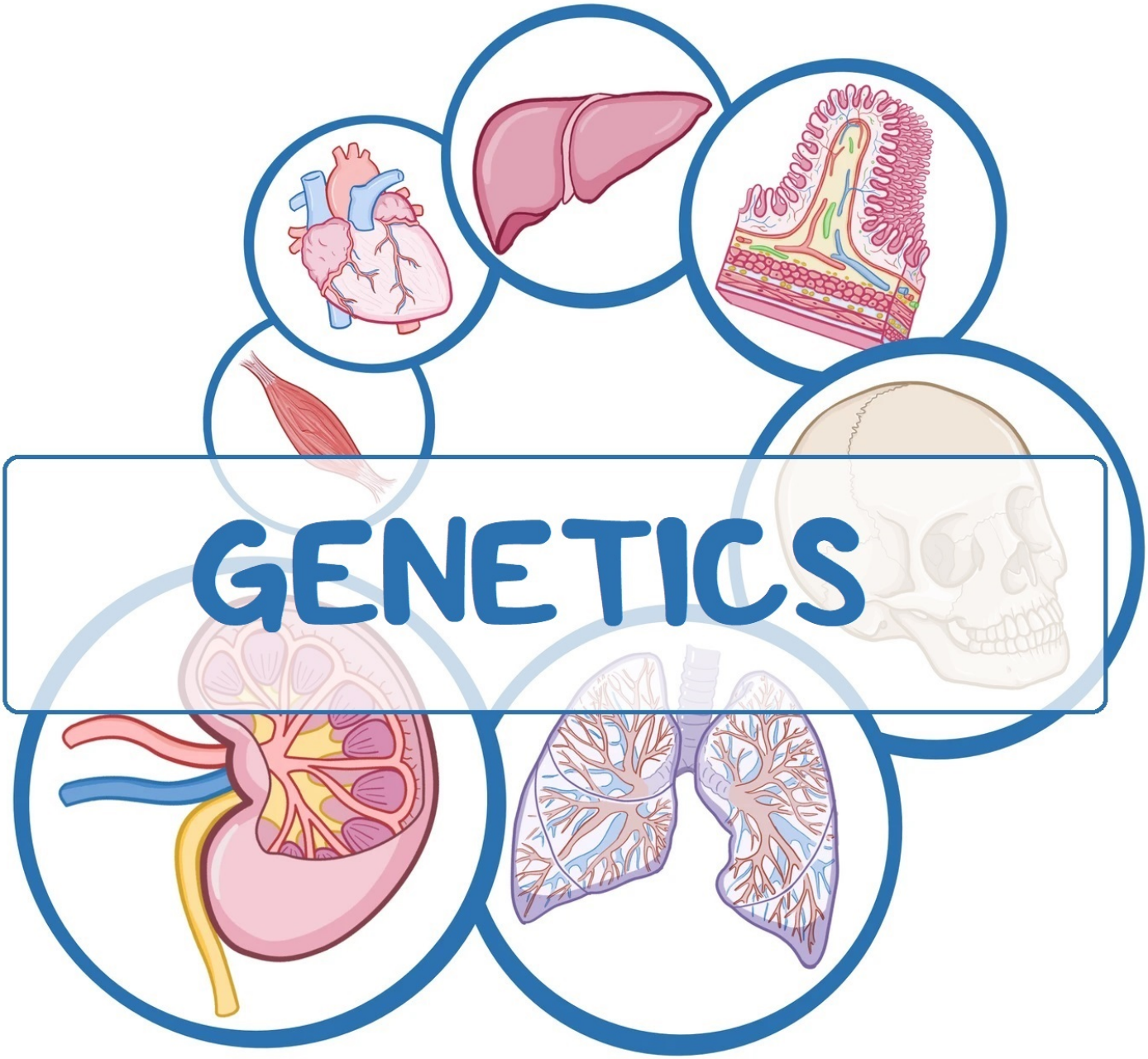
PHYSIOLOGY



GENETICS

HIGH-YIELD NOTES

AfraTafreeh.com

Table of Contents

NOTES
POPULATION GENETICS

MENDELIAN GENETICS & PUNNETT SQUARES

osms.it/mendelian-genetics-punnett-squares

- *Genetics:* science of inheritance
- Parental generation ("P") → 1st filial generation ("F1") → 2nd filial generation ("F2")
- *Homozygous:* male, female alleles are same
- *Heterozygous:* male, female alleles differ
- *Phenotype:* observable trait from genotype

Mendel's laws

- *Law of segregation:* alleles segregate, offspring acquire one allele from each parent
- *Law of dominance:* alleles can be dominant/recessive
  - Dominant traits appear when ≥ one dominant allele is present
- *Law of independent assortment:* separate genes assort independently
  - *Genetic linkage:* proximity of genes on chromosome can cause joint assortment

Punnett square

- Table showing possible combinations of genotypes

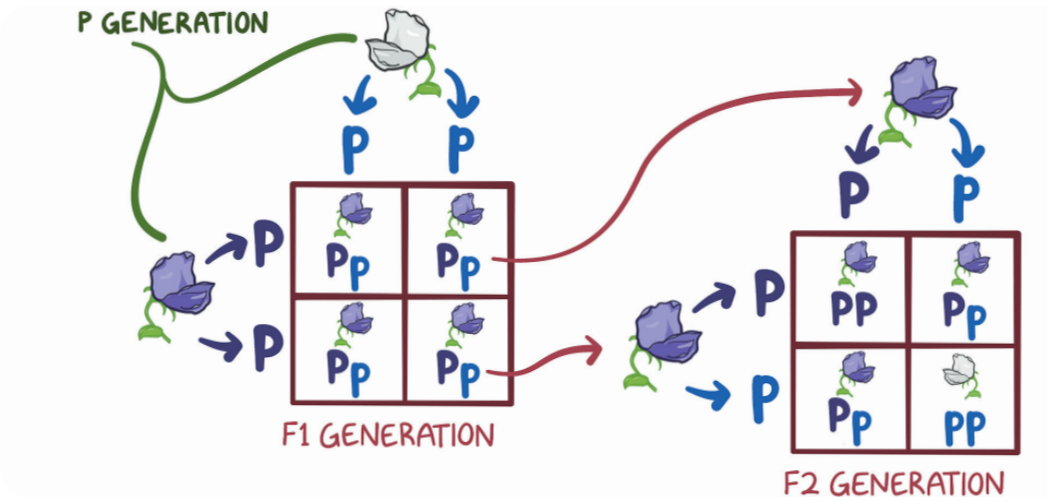


Figure 41.1 2x2 Punnett squares showing the allele combinations for one gene: flower color in pea plants. The parent plants are homozygous for the flower color trait. When they are crossbred (first Punnett square), each offspring in the F1 generation gets one dominant allele (P) and one recessive allele (p). The dominant P allele masks the recessive p allele, so all the flowers appear violet. When any two of the heterozygous F1 generation plants are bred (second Punnett square), the three plants in the F2 generation with at least one P allele have a violet flower phenotype and the one plant with the homozygous pp genotype has a white flower phenotype.

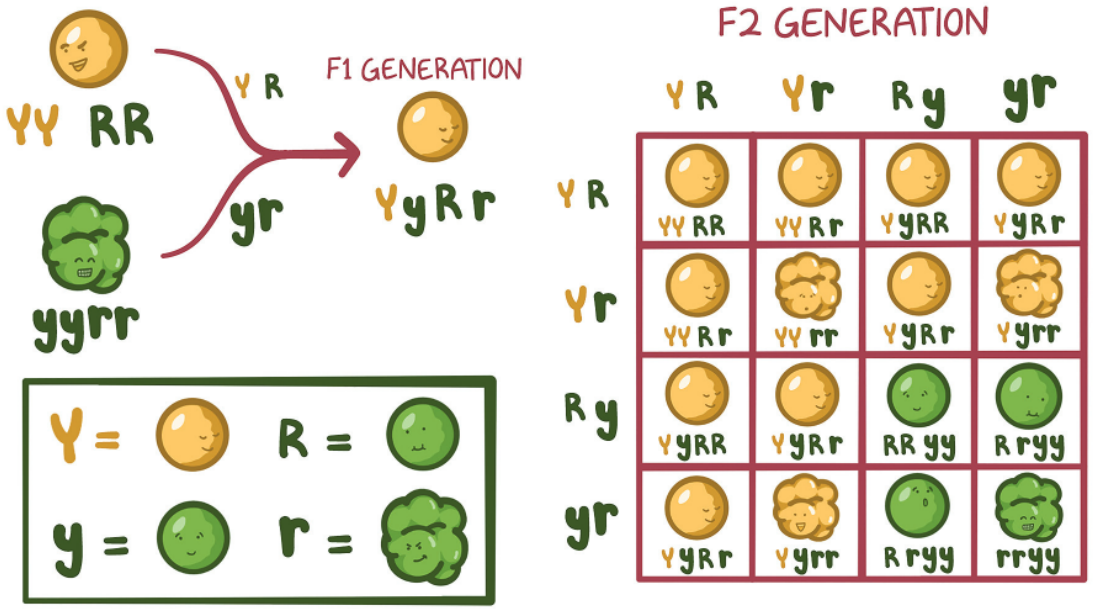


Figure 41.2 4x4 Punnett square showing the allele combinations for two genes: seed color (Y = yellow, y = green) and texture (R = round, r = wrinkly). One parent (P) plant is homozygous dominant (YYRR; yellow, round seeds), the second is homozygous recessive (yyrr; green, wrinkled seeds). When these plants are crossbred, all the F1 generation plants have the genotype YyRr and the phenotype of yellow, round seeds. When the F1 generation plants are bred (Punnett square), there are four possible combinations of the alleles for each parent: YR, Yr, yR, and yr. We can expect the F2 generation to have four phenotypes: yellow and round (≥ one Y and ≥ one R), yellow and wrinkled (≥ one Y and two r), green and round (two y and ≥ one R), green and wrinkled (yyrr). They appear in the ratio 9:3:3:1.

INDEPENDENT ASSORTMENT OF GENES & LINKAGE

osms.it/independent-assortment-and-linkage

- *Independent assortment:* separate genes assort independently
  - Apart from in genetic linkage
  - *Genetic linkage:* proximity of genes on chromosome can cause joint assortment
- *Crossing-over:* in prophase 1 of meiosis, genes can be exchanged between adjacent chromosomes
  - Homozygous genes can occur on different gametes
  - Even repetitions of crossing-over can reverse this effect
- Linked genes have < 50% chance of occurring on different gametes
  - *Parental gametes:* linked genes inherited together
  - *Recombinant gametes:* linked genes between which crossing-over has occurred

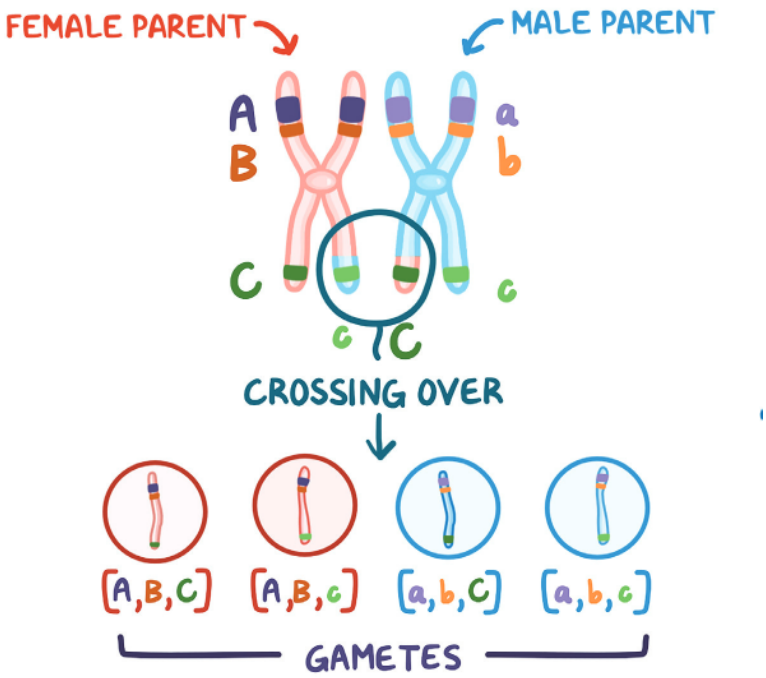


Figure 41.3 Red chromosome from female parent originally carried all dominant alleles for genes *A*, *B*, *C*; blue chromosome from male parent originally carried all recessive alleles for genes *A*, *B*, *C*. If crossing over occurs between the ends of the two chromosomes, dominant allele C from female parent ends up in the chromosome from male parent, vice versa.

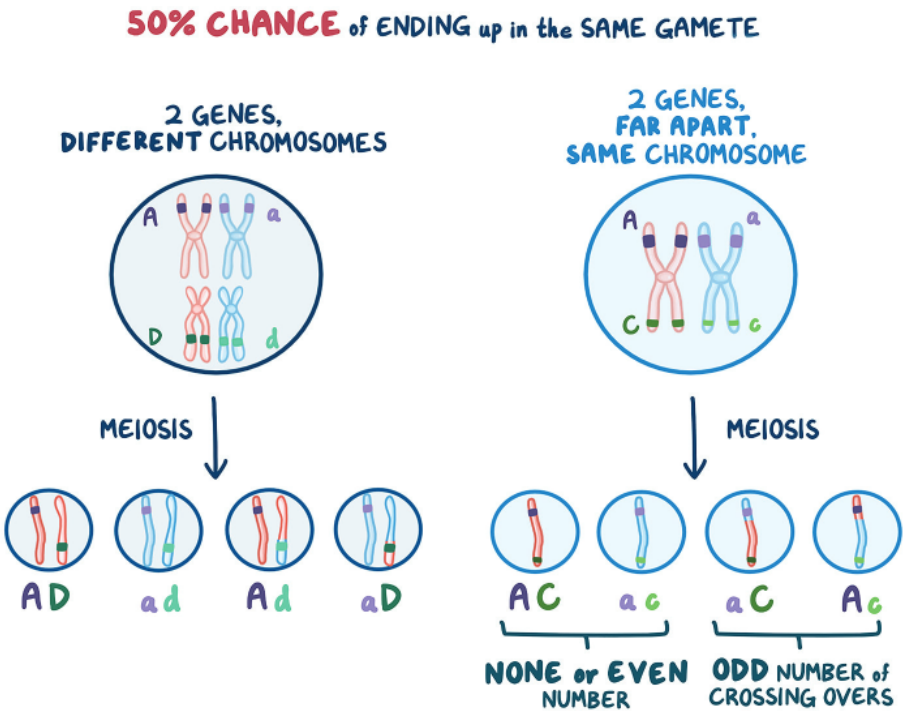


Figure 41.4 Any two genes on different chromosomes always have a 50% chance of going through crossing over in meiosis and showing up in the same gamete. The same is true for two genes very far apart on the same chromosome, because ending up in the same or a different gamete depends on whether there are an odd or even number of crossing over events.

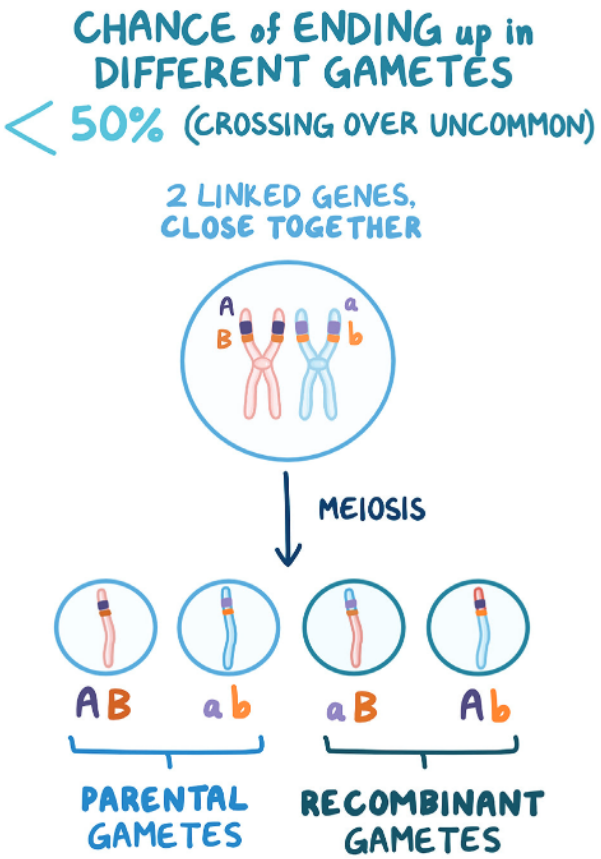


Figure 41.5 It is unlikely for a cut to occur in the small space between linked genes, which is why the chance of them crossing over and ending up in different gametes is < 50%. When linked genes are inherited together, the gametes are called "parental" because they carry same the alleles as the original chromosomes. When crossing over occurs, they are called "recombinant."

INHERITANCE PATTERNS

osms.it/inheritance-patterns

Dominant vs. recessive inheritance patterns

- *Dominant inheritance:* mutation affects dominant allele → one copy causes disease
- *Recessive inheritance:* mutation affects recessive allele → two copies cause disease

Autosomal vs. sexual vs. mitochondrial patterns

- *Autosomal inheritance:* mutation affects somatic chromosome
- *Sexual inheritance:* mutation affects sex chromosome; X-linked/Y-linked
- *Mitochondrial inheritance:* mutation on egg's mitochondrial DNA

Autosomal inheritance

- Autosomal dominant inheritance (e.g. Huntington's disease)
  - Dominant homozygotes (RR), heterozygotes (Rr) have disease
  - Recessive homozygotes (rr) unaffected
  - Disease too severe in homozygotes → don't reproduce

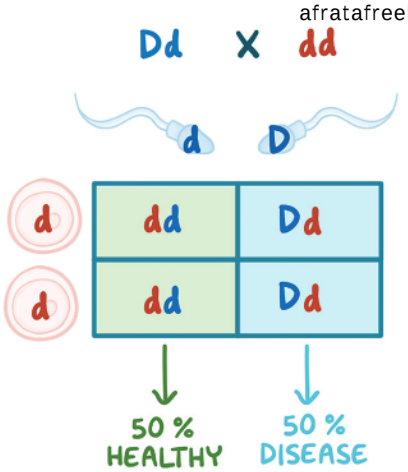


Figure 41.6 Autosomal dominant inheritance. Punnett square demonstrating probabilities of healthy and disease genotypes in offspring when a heterozygous dominant individual (Dd) reproduces with a healthy individual (dd).

- Autosomal recessive inheritance (e.g. cystic fibrosis)
  - Only recessive homozygotes have disease
  - Heterozygotes carriers
  - Tendency to skip generation
  - *Children of consanguineous unions:* ↑ likelihood of disease

Figure 41.7 Autosomal recessive inheritance. Punnett square demonstrating probabilities of healthy, disease, and carrier genotypes in the offspring when two healthy carriers reproduce.

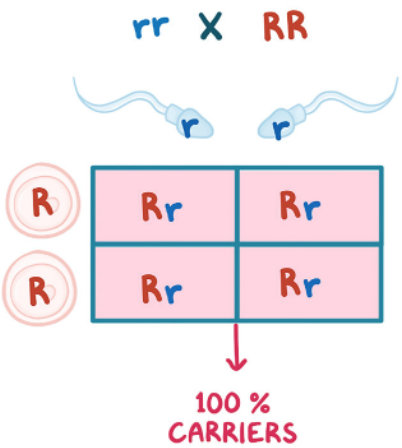


Figure 41.8 Autosomal recessive inheritance. When one affected and one unaffected individual reproduce, all offspring are carriers.

Sex-linked inheritance

- Males have one allele for genes on X, Y chromosomes (hemizygous)
- Females have two alleles for genes on X chromosomes (homozygous/heterozygous)
- X-linked dominant inheritance (e.g. fragile X syndrome)
  - Dominant hemizygotes, dominant homozygotes, heterozygotes have disease
  - Males reproducing with healthy females have 100% chance to pass onto female children, 0% chance to pass onto male children
  - Females reproducing with healthy males have 50% chance to pass onto children of both sexes
- X-linked recessive inheritance (e.g. hemophilia)
  - Recessive homozygotes, recessive hemizygotes have disease; heterozygotes are carriers
  - Males reproducing with healthy females have 100% chance of female children being carriers, 0% chance of passing disease onto male children
  - Heterozygous females reproducing with healthy males have 50% chance of female children being carriers, 50% chance of passing disease onto male children
- Y-linked inheritance (e.g. baldness)
- Only male heterozygotes have disease

- Always passed from biologically-male parent to biologically-male child

Mitochondrial inheritance

- Mitochondrial inheritance (e.g. DAD, AKA diabetes mellitus and deafness)
  - Males, females can develop disease
  - Only females can pass disease to offspring

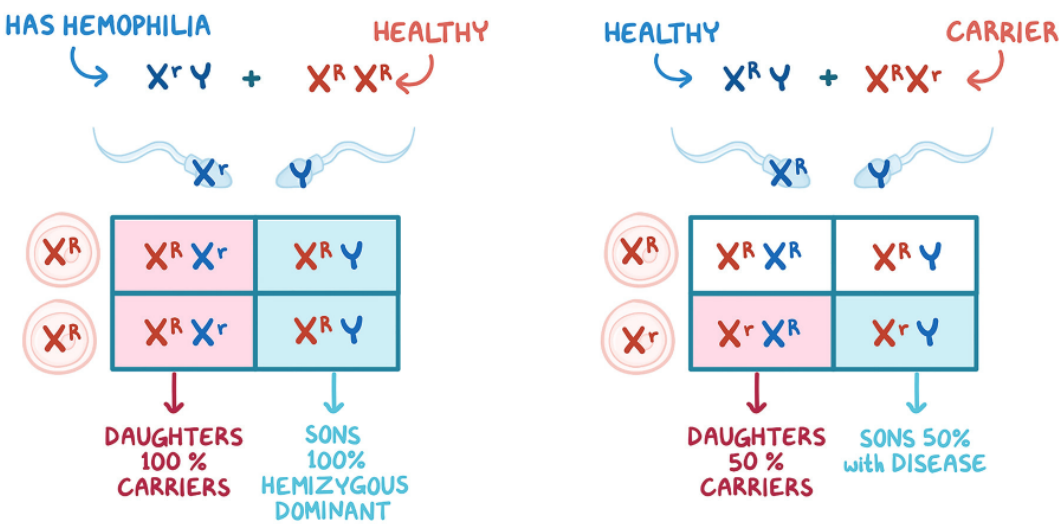


Figure 41.10 Punnett squares demonstrating the inheritance patterns for hemophilia, an X-linked recessive disease, with different combinations of parental genotypes.

EVOLUTION & NATURAL SELECTION

osms.it/evolution-natural-selection

Evolution

- Process by which populations change over time
  - *Population:* group of organisms within species that live in same place
  - *Species:* group of organisms with similar characteristics, ability to breed

Natural selection

- Premises
  - Individuals in species have different traits
  - Some individuals survive, reproduce
  - Some traits → ↑ survival, reproduction (AKA fitness)
  - → more offspring with these traits (AKA differential reproduction)
- Conclusion
  - Population slowly changes over time to favor useful traits (e.g. ↑ survival, reproduction)
- Artificial selection = selective breeding

HARDY–WEINBERG EQUILIBRIUM

osms.it/hardy-weinberg_equilibrium

- Population's genetic traits remain same from one generation to next in absence of evolutionary changes (e.g. natural selection, mutation, genetic drift)
  - Natural selection causes population to favor useful traits
  - Mutation causes new traits to arise
  - Genetic drift causes trait prominence to shift by chance (AKA sampling error)
- Given probability p of dominant allele A, probability q of recessive allele a
  - $p + q = 1$
  - prob(AA) = p^2
  - prob(aa) = q^2
  - prob(Aa) = $2pq$
- q can be calculated from phenotype
  - Square root of frequency of recessive phenotype
  - → frequency of other phenotypes can be calculated

EPIGENETICS

osms.it/epigenetics

- Mechanisms to selectively activate/silence genes without modifying nucleotide sequence

Histone modification

- Acetylation
  - Removes positive charge → less attraction to negative DNA phosphates → ↑ gene transcription
- Methylation
  - One methyl group → loosens histone tails → ↑ access for transcription factors → ↑ gene transcription
  - 2-3 methyl groups → tightens histone tails → ↓ access for transcription factors → ↓ gene transcription
- Direct DNA modification
  - Usually occurs in long sequences of cytosine,guanine nucleotides (AKA CpG)
  - Cytosine residues undergo methylation, silencing gene expression
- Modifications occur throughout lifetime
- Affected by environmental factors (e.g. drug usage, diet, exercise)
- Changes are reversible

LAC OPERON

osms.it/lac-operon

- Collection of genes in *E. coli*, other bacteria that code for proteins required to transport, metabolize lactose
- Includes structural genes like *lacZ*, *lacY*, *lacA* as well as regulatory genes like promoter, operator
  - *lacZ*: β-galactosidase (AKA lactase)
  - *lacY*: β-galactosidase permease
  - *lacA*: β-galactosidase transacetylase
  - *Promoter*: start transcription
  - *Operator*: prevent transcription with repressor (coded by *lacI*)
- Glucose, lactose concentrations can be used to regulate lac operon expression
  - ↑ glucose → repressor stays bound to operator, blocking RNA polymerase
  - ↑ glucose → catabolite activator protein inhibits transcription
  - ↓ glucose → repressor falls off
  - ↓ glucose → catabolite activator protein stimulates transcription

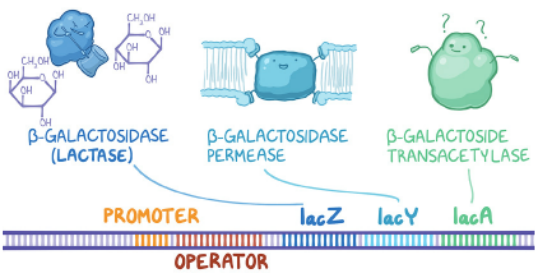


Figure 41.11 The lac operon. β-galactosidase breaks down lactose into glucose and galactose; β-galactosidase permease allows lactose to enter the cell; β-galactosidase transacetylase's function is not clearly understood.

GENE REGULATION

osms.it/gene-regulation

- Natural regulation of gene expression
- Occurs at transcription/post-transcription/translation level
- Transcriptional regulation
  - *Epigenetics:* chemical modifications activate/silence genes without modifying nucleotide sequence (e.g. by methylation/acetylation of histones)
  - *Activators:* bind to DNA enhancer → facilitate binding of general transcription factors, recruit histone acetyltransferases
  - *Repressors:* bind to DNA silencer → prevent RNA polymerase from binding to promoter, recruit histone deacetylases

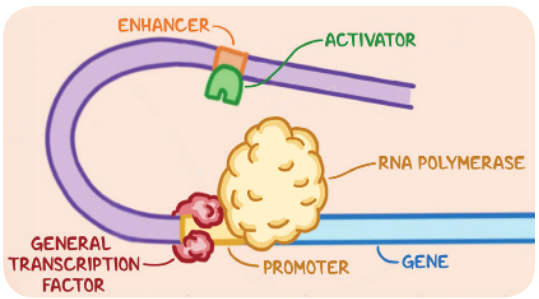


Figure 41.12 An activator looping DNA in the nucleus.

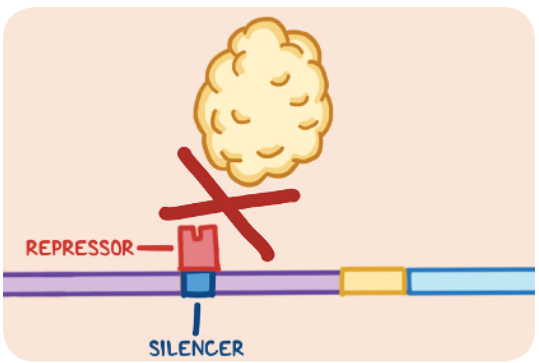


Figure 41.13 A repressor protein in the nucleus binding the DNA sequence called the silencer, which is on the same DNA strand as the gene.

- Post-transcriptional regulation
  - *Splicing:* spliceosomes remove introns (AKA non-coding sequences) from RNA → resulting mRNA codes for proteins more effectively
  - *Capping:* 5' end of RNA capped with protective 7-methyl-guanine → exonucleases unable to cleave off nucleotides
  - *Editing:* proteins convert certain nucleotides (e.g. ADAR: adenosine → inosine; CDAR: cytosine → uracil) to create sequence variation
- Translation regulation
  - Mainly occurs during initiation
  - Regulatory proteins (AKA initiation) factors must bind before ribosome can begin translation
  - Conditions like starvation, stress inhibit initiation factors to save energy

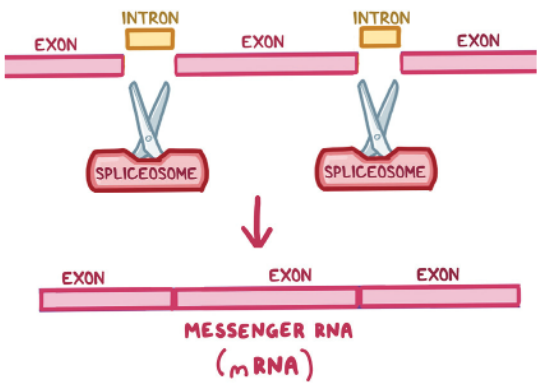


Figure 41.14 Illustration depicting the action of spliceosomes.

GEL ELECTROPHORESIS & GENETIC TESTING

osms.it/gel-electrophoresis-genetic-testing

- Method of separating, analyzing macromolecules (e.g. DNA, RNA, proteins), their fragments based on size, charge

Apparatus

- Clear box filled with gel, often agarose
  - Small depressions (AKA "wells") at one end
  - Sample macromolecules placed separately in wells
- Power source connected to gel

Premise

- Current applied → macromolecule fragments move through gel
- Charge of fragments determines
  - *Direction:* opposites attract
  - *Speed:* greater magnitude → faster
- Fragment size also determines speed
  - Gel contains small pores; smaller size → faster
- Fast-moving fragments travel further over given period → production of multiple bands (one per fragment)

Applications

- DNA analysis (e.g. genetic fingerprinting)
  - DNA chopped up with restriction enzymes (e.g. EcoRI cuts at GAATTC)
  - Fragments poured into wells, current applied
  - Fragments move towards positive terminal, form bands at isoelectric point
- Identifying DNA mutations
  - Mutation → restriction enzymes create different fragments → bands change
  - Smaller fragments → bands are further apart
  - More abundant fragments → bands (thicker, brighter)
- *Other applications:* estimation of molecule size, macromolecule separation

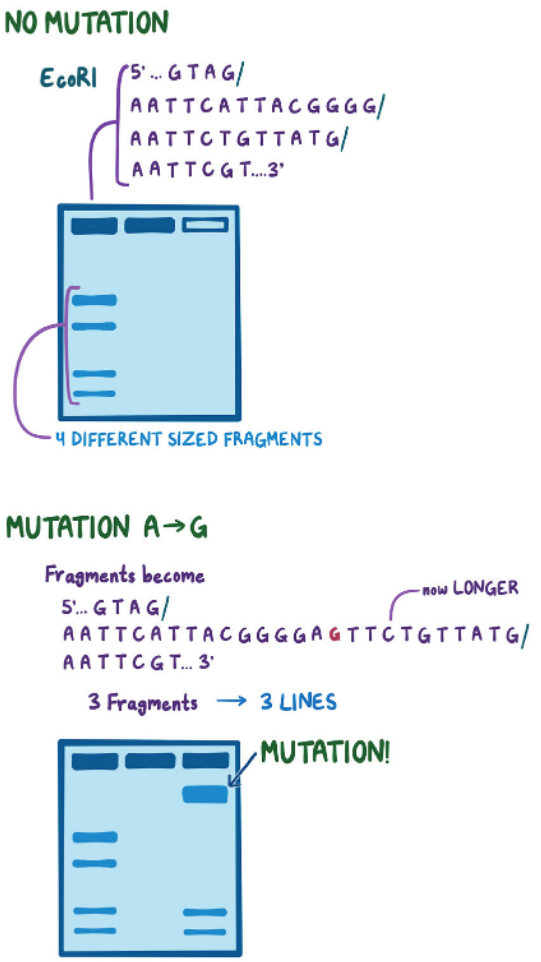


Figure 41.15 Identifying DNA mutations using EcoRI. A mutation in a single nucleotide from A to G in the EcoRI binding site prevents the enzyme from binding and cutting at that location. Now, in gel electrophoresis, there will be only three lines (instead of four) and one fragment will be longer, indicating that the DNA contains a mutation.

POLYMERASE CHAIN REACTION

osms.it/polymerase-chain-reaction

- Technique used to amplify desired DNA segment
- Based on DNA melting, enzyme-driven DNA replication
- Takes place in thermal cycler
- Four essential components
  - *Template DNA:* strand to be replicated
  - *Nucleotides:* building blocks of DNA
  - *Primers:* short complementary DNA strands to the 3' end of each strand
  - *DNA polymerase:* enzyme that synthesizes DNA from nucleotides (e.g. Taq polymerase)

Process

- *Denaturation:* sample heated to 96°C/205°F → bonds between DNA strands separate, forming two template strands
- *Annealing:* sample cooled to 55°C/131°F → primers bind to template strands
- *Extension:* sample heated to 72°C/162°F → Taq polymerase synthesizes complete complementary DNA strands, starting from end of each primer

Applications

- Cloning DNA into plasmids, replicating DNA for analysis (e.g. research and practice)

NOTES
TRANSCRIPTION, TRANSLATION, & REPLICATION

DNA STRUCTURE

osms.it/DNA-structure

DNA (DEOXYRIBONUCLEIC ACID)

- Two polynucleotide chains (double helix shape)

Nucleotides

- 5-carbon sugar, phosphate group, nitrogenous base

Sugar

- Deoxyribose in DNA, ribose in RNA

Nucleobases

- *Purines:* adenine (A), guanine (G)
  - *Pure silver:* purines (pure), adenine, guanine (AG)
- *Pyrimidines:* cytosine (C), thymine (T) for DNA, uracil (U) for RNA
  - *Mnemonic:* CUT the PYE

MNEMONIC: CUT the PYE
Pyrimidines
Cytosine
Uracil
Thymine
The
PYrimidin**E**s

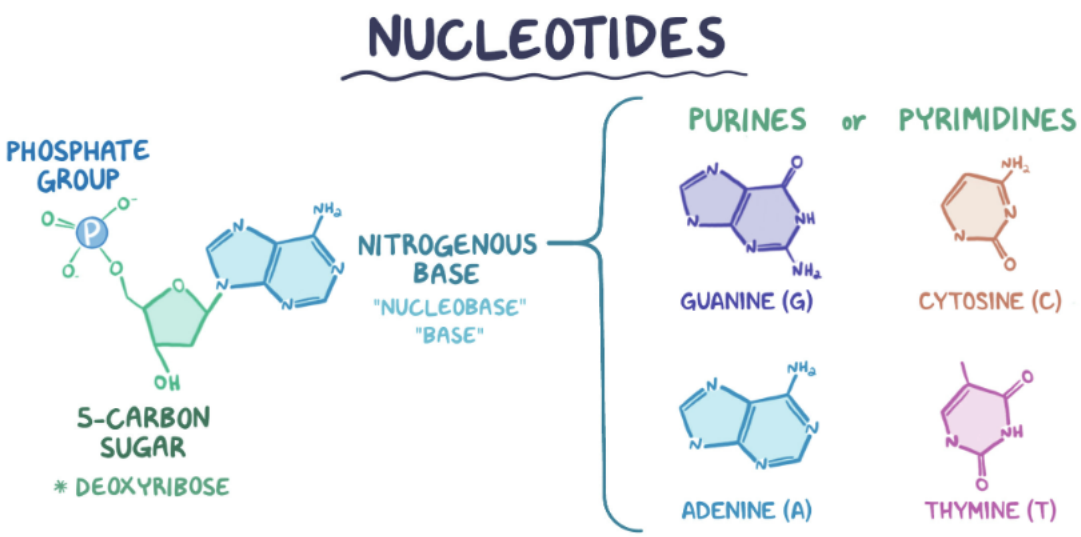


Figure 42.1 Nucleotides consist of a phosphate group, 5-carbon sugar (deoxyribose for DNA) and a nitrogenous base. The base can be a purine, which has two rings (adenine, guanine), or a pyrimidine, which has one ring (cytosine, guanine).

Nucleotide binding and bonding

- Nucleotides bind using sugar, phosphate groups (phosphate group on 5th carbon of sugar binds covalently to 3rd carbon of sugar) → sugar-phosphate backbone
- Nucleotides form hydrogen bonds with bases on opposing strand
  - *Complementary base pairing:* A pairs with T/U (two hydrogen bonds), C pairs with G (three hydrogen bonds)

DNA structure and packing

- Strands coil around each other once every 10 base pairs → major, minor grooves
- In order to be packed tightly, DNA wrapped around histones (positive charge attracts to negative charge of phosphate backbone) → nucleosomes
- Nucleosomes further packed as chromatin fibers
  - *Euchromatin:* loosely packed (genes frequently used)
  - *Heterochromatin:* densely packed (genes rarely used)

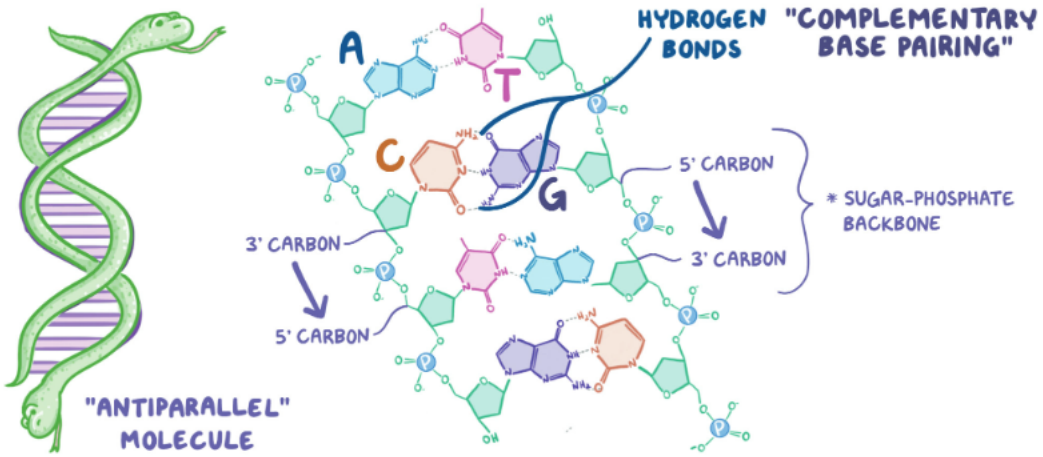


Figure 42.2 *Nucleotide binding:* phosphate group on 5th carbon of sugar on one nucleotide (called 5 prime carbon) binds covalently to 3rd carbon of sugar on another nucleotide (called 3 prime carbon. This gives each DNA strand a sugar-phosphate backbone and a direction (5' to 3' and 3' to 5'). *Nucleotide bonding:* nucleotide bases form hydrogen bonds with the complementary base on the opposing strand, A with T (U in RNA) and C with G.

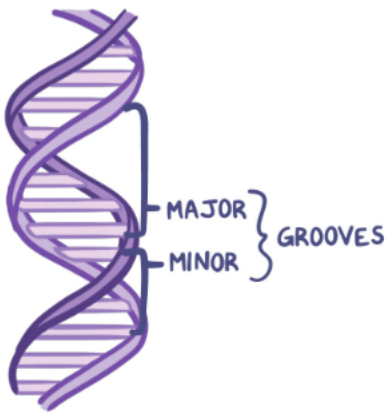


Figure 42.3 Major and minor grooves: larger/smaller spaces between DNA strands where proteins can bind to regulate functions.

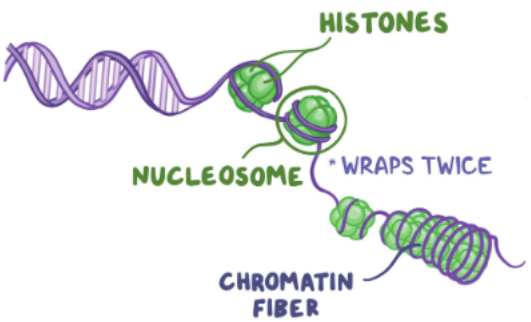


Figure 42.4 DNA wraps around histone proteins to form nucleosomes, which pack tighter again to form chromatin fibers.

DNA REPLICATION

osms.it/DNA-replication

- Occurs in S phase of cell cycle (before cell division)
- 46 chromosomes duplicated → each daughter cell gets genetic material
- DNA replication semiconservative → each strand of double helix template

PROCESS

Initiation

- Pre-replication complex seeks origin of replication, DNA helicase splits strands → replication fork
  - Single-stranded DNA binding proteins improve stability of lone strands
  - DNA topoisomerase prevents overwinding of later DNA

Elongation

- RNA primase creates multiple RNA primers → randomly bind → DNA polymerase adds complementary nucleotides in 3', 5' direction
  - Forms single leading strand
  - Forms single lagging strand by attaching (with DNA ligase) multiple Okazaki fragments

Termination

- DNA polymerase leaves strand at telomere (TTAGGG nucleotide sequences)
- *Hayflick limit:* maximum number of times cell's DNA can be replicated
  - Due to repeated shortening of telomeres during termination step

DNA CLONING

- Technique used to duplicate segment of DNA within host organism
- *Uses "plasmids"*: genetic structures outside of chromosomes, replicate independently

Process

- Extract desired DNA segment using specific restriction enzymes
- Paste segment into plasmid with DNA ligase → "recombinant DNA"
- Insert plasmid into host organism (e.g. *E. coli*), encouraging uptake with shock (e.g. heat)
- Identify bacteria carrying plasmid with antibiotics (plasmids given antibiotic resistance gene)
- Leave bacteria to replicate DNA segment, mass-manufacture protein(s)

Applications

- Producing biopharmaceuticals (e.g. insulin), gene therapy (e.g. cystic fibrosis)

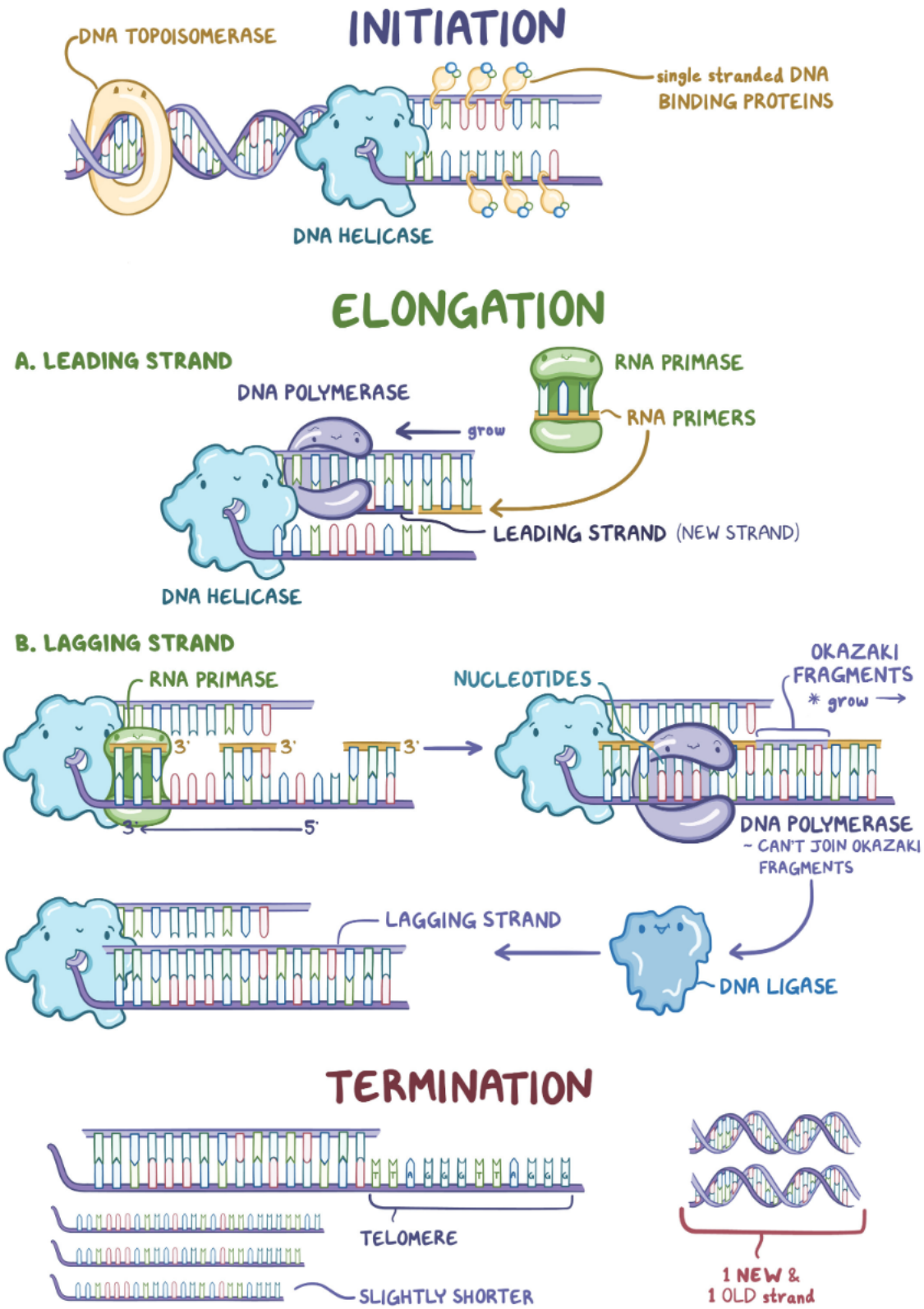


Figure 42.5 Three steps of DNA replication: initiation, elongation, and termination. DNA replication results in two sets of identical DNA, each containing one old strand and one new one.

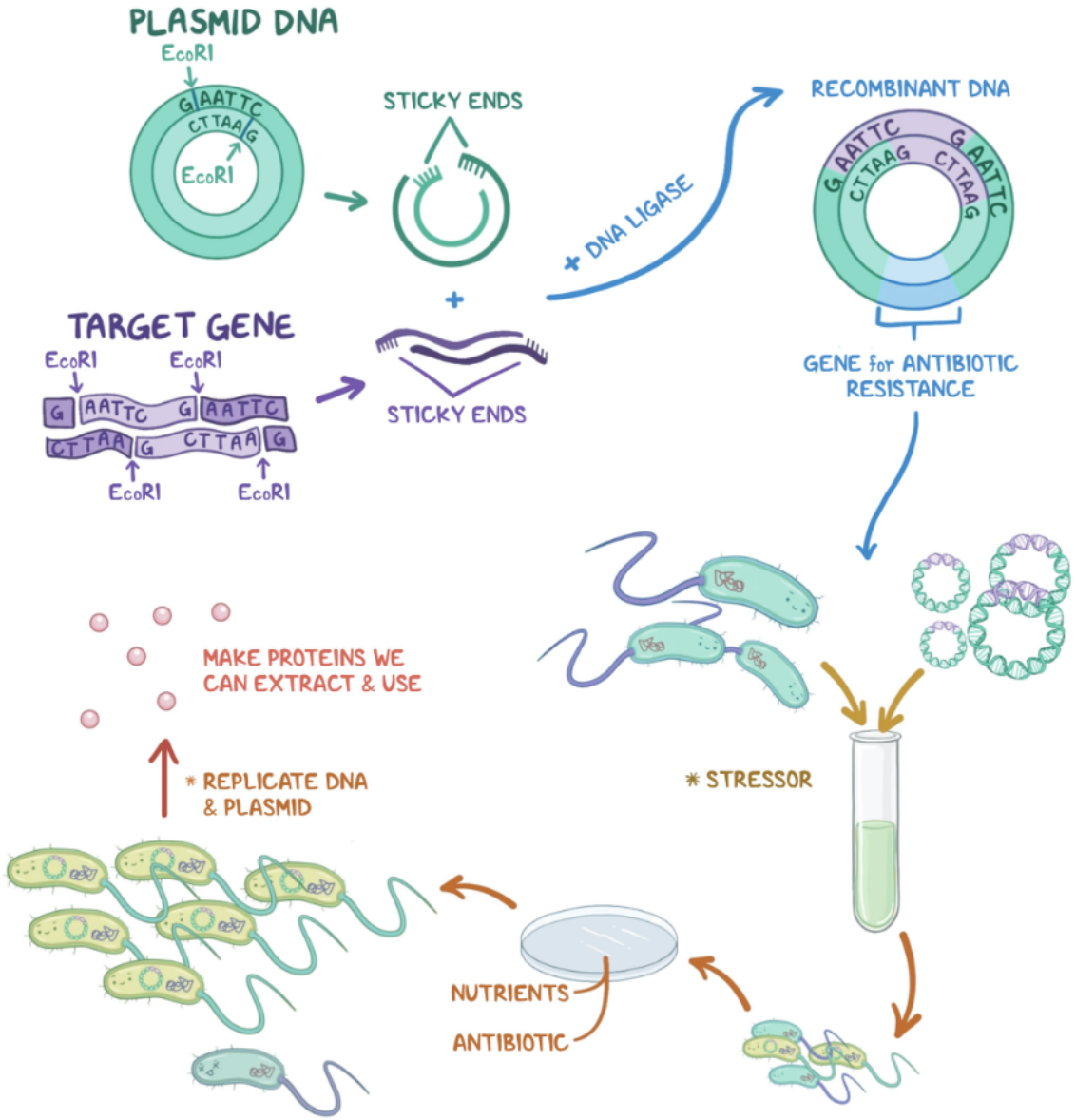


Figure 42.6 DNA cloning. Restriction enzyme (in this case, EcoRI) cleaves a known sequence surrounding a target gene and a plasmid, creating pieces with sticky ends. When DNA ligase is added, these pieces form recombinant DNA (plasmid containing target gene), as well as a gene for antibiotic resistance. A host, in this case *E. coli*, is combined with recombinant plasmids and subjected to a stressor so that some bacteria take up plasmid. Bacteria are allowed to replicate on plate containing antibiotic, so that only ones that have taken up plasmid can survive. These bacteria produce desired protein from target gene in plasmid.

TRANSCRIPTION

osms.it/transcription

- First step in creating protein from gene
- Gene read, copied on individual messenger RNA (mRNA)

PROCESS

- DNA unpacked from chromatin, undergoes dehelicization
- Promoter region identifies starting point for transcription (e.g. TATA box)
- RNA polymerase shears hydrogen bonds between two strands → transcription bubble
- RNA polymerase follows template strand to assemble mRNA molecule (complementary to template strand)
- Hydrogen bonds reform on nucleotides (already transcribed)
- Termination sequences contains two complementary sequences → resulting mRNA binds with itself forming hairpin loop
- RNA polymerase detaches, DNA closes back up
- Polyadenylate polymerase adds 7-methyl guanosine cap to 5', polyadenine tail to 3' end of mRNA
- Spliceosomes remove introns (don't code proteins) to leave behind exons (do code proteins)
- Resulting mRNA processed by ribosome to create desired protein (translation)

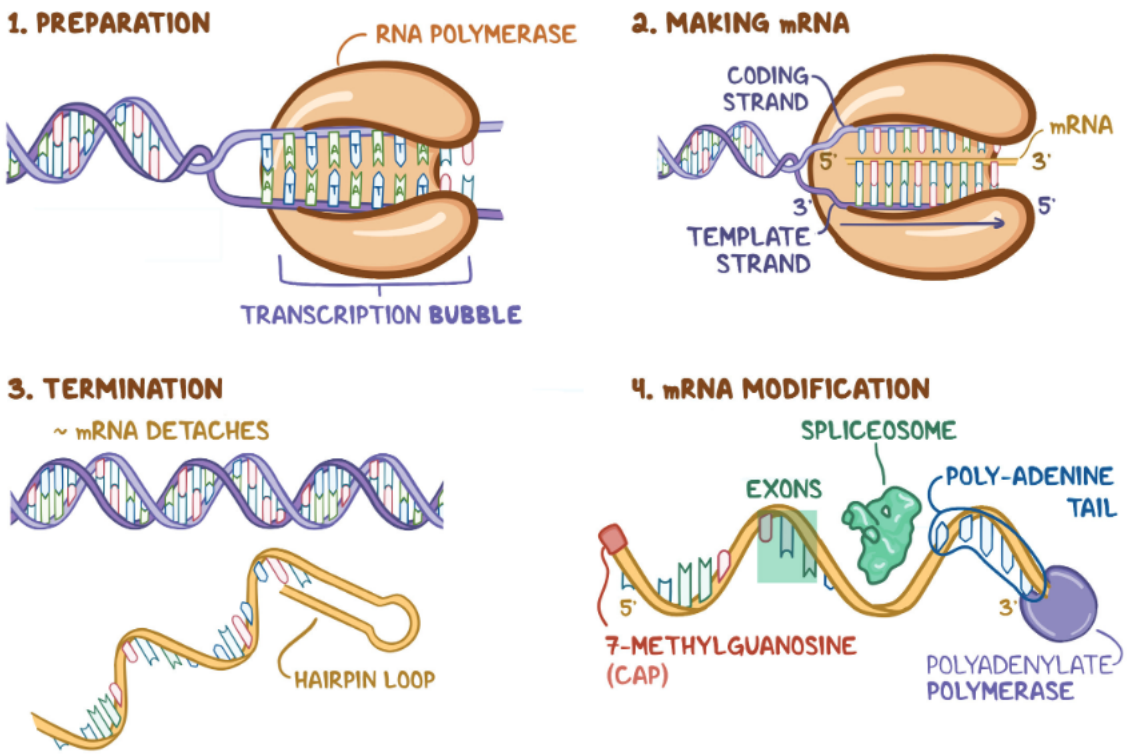


Figure 42.7 Transcription. 1: DNA unpackaging, dehelicization; promoter region identified (TATA box); RNA polymerase shears hydrogen bonds between strands → transcription bubble. 2: RNA polymerase assembles mRNA strand complementary to template strand. Hydrogen bonds reform between DNA nucleotides already transcribed. 3: Termination sequence causes mRNA to form hairpin loop, detach. 4: Cap and tail added, introns spliced out.

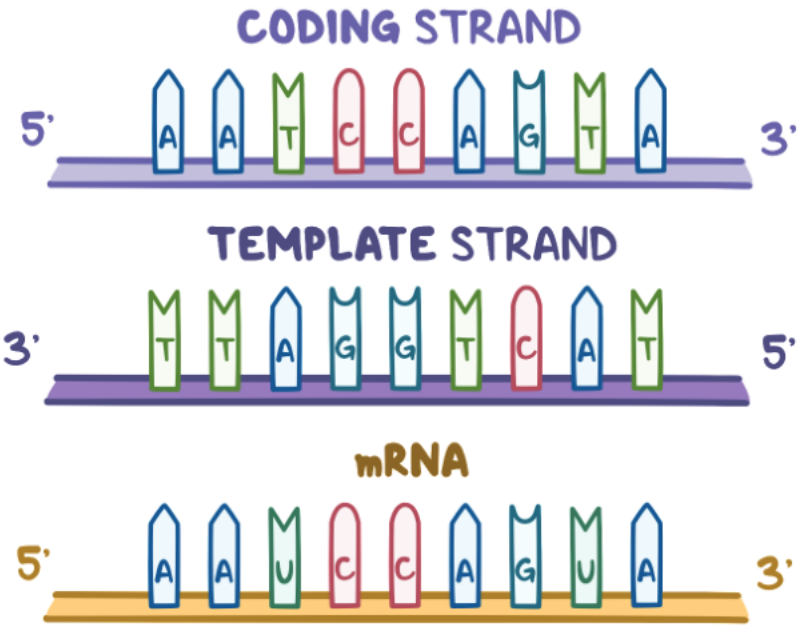


Figure 42.8 One strand of DNA is called the coding strand and the other is called the template strand. They have complementary nucleotide sequences. RNA polymerase builds an mRNA molecule by reading the template strand and adding complementary nucleotides. Therefore, the mRNA will have the same sequence and directionality as the coding strand, only with U instead of T.

TRANSLATION

osms.it/translation

- Second step in creating protein from gene
- Ribosomes assemble protein from mRNA template produced in transcription

PROCESS

- mRNA floats out of nucleus through pore
- *Initiation:* ribosome grabs mRNA, finds start codon (e.g. AUG)
- *Elongation:* ribosome moves along mRNA, producing specific amino acid for each codon
- *Termination:* ribosome reaches stop codon, releases polypeptide (e.g. UGA)

TRANSFER RNA (tRNA)

- Finds, carries amino acids to ribosome
- Three-letter coding sequence (complementary to mRNA)
- Binds to ribosome on aminoacyl/peptidyl/exit site
  - *Aminoacyl:* binds transfer RNA (tRNA) with complementary mRNA codon
  - *Peptidyl:* holds tRNA with polypeptide
  - *Exit:* holds tRNA after amino acid released

Figure 42.9 Ribosome binding sites.

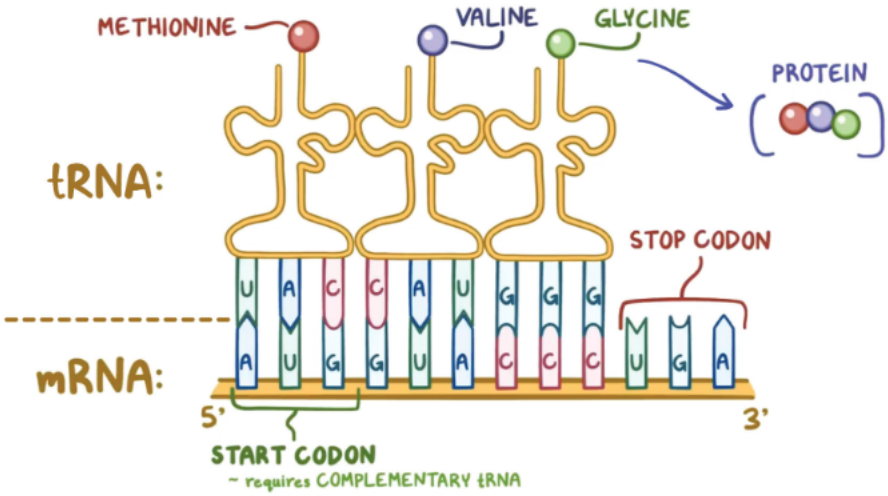


Figure 42.10 One strand of DNA is called the coding strand and the other is called the template strand. They have complementary nucleotide sequences. RNA polymerase builds an mRNA molecule by reading the template strand and adding complementary nucleotides. Therefore, the mRNA will have the same sequence and directionality as the coding strand, only with U instead of T.

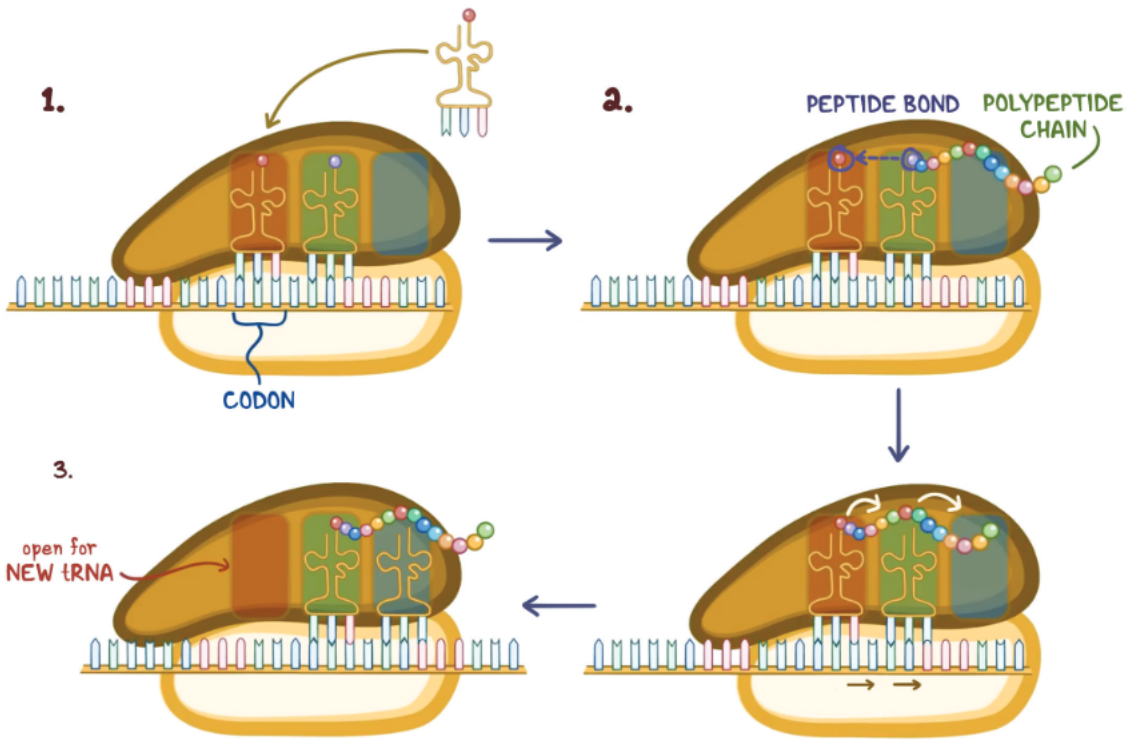


Figure 42.11 Translation extending an existing polypeptide chain.
1: tRNA with amino acid and codon complementary to that of mRNA binds at ribosome A site.
2: Peptide bond forms between amino acid on new tRNA and tRNA in P site holding polypeptide chain, polypeptide chain is transferred to tRNA in A site.
3: Everything moves by one site. A site is now open for a new tRNA.

CELL CYCLE

osms.it/cell-cycle

- Sequence of events between formation, division of somatic cell
- Two phases
  - *Interphase:* preparatory phase; cell performs basic functions, replicates DNA
  - *Mitosis:* cellular division

G0 (G-ZERO) PHASE

- Cells function but not dividing/preparing to divide
- Considered outside cell cycle

INTERPHASE

- *Three subphases:* G1, S, G2 phases

Gap/Growth 1 (G1) phase

- Longest phase
- Cell grows while organelles function as usual
- Terminates with G1 checkpoint
  - Cells with damaged DNA → G0 phase/ apoptosis

Synthesis (S) phase

- DNA replicated (identical chromatids created)

Gap/Growth 2 (G2) phase

- Organelles duplicated
- Terminates with G2 checkpoint

MITOSIS (M) PHASE

- Cell divides into two daughter cells

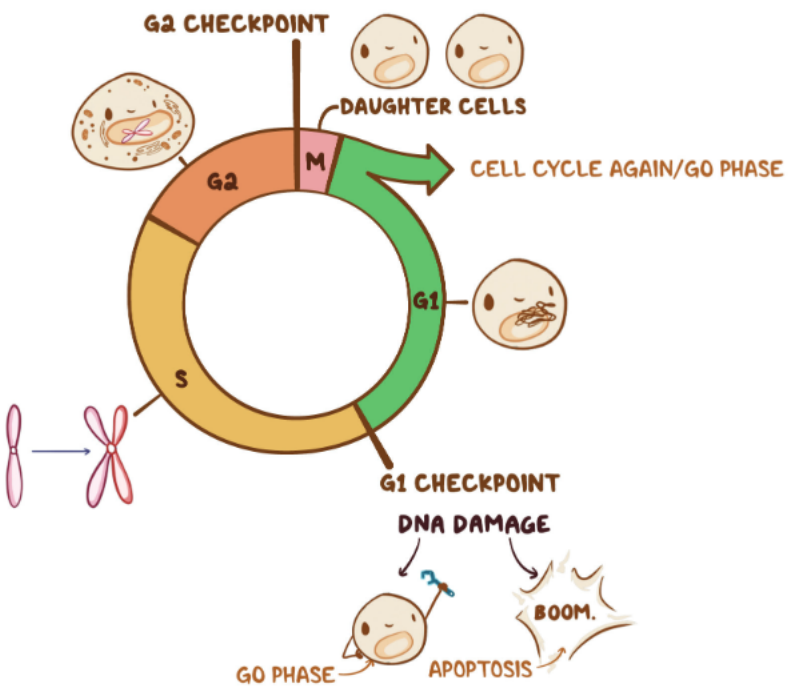


Figure 42.12 Cell cycle summary.

MITOSIS & MEIOSIS

osms.it/mitosis-and-meiosis

- Two processes of cell division

MITOSIS

- Division of cell into two identical daughter cells
- Part of cell cycle
- Consists of prophase, metaphase, anaphase, telophase

Prophase

- Chromatin fibers condense
- Centrioles align chromosomes between centrosomes

Metaphase

- *Prometaphase:* nuclear membrane, nucleolus disintegrate
- *Metaphase:* chromosomes align along metaphase plate, spindle fibers attach to kinetochores

Anaphase

- Centrosomes pull on spindle fibers to separate chromatids

Telophase

- New nuclear envelopes form

MEIOSIS

- Division of cell into four haploid daughter cells
- Consists of
  - *Meiosis I:* prophase I, metaphase I, anaphase I, telophase I
  - *Meiosis II:* prophase II, metaphase II, anaphase II, telophase II

Meiosis I

- Prophase I
  - *Leptotene:* 46 chromosomes condense, nuclear membrane disintegrates
  - *Zygotene:* chromosomes find homologues, bind, forming tetrads (AKA synapsis)

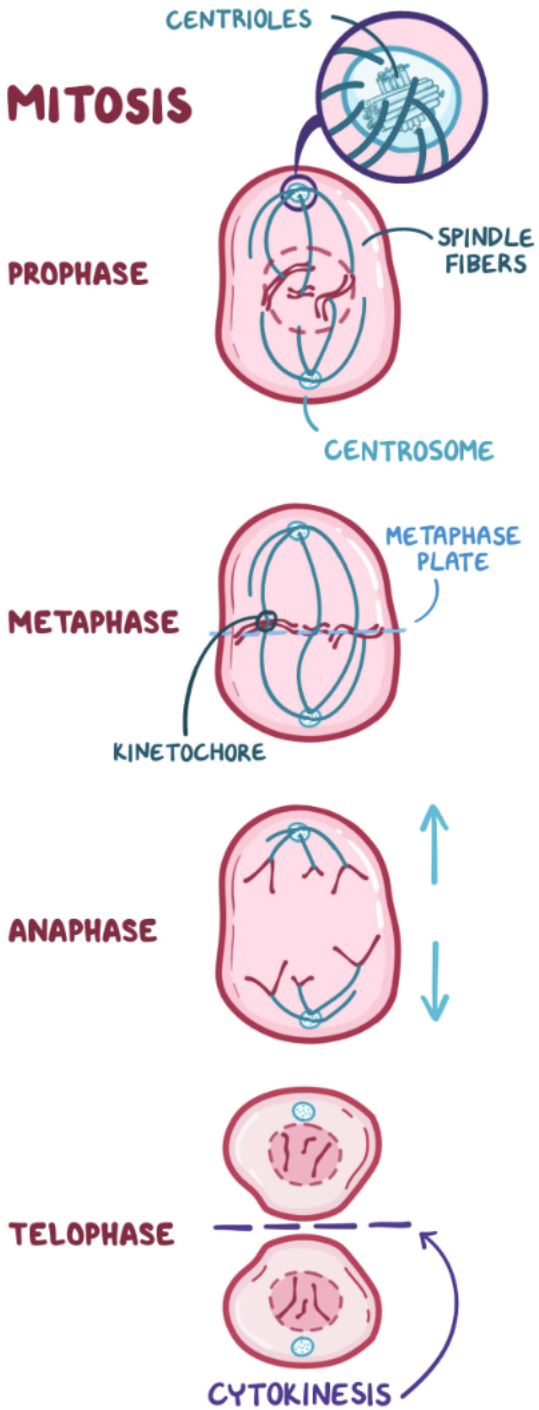


Figure 42.13 Stages of mitosis: division of one cell into two identical daughter cells.

- *Pachytene:* homologous chromosomes exchange genetic material (AKA crossing-over)
- *Diplotene:* homologous chromosomes uncoil, slide toward ends (AKA chiasmata)
- *Diakinesis:* terminalization completed

- Metaphase I
  - Tetrads migrate to metaphase plate
- Anaphase I
  - Tetrads split up
  - Chromosomes pulled to each pole by spindle fibers
  - Diploid cell → haploid cell
- Telophase I
  - Cleavage furrow appears, cytokinesis occurs
- Followed by interphase without chromosome duplication in S phase

Meiosis II

- Meiosis II progresses exactly as mitosis
  - Two haploid cells → four haploid cells
  - Same phase names

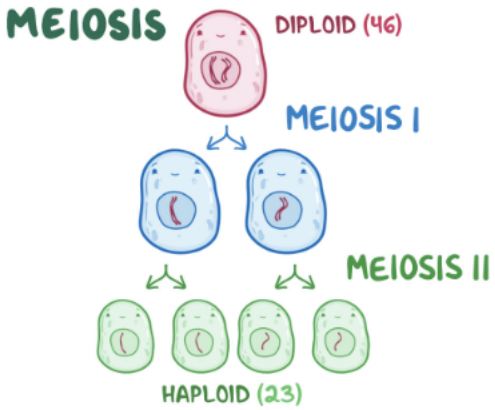


Figure 42.15 Meiosis produces haploid daughter cells with 23 chromosomes each.

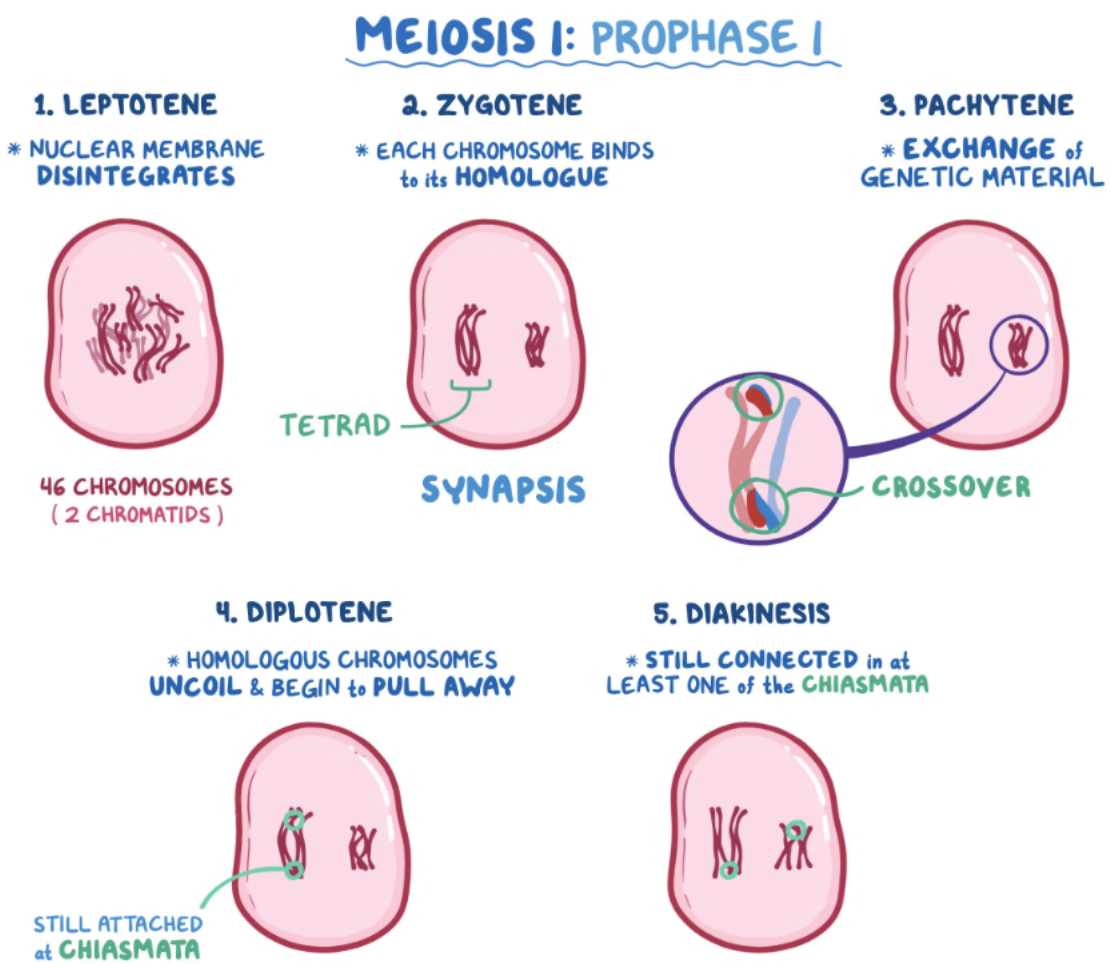


Figure 42.14 Steps of meiosis I, prophase I.

GENETIC MUTATIONS & REPAIR

osms.it/DNA-mutations
osms.it/DNA-damage-and-repair

DNA MUTATIONS

- Alterations in nucleotide (A, T, G, C) sequence of ≥ one gene
  - Affect somatic cells (AKA non-reproductive cells), gametes → germline mutations
  - Arise spontaneously/due to mutagens

SMALL-SCALE MUTATIONS

- Single gene
- *Substitutions:* nucleotide replaced by another
- May result in
  - *Silent mutation:* same amino acid
  - *Missense mutation:* different amino acid (e.g. sickle cell disease)
  - *Nonsense mutation:* stop codon

INSERTIONS & DELETIONS

- Nucleotide added/removed from sequence
- Multiples of three → nonframeshift mutation
  - Reading frame displaced by entire codon → remaining amino acids unchanged → similar resulting protein
- *Frameshift mutation:* resulting protein abnormally long/short, most likely nonfunctional

LARGE-SCALE MUTATIONS

- Often occur due to errors in gamete formation

Abnormal number of chromosomes

- *Aneuploidy*
  - Additional chromosomes (e.g. Down syndrome)
  - Missing chromosomes (e.g. Turner's syndrome)
- *Polyploidy*
  - Increased number of chromosomes per set (e.g. triploidy)

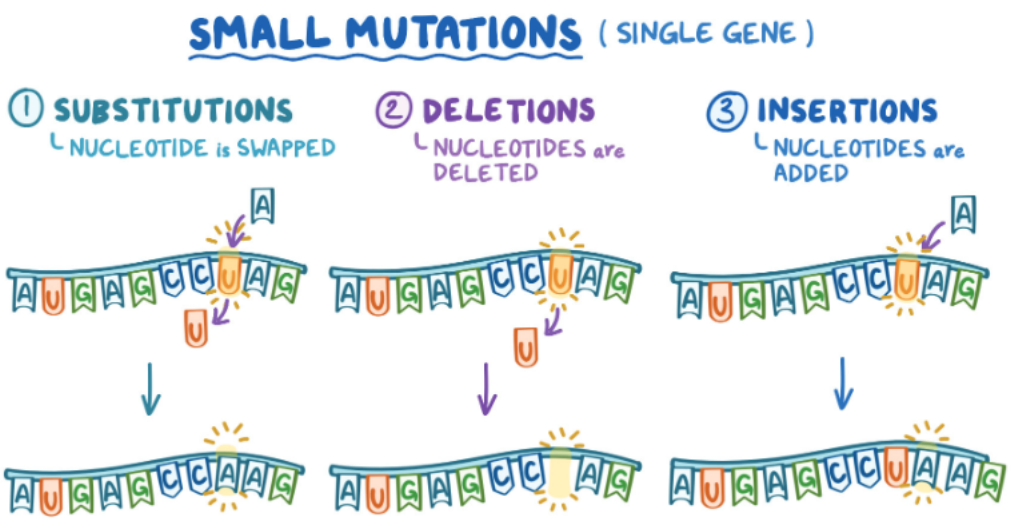


Figure 42.16 Small-scale mutations include: substitutions, deletions, and insertions. They may have a small or large effect on protein function depending on how the new nucleotide affects the translation of the codon sequence into amino acids.

Structurally abnormal

- Movement of sections of chromosomes
- *Deletion*: part of chromosome goes missing (e.g. cri du chat syndrome)
- *Duplication*: part of chromosome duplicated
- *Inversion*: part of chromosome breaks off, reattaches
- *Translocation*: parts of two chromosomes switched

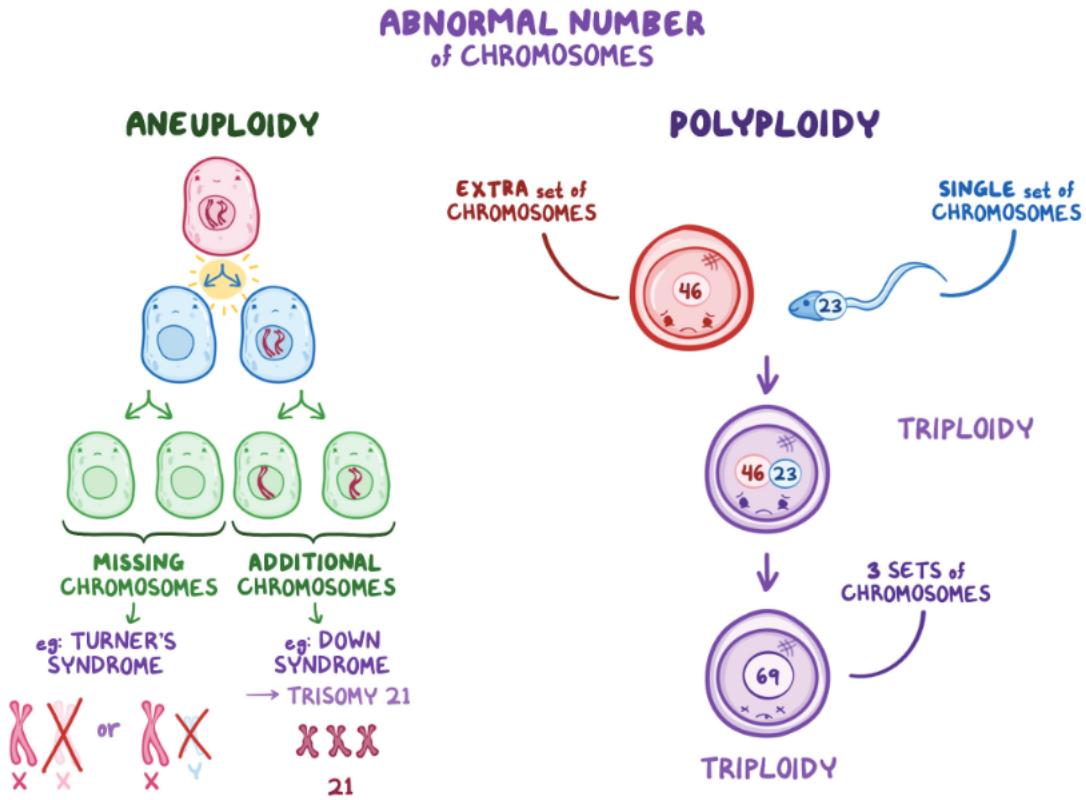


Figure 42.17 Aneuploidy and polyploidy are types of large-scale mutations which result in an abnormal number of chromosomes.

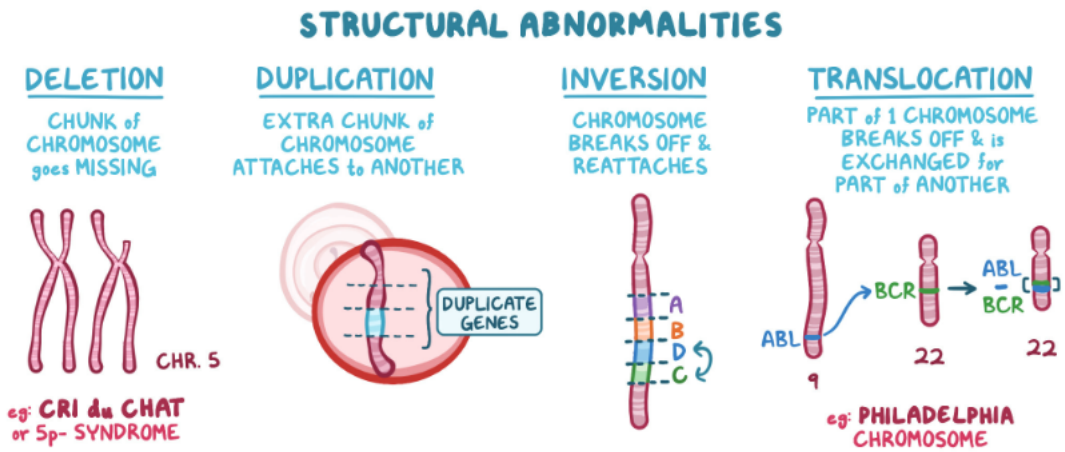


Figure 42.18 Illustration of types of structural abnormalities.

DNA DAMAGE

- DNA damaged by endogenous, exogenous (environmental) factors
- If damaged DNA cannot be fixed → multiple paths
  - *Senescence:* stops dividing
  - *Apoptosis:* programmed cell death
  - *Uncontrolled cell division:* develops into tumor
- If damaged DNA can be fixed → G0 phase

Single strand damage

- Causes
  - Endogenous (errors in DNA replication)
  - Exogenous (harmful chemical/physical agents)
- Repaired with mismatch/base excision/ nucleotide excision repair
  - Endonucleases cleave damaged segment
  - Exonucleases remove damaged segment
  - DNA polymerase rebuilds segment
  - DNA ligase glues new segment

Double stranded breaks

- May be due to ionizing radiation

Repair mechanisms

- Non-homologous end joining
  - DNA protein kinase binds to each end of the broken DNA → artemis cuts off rough ends → ends are rejoined with DNA ligase
- Homologous end joining
  - MRN protein complex binds to each end and removes affected nucleotides → DNA polymerase copies genetic information from sister chromatid

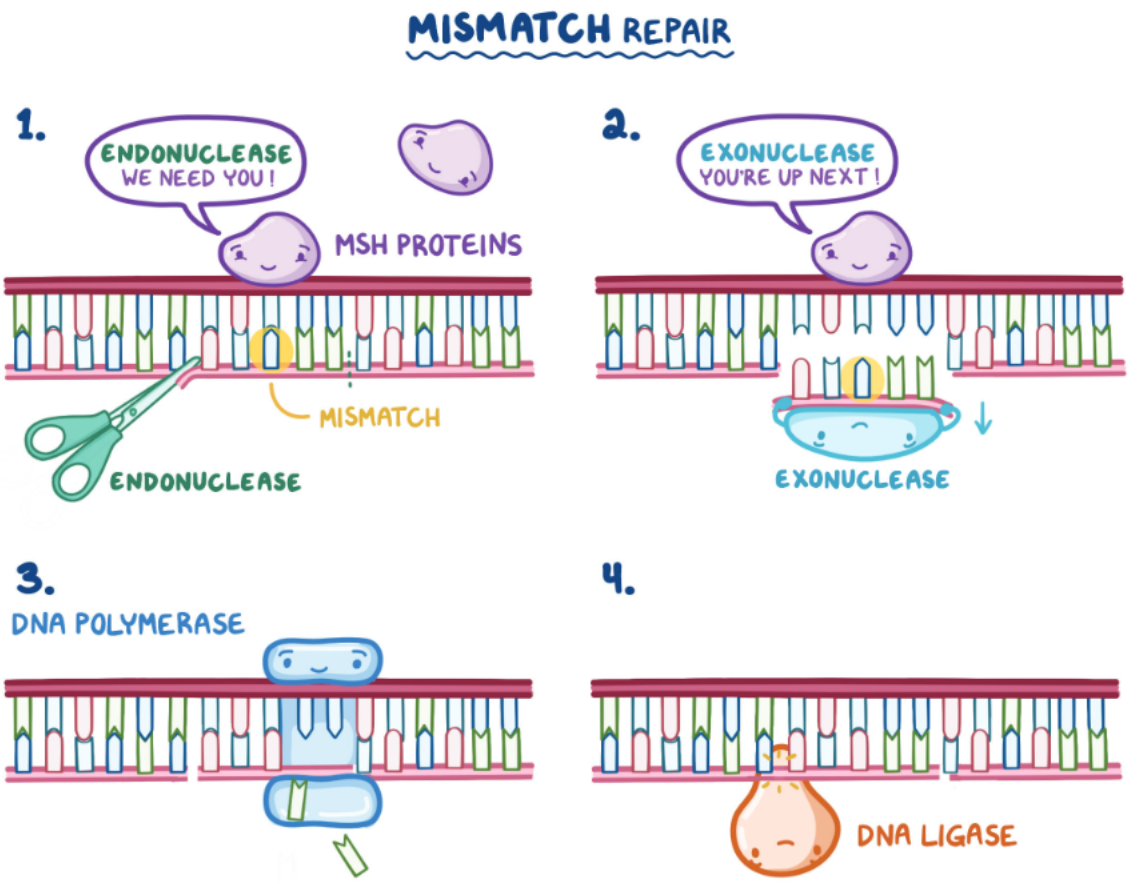


Figure 42.19 Repair of a mismatched nucleotide on a newly synthesized DNA strand. **1:** Endonucleases cleave either side of damaged segment; **2:** Exonucleases remove damaged segment; **3:** DNA polymerase rebuilds segment; **4:** DNA ligase connects new segment to strand.

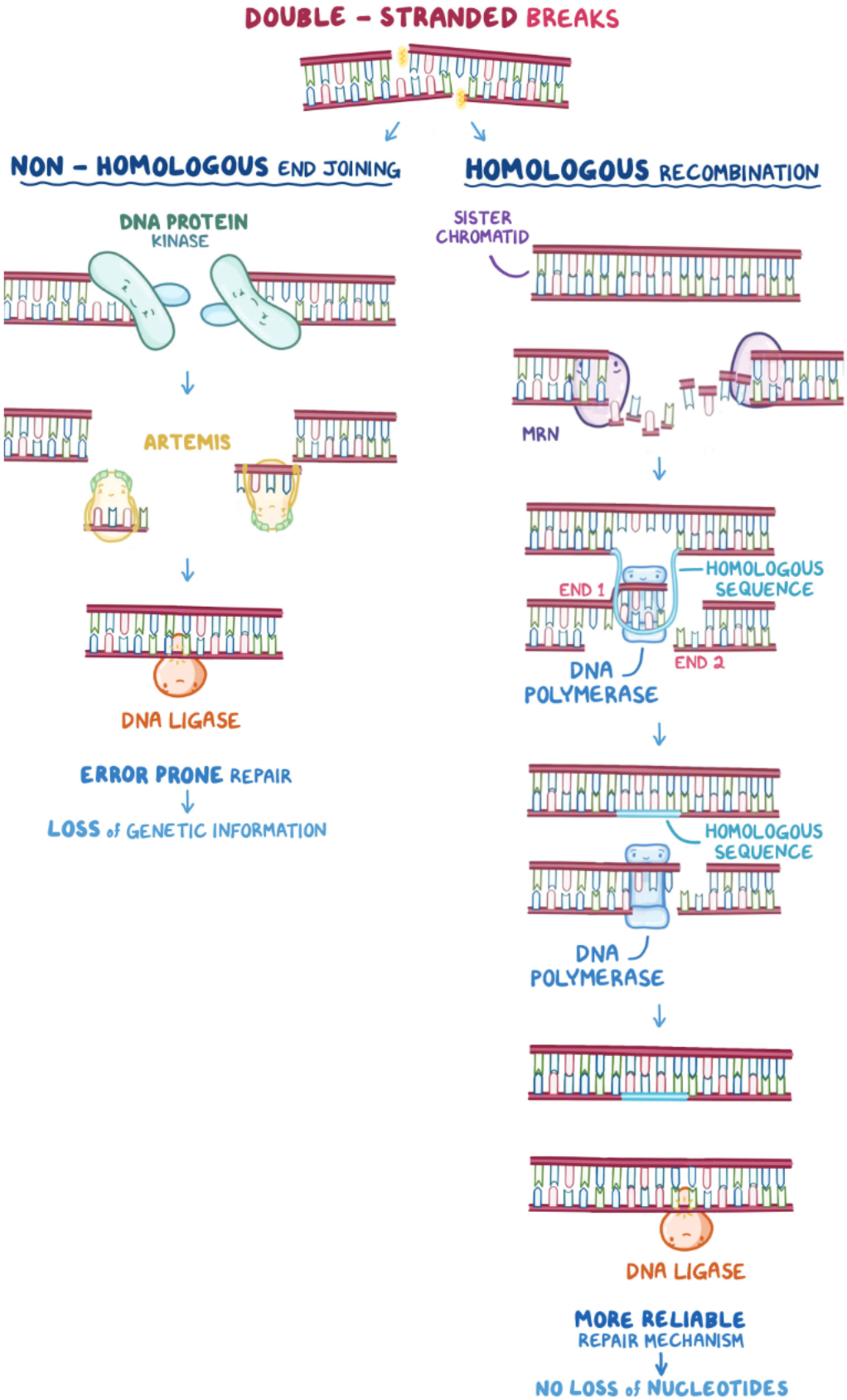


Figure 42.20 Two repair mechanisms for double-stranded breaks: non-homologous end joining and homologous recombination.