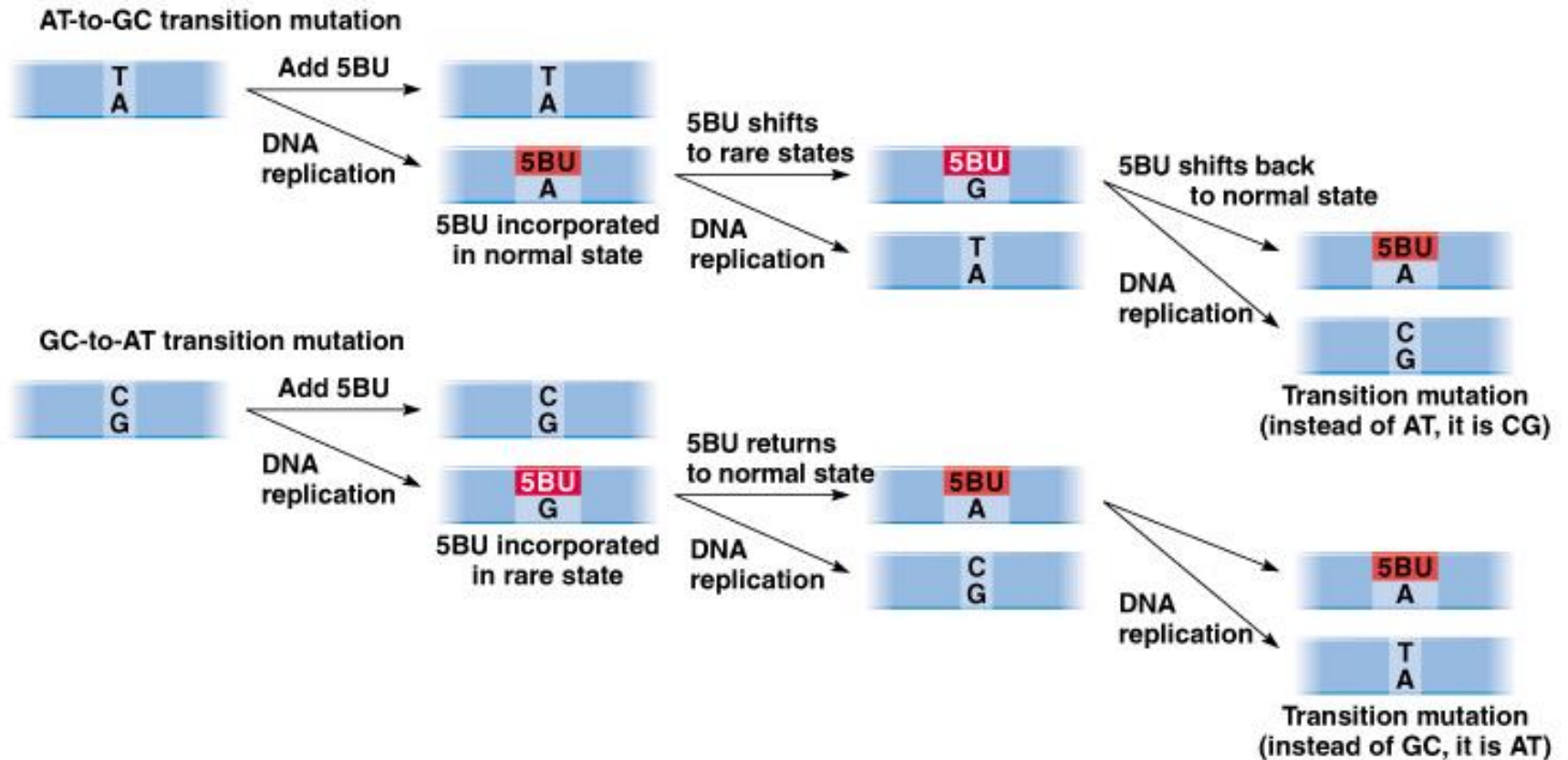


b) Base-pairing of 5-bromouracil in its rare state



Mutagenic effects of 5-bromouracil

c) Mutagenic action of 5BU



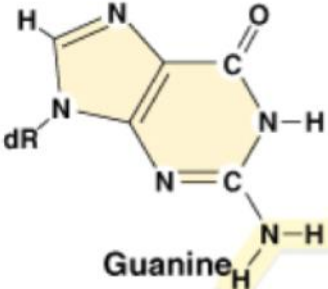
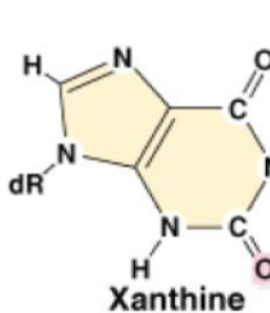
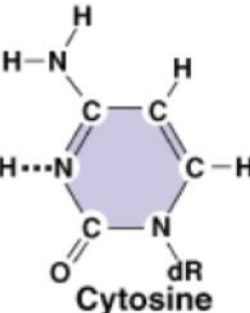
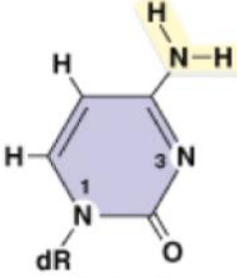
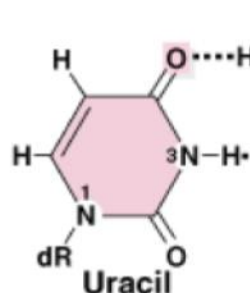
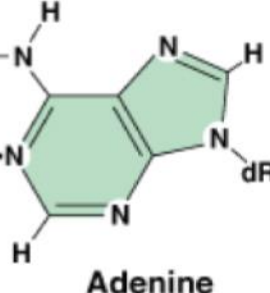
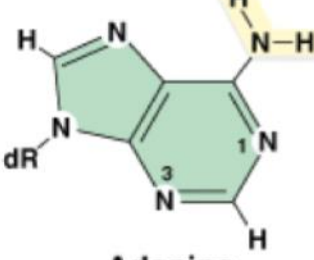
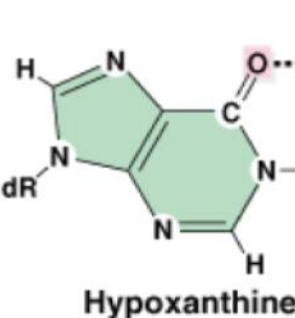
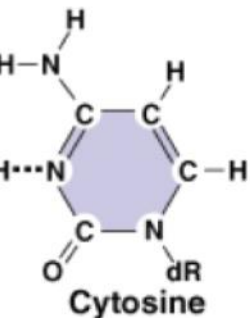
Induced mutations:

Chemical mutagens

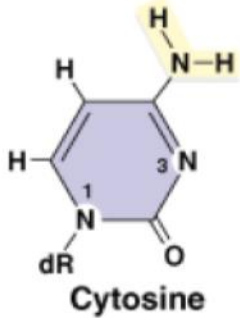
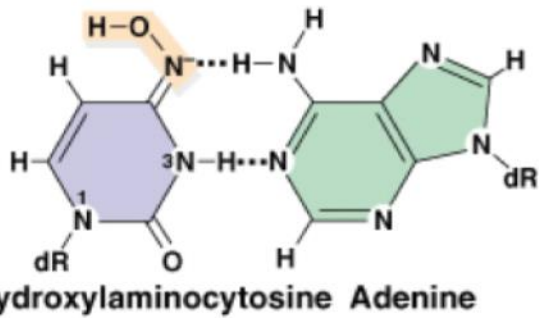
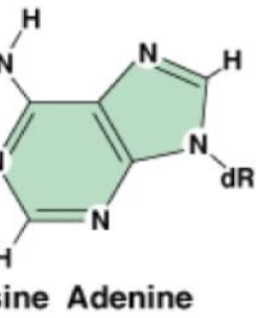
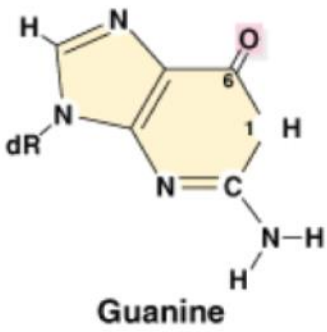
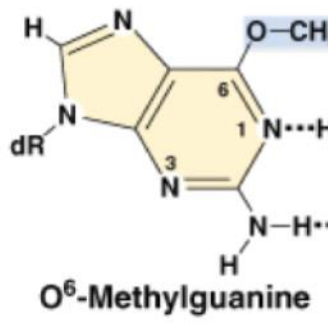

Base modifying agents, act at any stage of the cell cycle:

- Deaminating agents
- Hydroxylating agents
- Alkylating agents

Base-modifying agents

Original base	Mutagen	Modified base	Pairing partner	Predicted transition
<p>a)</p> <p>1)</p>  <p>Guanine</p>	<p>Nitrous acid (HNO_2)</p>	 <p>Xanthine</p>	 <p>Cytosine</p>	None
<p>2)</p>  <p>Cytosine</p>	<p>Nitrous acid (HNO_2)</p>	 <p>Uracil</p>	 <p>Adenine</p>	$\text{CG} \rightarrow \text{TA}$
<p>3)</p>  <p>Adenine</p>	<p>Nitrous acid (HNO_2)</p>	 <p>Hypoxanthine</p>	 <p>Cytosine</p>	$\text{AT} \rightarrow \text{GC}$

Base-modifying agents

Original base	Mutagen	Modified base	Pairing partner	Predicted transition
<p>b)</p>  <p>Cytosine</p>	<p>Hydroxylamine (NH₂OH)</p>	 <p>Hydroxylaminocytosine</p>	 <p>Adenine</p>	CG → TA
<p>c)</p>  <p>Guanine</p>	<p>Methylmethane sulfonate (MMS) (alkylating agent)</p>	 <p>O⁶-Methylguanine</p>	 <p>Thymine</p>	GC → AT

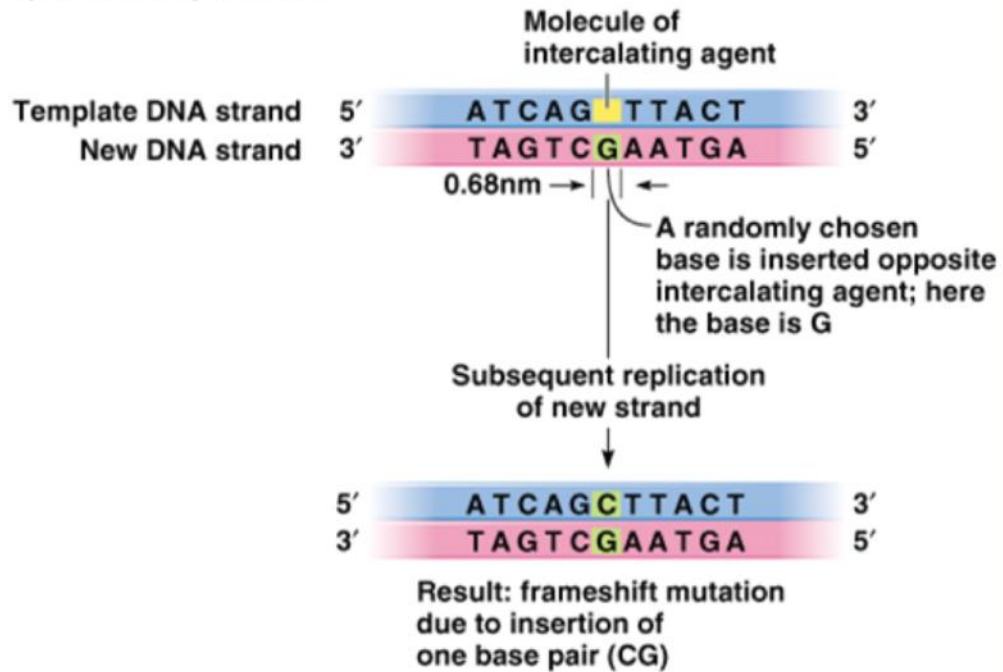
Induced mutations:

Chemical mutagens

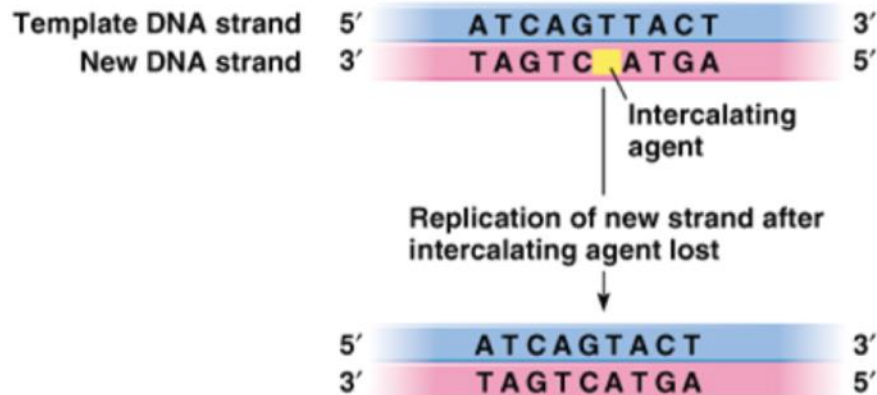
Intercalating agents:

- Thin, plate-like hydrophobic molecules insert themselves between adjacent base-pairs,
- Mutagenic intercalating agents cause insertions during DNA replication.
- Loss of intercalating agent can result in deletion.
- Examples: Proflavin, Ethidium bromide

a) Mutation by addition



b) Mutation by deletion



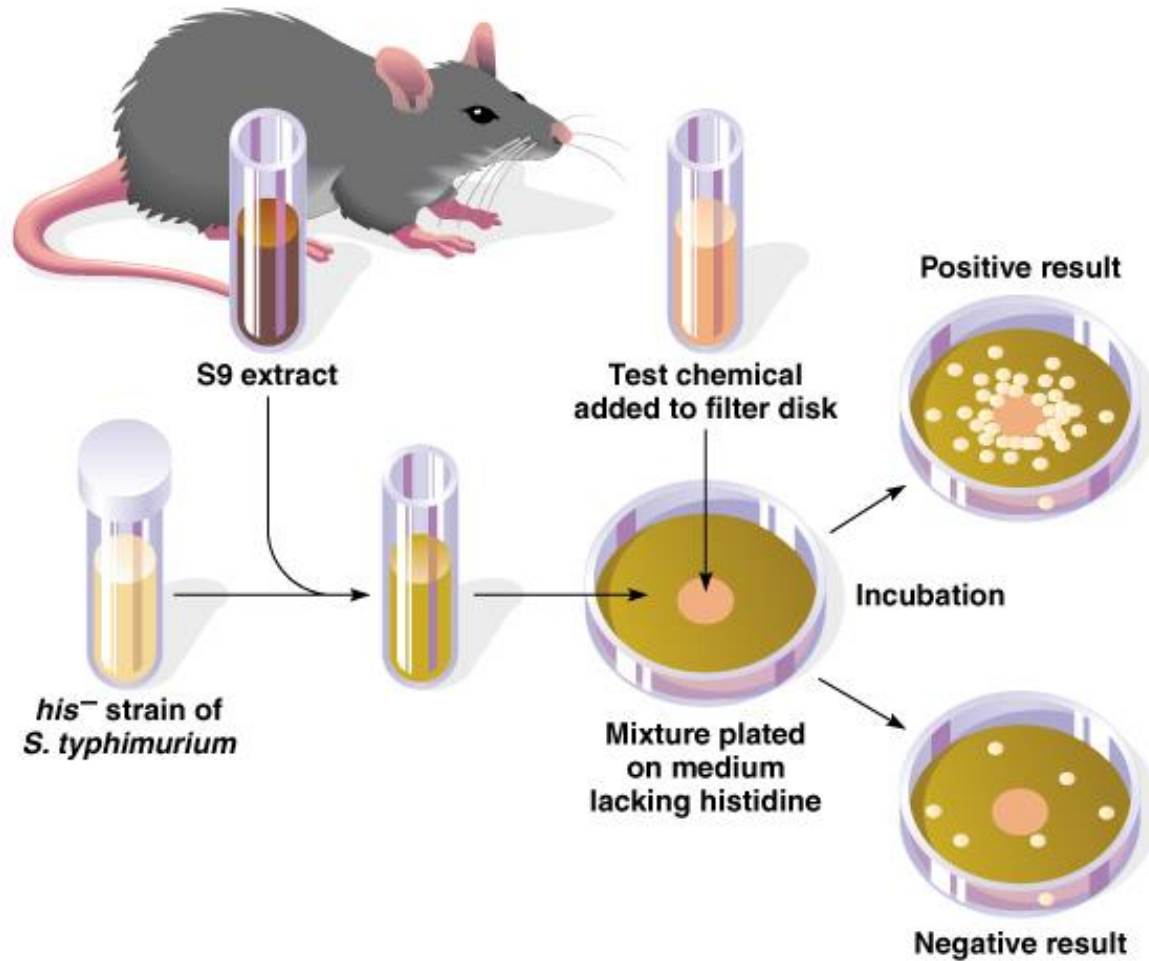
Detecting environmental mutations:

Ames Test (after Bruce Ames)

Ames Test is an inexpensive method used to screen possible carcinogens and mutagens.

- Histidine auxotroph *Salmonella typhimurium* (requires Histidine to grow) are mixed with rat liver enzymes and plated on media lacking histidine.
- Liver enzymes are required to detect mutagens that are converted to carcinogenic forms by the liver (e.g., procarcinogens).
- Test chemical is then added to medium.
- Control plates show only a small of revertants (bacteria cells growing without histidine).
- Plates innoculated with mutagens or procarcinogens show a larger of revertants.
- Auxotroph will not grow without Histidine unless a mutation has occurred.

Ames test

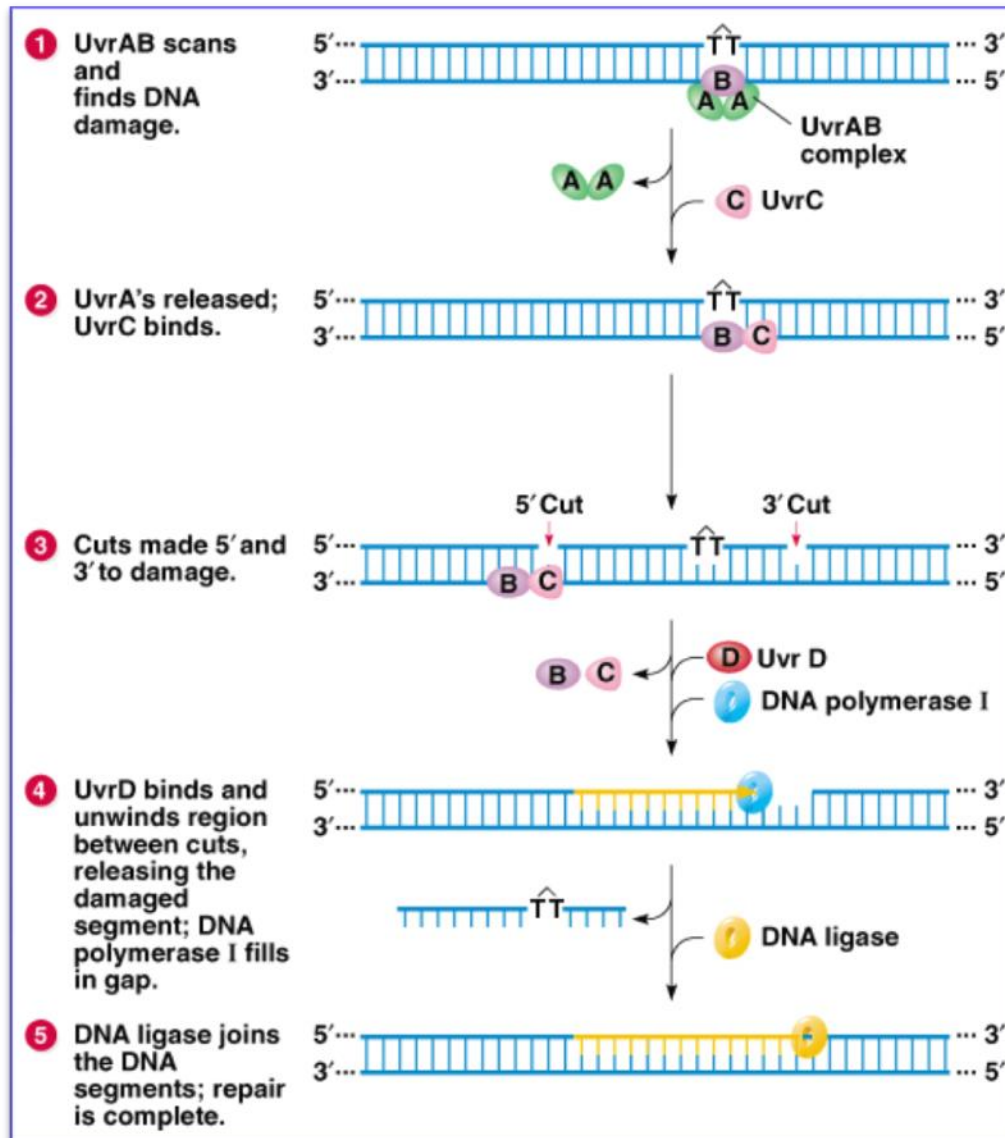


DNA repair mechanisms:

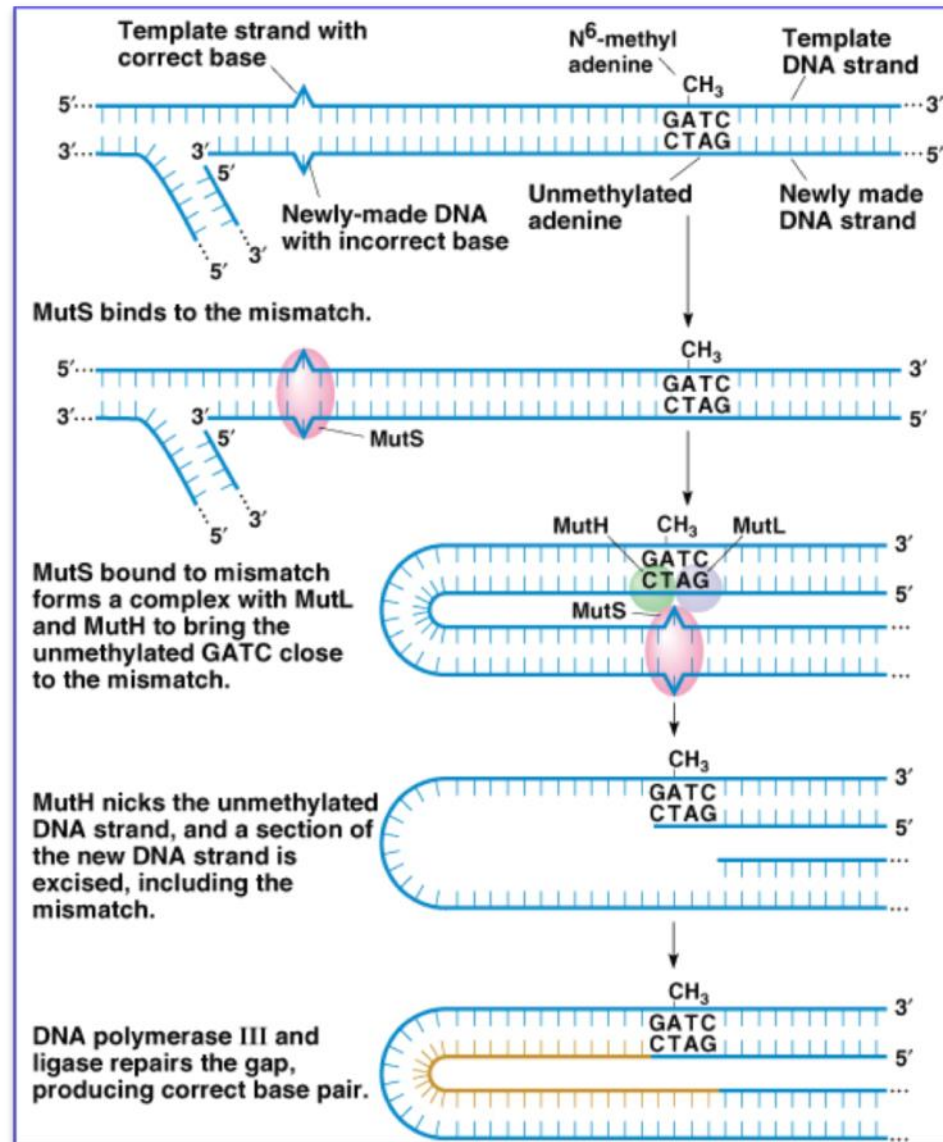
Types of mechanisms

- **DNA polymerase proofreading** - 3' -5' exonuclease activity corrects errors during the process of replication.
- **Photoreactivation** (also called **light repair**) - photolyase enzyme is activated by UV light (320-370 nm) and splits abnormal base dimers apart.
- **Demethylating DNA repair enzymes** - repair DNAs damaged by alkylation.
- **Nucleotide excision repair (NER)** - Damaged regions of DNA unwind and are removed by specialized proteins; new DNA is synthesized by DNA polymerase.
- **Methyl-directed mismatch repair** - removes mismatched base regions not corrected by DNA polymerase proofreading. Sites targeted for repair are indicated in *E. coli* by the addition of a methyl (CH₃) group at a GATC sequence.

Nucleotide excision repair (NER) of pyrimidine dimer and other damage-induced distortions of DNA



Mechanism of mismatch correction repair



Thank you....