Cerebrum Biology Academy

Genetics & Heredity Complete Guide
For NEET Biology Excellence

Complete guide covering inheritance patterns, molecular genetics, and gene expression. From Mendel's laws to modern genetic disorders, DNA structure to genetic engineering. Essential for NEET and competitive exams.

- Classical & Molecular Genetics
- Inheritance Patterns
- Nucleic Acid Biology
- Gene Expression
- Human Genetic Disorders

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Mendel's Laws

Gregor Mendel's experiments with pea plants (1866) established the foundation of genetics. Law of Segregation states that alleles segregate during gamete formation, with each gamete receiving only one allele. Law of Independent Assortment states that alleles of different genes assort independently during gamete formation. Monohybrid cross (Tt x Tt) produces 3:1 phenotypic ratio in F2 (3 dominant: 1 recessive). Dihybrid cross (AaBb x AaBb) produces 9:3:3:1 phenotypic ratio in F2.

Key Facts & Ratios:

• Monohybrid F2 ratio: 1 homozygous dominant (AA) : 2 heterozygous (Aa) : 1 homozygous recessive (aa)

• Phenotypic ratio: 3 dominant : 1 recessive (3:1)

• Genotypic ratio: 1:2:1

• Test cross: Aa x aa produces 1:1 ratio, revealing heterozygosity

• Dihybrid F2 ratio: 9 A_B_ : 3 A_bb : 3 aaB_ : 1 aabb

NEET Previous Year Trend:
Segregation law, test cross interpretation, dihybrid cross ratios appear frequently

Incomplete Dominance & Codominance

Incomplete dominance occurs when neither allele is completely dominant, resulting in intermediate phenotypes. Heterozygotes show blended characteristics different from both homozygotes. Classic example: red x white snapdragons produce pink F1. Codominance occurs when both alleles are fully expressed in heterozygotes without blending. Example: ABO blood type AB individuals express both A and B antigens on RBCs.

Key Facts & Ratios:

• Incomplete dominance F1: Aa produces intermediate phenotype

• Incomplete dominance F2 ratio: 1:2:1 phenotypic and genotypic (Red : Pink : White)

• Codominance: both alleles fully expressed simultaneously in heterozygotes

• AB blood group: codominant expression of IA and IB alleles

• No dominant/recessive relationship in incomplete dominance or codominance

NEET Previous Year Trend:
Blood groups, flower colors, incomplete dominance ratios tested repeatedly

Multiple Allelism

Multiple allelism occurs when a gene has more than two alleles in a population. ABO blood groups are the classic example with three alleles: IA, IB, i. IA and IB are codominant to each other, and both are dominant over i. Blood type AB (IAIB) shows codominance; A (IAIA or IAi) and B (IBIB or IBi) are dominant; O (ii) is recessive. Blood groups also involve Rh factor compatibility for transfusions.

Key Facts & Ratios:

• ABO system: 3 alleles (IA, IB, i) produce 4 phenotypes (A, B, AB, O)

• Type A: IAIA or IAi; Type B: IBIB or IBi; Type AB: IAIB; Type O: ii

• Blood group antigens are glycoproteins on RBC surface

• Rh factor: Rh+ (RhD antigen present) dominant over Rh- (recessive)

• Transfusion: O is universal donor (no A/B antigens); AB is universal recipient

NEET Previous Year Trend:
Blood group inheritance, transfusion compatibility, Rh incompatibility in pregnancy

Sex-linked Inheritance

Sex-linked traits are controlled by genes on sex chromosomes (X or Y). X-linked genes show different patterns in males (XaY) and females (XAXA, XAXa, XaXa). Males hemizygous for X-linked traits express recessive alleles. Females must be homozygous recessive to express X-linked recessive phenotypes. Examples: red-green color blindness, hemophilia. X-linked crosses often produce 1:1 ratios in males.

Key Facts & Ratios:

• X-linked recessive trait: males (1/2 affected), females (1/4 affected)

• Heterozygous females are carriers; show no symptoms but can transmit

• Color blindness: XcY (male affected); XcXC or XcXc (female carrier or affected)

• Hemophilia (Factor VIII/IX deficiency): X-linked recessive bleeding disorder

• Y-linked traits: only males affected; father to son transmission exclusively

NEET Previous Year Trend:
Color blindness ratios, hemophilia inheritance, carrier females, sex-linked cross interpretations

Chromosomal Theory of Inheritance

The chromosomal theory states that genes are located on chromosomes and that hereditary information is transmitted via chromosomes during reproduction. Thomas Hunt Morgan's experiments with Drosophila proved this theory using white-eye mutation, which mapped to the X chromosome. Homologous chromosomes separate during meiosis I, distributing alleles to gametes.

Key Facts & Ratios:

• Genes are units of inheritance located on chromosomes

• Chromosomes are the physical basis of heredity

• Homologous chromosome pairs separate during meiosis I (reduction division)

• Sister chromatids separate during meiosis II (equational division)

• Morgan's work: white-eye (w) in Drosophila mapped to X chromosome

NEET Previous Year Trend:
Chromosome number, meiosis stages, sex chromosome inheritance patterns

Linkage & Crossing Over

Linkage is the tendency of genes located close together on the same chromosome to be inherited together. Crossing over (recombination) occurs during prophase I of meiosis when homologous chromosomes exchange segments. Recombination frequency between two genes is proportional to their distance apart (1% recombination = 1 map unit/centimorgan). Thomas Hunt Morgan mapped Drosophila genes using test cross data.

Key Facts & Ratios:

• Linked genes don't assort independently; violate Mendel's law of independent assortment

• Recombination frequency = (recombinant offspring / total offspring) × 100%

• 1 map unit (centimorgan) = 1% recombination frequency = 1 million base pairs average

• Double crossover rarer than single crossover; triple crossover rarest

• Genetic map: linear arrangement of genes with distances calculated from recombination frequencies

NEET Previous Year Trend:
Recombination frequency calculation, three-point crosses, gene mapping, linkage detection

DNA Structure

Watson and Crick determined DNA structure (1953) as a double helix of two antiparallel strands. Each strand has a sugar-phosphate backbone with nitrogenous bases (purines: A, G; pyrimidines: C, T) extending into the helix. Base pairing follows Chargaff's rules: A=T (2 H-bonds), G≡C (3 H-bonds). DNA diameter ~2 nm; pitch ~3.4 nm; 10 base pairs per turn.

Key Facts & Ratios:

- Double helix: antiparallel strands (one 5' to 3', other 3' to 5')
- Base pairing: A-T (2 bonds), G-C (3 bonds)
- Chargaff's rules: %A = %T, %G = %C, (A+G) = (T+C) = 50%
- Sugar-phosphate backbone: 5' phosphate to 3' hydroxyl linkage
- B-form DNA (Watson-Crick): 10.5 bp/turn, 11 Å wide helix

NEET Previous Year Trend:
Base pairing, Chargaff's rules, antiparallel strands, DNA dimensions

DNA Replication

DNA replication is semi-conservative: each strand serves as template; new complementary strand synthesized by DNA polymerase. Origin of replication initiates replication; DNA helicase unwinds helix; primase synthesizes RNA primers; DNA polymerase III extends primers; DNA polymerase I removes primers; DNA ligase seals nicks. Leading strand: continuous synthesis 5' to 3'. Lagging strand: Okazaki fragments (1000-2000 nucleotides in eukaryotes).

Key Facts & Ratios:

• Semi-conservative: each new DNA molecule has one original and one new strand

• DNA polymerase: requires RNA primer, synthesizes 5' to 3', has 3' to 5' exonuclease (proofreading)

• Leading strand: continuous synthesis in 5' to 3' direction

• Lagging strand: discontinuous; Okazaki fragments joined by ligase

• Meselson-Stahl experiment proved semi-conservative replication (N15 labeling)

NEET Previous Year Trend:
Semi-conservative replication, leading/lagging strands, Okazaki fragments, DNA polymerase function

Transcription

Transcription synthesizes mRNA from DNA template. RNA polymerase II (eukaryotes) initiates at promoter (-10 TATA box, -25 CAAT box). Transcription proceeds 5' to 3' on mRNA (3' to 5' on template strand). Three mRNA types: mRNA (protein coding), tRNA (amino acid transport), rRNA (ribosome structure). Eukaryotic mRNA undergoes 5' capping, 3' polyadenylation, and splicing to remove introns.

Key Facts & Ratios:

• Promoter: TATA box (TATAAA) at -10, CAAT box at -25 in eukaryotes

• RNA polymerase I: rRNA; II: mRNA, miRNA; III: tRNA, 5S rRNA

• mRNA processing: 7-methylguanosine 5' cap, poly-A tail (200 adenines), splicing

• Introns: non-coding sequences removed; exons: expressed sequences retained

• One gene can produce multiple proteins via alternative splicing

NEET Previous Year Trend:
Gene expression, mRNA processing, promoter sequences, transcription in prokaryotes vs eukaryotes

Translation

Translation synthesizes proteins from mRNA template. Codons (3 nucleotides) code for amino acids; tRNA molecules (anticodon) deliver specific amino acids to ribosome. Genetic code: 64 codons (61 sense, 3 stop). Start codon: AUG (methionine); Stop codons: UAA, UAG, UGA. Ribosome reads mRNA 5' to 3'; protein synthesized N-terminal to C-terminal. Initiation, elongation, termination phases.

Key Facts & Ratios:

• Genetic code: universal, triplet, degenerate (multiple codons/amino acid), non-overlapping

• Codon table: UUU/UUC = Phe, UUA/UUG = Leu, UCU/UCC/UCA/UCG = Ser, etc.

• tRNA: anticodon binds codon; amino acid attached by aminoacyl-tRNA synthetase

• Start codon AUG; stop codons UAA (ochre), UAG (amber), UGA (opal)

• Wobble position: 3rd codon position allows non-standard pairing (U-G wobble)

NEET Previous Year Trend:
Genetic code table, codon-anticodon pairing, start/stop codons, degeneracy

Gene Regulation

Gene regulation controls when genes are expressed. Lac operon (prokaryotic) model: structural genes (lacZ, lacY, lacA) under control of promoter and operator. Repressor protein blocks transcription when lactose absent; lactose (allolactose) inactivates repressor. CAP-cAMP enhances transcription when glucose low. Eukaryotic regulation: transcription factors, chromatin remodeling, DNA methylation, histone acetylation.

Key Facts & Ratios:

• Lac operon: inducible system (turned on by substrate); negative control (repressor)

• Repressor binds operator in absence of lactose, blocks RNA polymerase

• Allolactose (lactose metabolite) inactivates repressor; derepression occurs

• CAP-cAMP: positive control; cAMP increases when glucose low

• Trp operon: repressible system (turned off by end product); tryptophan = corepressor

NEET Previous Year Trend:
Lac operon function, operon model, inducible vs repressible, eukaryotic gene regulation

Human Genome Project

The Human Genome Project (completed 2003) determined the DNA sequence of the entire human genome (~3 billion base pairs). International collaboration used physical mapping and shotgun sequencing methods. Key findings: ~20,000-25,000 genes (not 100,000 predicted), significant non-coding DNA, high sequence similarity (99.9%) between individuals.

Key Facts & Ratios:

• Human genome: 3.2 × 10^9 base pairs; 46 chromosomes (23 pairs); haploid = 1.6 × 10^9 bp

• Gene density: ~1 gene per 100,000 bp; coding sequence = 1.5% of genome

• Non-coding DNA: introns, regulatory regions, repetitive sequences, transposable elements

• SNPs (single nucleotide polymorphisms): ~10 million in human genome; 1 per 300 bp average

• Genetic variation: 99.9% similarity between humans; 0.1% accounts for individual differences

NEET Previous Year Trend:
Gene number, genome size, coding vs non-coding DNA, DNA sequencing methods

DNA Fingerprinting

DNA fingerprinting (profiling) identifies individuals based on unique DNA patterns. Uses VNTRs (variable number tandem repeats) or microsatellites (STRs - short tandem repeats). VNTR analysis by Southern blotting detects restriction fragment length polymorphisms (RFLPs). STR analysis via PCR is faster, requires less DNA. Probability of two unrelated individuals having identical profile extremely low (<1 in billions).

Key Facts & Ratios:

• VNTRs: highly polymorphic; varies in copy number; creates unique banding patterns

• STRs: 2-6 bp repeats; PCR-amplified; 13 core loci in CODIS database for forensics

• RFLPs: restriction fragment length differences detected by Southern blot

• Paternity testing: match alleles at multiple loci (>99.99% conclusive)

• Forensic application: hair, blood, saliva identify suspects; match crime scene DNA

NEET Previous Year Trend:
VNTR vs STR, fingerprinting principles, paternity testing, forensic DNA analysis

Genetic Disorders

Genetic disorders result from mutations causing altered protein function. Autosomal dominant (e.g., huntingtin - Huntington's disease) appear in heterozygotes. Autosomal recessive (e.g., hemoglobin S - sickle cell) require homozygosity. X-linked disorders (e.g., Factor VIII - hemophilia A) affect males primarily. Chromosomal abnormalities: trisomy 21 (Down syndrome), Turner syndrome (45,X), Klinefelter (47,XXY).

Key Facts & Ratios:

• Huntington's disease: CAG repeat expansion (>40 repeats); progressive neurodegeneration

• Sickle cell: glutamic acid → valine at position 6; polymerization under low O2

• Cystic fibrosis: CFTR protein mutation; thick secretions; lung/pancreatic damage

• Hemophilia A/B: Factor VIII/IX deficiency; X-linked recessive; bleeding disorder

• Down syndrome (Trisomy 21): intellectual disability; heart defects; life expectancy ~60 years

NEET Previous Year Trend:
Autosomal vs X-linked disorders, mutation types, chromosomal abnormalities, genetic counseling

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