Collegedunia NCERT Formula Sheet

Class 12 / 12th Biology — Chapter 6 (NCERT 2024-25 / Latest Edition)

Chapter 6: Evolution

Hardy-Weinberg | Population Genetics | Selection & Drift | Radiometric Dating

Quantity / Constant	Symbol & Value	Where it appears
Age of the Earth	$\approx 4.5 \times 10^9$ yr	Geological-age calibration; radiometric dating baseline
Age of the Universe (Big Bang)	$\approx 13.7 \times 10^9$ yr	Origin of life timeline (NCERT 6.1)
First cellular life on Earth	≈ 3.8–4.0×10^9 yr ago	Chemical evolution $\rightarrow$ biogenesis transition
Half-life of ^{14}C	$T_{1/2} = 5730$ yr	Dating of recent fossils (last $\sim$50,000 yr)
Half-life of ^{40}K $\rightarrow$ ^{40}Ar	$T_{1/2} = 1.25 \times 10^9$ yr	Dating of very old volcanic/igneous rocks
Half-life of ^{238}U $\rightarrow$ ^{206}Pb	$T_{1/2} = 4.47 \times 10^9$ yr	Oldest terrestrial & meteorite rocks
Hardy-Weinberg sum of allele freq.	$p + q = 1$	Two-allele locus baseline
Hardy-Weinberg sum of genotypes	$p^2 + 2pq + q^2 = 1$	Equilibrium genotype frequencies
Selection coefficient range	$0 \leq s \leq 1$	$s = 0$: neutral; $s = 1$: lethal
Fitness coefficient range	$0 \leq w \leq 1$	$w = 1$: most fit; $w = 0$: zero offspring
Fixation index range	$0 \leq F_{ST} \leq 1$	0: no differentiation; 1: complete fixation

1 1. Hardy-Weinberg Principle (Core Equations)

The Hardy-Weinberg (HW) principle predicts allele and genotype frequencies in a non-evolving population. It is the **null model** of evolution: if a real population deviates from these equations, evolution is acting.

Allele frequency sum (two alleles)

$$p + q = 1$$

where p = frequency of dominant allele A (dimensionless, between 0 and 1); q = frequency of recessive allele a (dimensionless).

Total of all allele frequencies at a locus always equals 1. For a **two-allele locus**, knowing p instantly fixes $q = 1 - p$.

Hardy-Weinberg genotype equation

$$p^2 + 2pq + q^2 = 1$$

where p^2 = frequency of homozygous dominant (AA); $2pq$ = frequency of heterozygotes (Aa); q^2 = frequency of homozygous recessive (aa).

Binomial expansion of $(p + q)^2 = 1$. Holds only when the **five HW conditions** are met (see conceptbox). The frequencies stay constant generation after generation if undisturbed — this is **genetic equilibrium**.

The five Hardy-Weinberg conditions

A population stays in HW equilibrium only if all five hold simultaneously:

1. **No mutation** — alleles do not change into other alleles.
2. **No gene flow / migration** — no alleles enter or leave the gene pool.
3. **Random mating (panmixia)** — mate choice is independent of genotype.
4. **No genetic drift** — population size is effectively infinite (very large).
5. **No natural selection** — all genotypes have equal fitness.

A breach of **any one** of these conditions causes the gene-pool frequencies to change with time — the operational definition of **evolution**.

Allele frequencies from genotype counts

$$p = \frac{2N_{AA} + N_{Aa}}{2N} \qquad q = \frac{2N_{aa} + N_{Aa}}{2N}$$

where N_{AA}, N_{Aa}, N_{aa} = counts of each genotype in the sample; N = total number of individuals; $2N$ = total number of alleles (each diploid carries 2).

Each homozygote contributes **two** of its allele; each heterozygote contributes **one of each**. Use this to estimate p and q from observed counts.

Shortcut for recessive trait frequency

If the recessive phenotype frequency is observed (e.g., albinism in 1 in 10,000): $q^2 = 1/10000 \Rightarrow q = 0.01$, so $p = 0.99$ and carrier frequency $2pq \approx 0.0198$ (i.e. ≈ 1 in 50 are carriers). Useful for genetic-counselling problems in NEET.

2 2. Disturbing Forces (Causes of Evolution)

The five factors that break HW equilibrium and drive allele-frequency change are gene migration (flow), genetic drift, mutation, recombination, and natural selection. Each can be quantified with a simple expression.

Gene flow / migration: allele-frequency change

$$\Delta p = m\,(p_M - p)$$

where Δp = change in allele frequency per generation due to migration; m = migration rate (fraction of population replaced by migrants per generation); p_M = allele frequency among migrants; p = allele frequency in resident population.

Migration pulls the recipient population's p toward the donor's p_M. Strong gene flow **homogenises** populations and **opposes speciation**.

Mutation pressure: allele-frequency change

$$\Delta q = \mu\, p - \nu\, q$$

where μ = forward mutation rate $A \to a$ per generation; ν = reverse mutation rate $a \to A$ per generation; p, q = current allele frequencies.

At mutation-only equilibrium, $\Delta q = 0 \Rightarrow \hat{q} = \mu/(\mu + \nu)$. Mutation rates are typically 10^{-5} to 10^{-8} per locus per generation, so this force is **slow on its own** but supplies the raw variation that selection acts on.

Genetic drift: variance in allele frequency

$$\sigma^2_{\Delta p} = \frac{p\,q}{2N_e}$$

where $\sigma^2_{\Delta p}$ = variance of allele-frequency change per generation; p, q = current allele frequencies; N_e = **effective population size** (the number of breeding individuals contributing genes).

Drift is **random sampling error** in passing alleles to the next generation. Variance is **inversely proportional to** N_e — small populations drift hard, large populations barely budge. Strong in **founder effect** and **bottleneck** events.

Probability of allele fixation by drift

$$P_{\text{fix}}(A) = p_0 \quad ; \quad \text{expected time } \bar{t}_{\text{fix}} \approx 4N_e \text{ generations}$$

where p_0 = initial frequency of allele A; N_e = effective population size.

A **neutral allele**'s probability of eventually becoming fixed equals its current frequency. A brand-new mutation has $p_0 = 1/(2N_e)$, so its chance of fixation is tiny but non-zero. Small N_e $\Rightarrow$ fast fixation.

3 3. Selection Coefficient and Fitness

Natural selection differentially keeps or removes genotypes from the breeding pool. Fitness and the selection coefficient are two sides of the same coin — both measure relative reproductive success.

Fitness coefficient

$$w = \frac{\text{mean offspring of a given genotype}}{\text{mean offspring of fittest genotype}}$$

where w = relative (Darwinian) fitness; range $0 \le w \le 1$.

Fitness measures **reproductive success relative to the fittest genotype**, not survival alone.

Fittest genotype: $w = 1$. Lethal/sterile genotype: $w = 0$. The **currency of evolution is offspring**, not lifespan.

Selection coefficient

$$s = 1 - w$$

where s = selection coefficient against the genotype; range $0 \leq s \leq 1$.

s is the **fractional reduction in fitness** relative to the best genotype. $s = 0$: neutral (no selection). $s = 1$: completely lethal/sterile. Small s (~ 0.01) accumulates over many generations to produce substantial allele-frequency shifts.

Allele-frequency change under selection (recessive lethal)

$$\Delta q = -\frac{s\,q^2(1-q)}{1 - s\,q^2}$$

where q = frequency of recessive deleterious allele; s = selection coefficient against aa.

Selection against a **recessive lethal** ($s = 1$) becomes inefficient as q falls — because rare a alleles hide inside heterozygotes (Aa) and escape selection. This is why deleterious recessives **persist** in human populations.

Selection-mutation balance

$$\hat{q} \approx \sqrt{\frac{\mu}{s}} \quad \text{(recessive deleterious allele)}$$

where $\hat{q}$ = equilibrium frequency of harmful allele; μ = mutation rate creating it; s = selection coefficient against the homozygote.

At equilibrium, new mutations introduce the allele as fast as selection removes it. Explains **baseline incidence** of recessive genetic disorders (e.g. cystic fibrosis, phenylketonuria).

JEE/NEET Extension — Three modes of natural selection

Stabilising: intermediate phenotype favoured; variance *decreases* (e.g. human birth weight ~ 3.5 kg). **Directional**: one extreme favoured; mean *shifts* (e.g. industrial melanism of *Biston betularia*). **Disruptive**: both extremes favoured; variance *increases*, can drive sympatric speciation.

4 4. Population Differentiation: Fixation Index

When a species is split into subpopulations, allele frequencies drift apart. Wright's fixation index F_{ST} quantifies how genetically distinct those subpopulations have become.

Fixation index F_{ST}

$$F_{ST} = \frac{H_T - H_S}{H_T}$$

where H_T = expected heterozygosity if the total population mated at random ($= 2\bar{p}\bar{q}$, using mean allele freq.); H_S = average expected heterozygosity within subpopulations.

F_{ST} is the **fraction of total genetic variation due to between-population differences**. $F_{ST} = 0$: subpopulations identical. $F_{ST} = 1$: fully differentiated (different alleles fixed in each).

Inbreeding coefficient F (Wright's F)

$$F = \frac{H_{\text{exp}} - H_{\text{obs}}}{H_{\text{exp}}}$$

where $H_{\text{exp}} = 2pq$ (HW expectation); H_{obs} = observed heterozygote frequency.

Measures the **deficit of heterozygotes** relative to HW prediction. $F > 0$: inbreeding (excess homozygotes). $F < 0$: outbreeding/heterozygote advantage. Bridges HW theory and real-population genotype counts.

Qualitative F_{ST} scale for natural populations

- $F_{ST} = 0$–0.05: little differentiation
- $F_{ST} = 0.05$–0.15: moderate differentiation
- $F_{ST} = 0.15$–0.25: great differentiation
- $F_{ST} > 0.25$: very great differentiation, often incipient speciation

Human worldwide $F_{ST} \approx 0.05$–0.15 — humans are a remarkably **undifferentiated species** despite geographic spread.

5 5. Radioactive Decay & Radiometric Dating

Fossils and rocks are dated by the radioactive decay of isotopes locked into the rock at formation. This converts the textbook's "Devonian / Cretaceous / Eocene" labels into hard numbers.

Radioactive decay law

$$N(t) = N_0\, e^{-\lambda t}$$

where $N(t)$ = number of parent atoms remaining at time t; N_0 = original number at $t = 0$; λ = decay constant (per unit time); t = elapsed time.

Exponential decline: same fraction decays per unit time, regardless of how much remains. The **rate is independent** of temperature, pressure, or chemistry — this is why isotopic clocks are reliable.

Half-life and decay constant

$$T_{1/2} = \frac{\ln 2}{\lambda} = \frac{0.693}{\lambda}$$

where $T_{1/2}$ = half-life (time for half the parent atoms to decay); λ = decay constant.

After one half-life: $\frac{1}{2}$ of parent remains. After two: $\frac{1}{4}$. After n half-lives: $\left(\frac{1}{2}\right)^n$ of parent remains. **Choice of isotope** must match the age range being dated.

Age of a fossil / rock

$$t = \frac{1}{\lambda}\ln\left(\frac{N_0}{N}\right) = \frac{T_{1/2}}{\ln 2}\ln\left(1 + \frac{D}{P}\right)$$

where N_0, N = initial & current parent counts; D = daughter atoms now present; P = parent atoms now present (assuming all D came from decay of P).

The **parent–daughter ratio** D/P is measured by mass-spectrometry; the formula then directly returns the age t. Used to date everything from Lucy (~ 3.2 Mya) to the oldest zircons (~ 4.4 Gya).

n half-life rule (quick mental form)

$$\frac{N}{N_0} = \left(\frac{1}{2}\right)^n \quad ; \quad t = n\,T_{1/2}$$

where n = number of half-lives elapsed (can be a fraction).

If only $1/8$ of the parent remains $\Rightarrow n = 3$ half-lives $\Rightarrow t = 3\,T_{1/2}$. **Fastest way** to solve NEET-style "what age?" problems without a calculator.

Carbon-14 dating equation

$$t = \frac{T_{1/2}}{\ln 2}\ln\left(\frac{A_0}{A}\right) = \frac{5730}{0.693}\ln\left(\frac{A_0}{A}\right)$$

where A_0 = ^{14}C activity of a living/modern sample (Bq/g); A = activity of the fossil sample now; $T_{1/2}(^{14}\mathrm{C}) = 5730$ yr.

^{14}C is continuously produced in the upper atmosphere and incorporated into living tissue. After death, intake stops and ^{14}C decays. **Useful range:** $\sim$ **100–50,000 yr** — beyond this, ^{14}C is too depleted to measure.

Don't confuse ^{14}C with ^{40}K

^{14}C dates **recent** biological material (last ~ 50 kyr). ^{40}K–^{40}Ar dates **ancient volcanic rocks** ($> 10^5$ yr). Using ^{14}C on a million-year-old fossil gives zero signal — all the ^{14}C is long gone. NEET MCQs trap students with this isotope-vs-age mismatch.

JEE/NEET Extension — Geological-age dating isotope pairs

Parent → Daughter	$T_{1/2}$	Useful range / material
^{14}C → ^{14}N	5.73×10^3 yr	Recent fossils, wood, bone (up to ~ 50 kyr)
^{40}K → ^{40}Ar	1.25×10^9 yr	Volcanic rocks; hominin fossil beds
^{238}U → ^{206}Pb	4.47×10^9 yr	Oldest rocks; meteorites; zircon
^{87}Rb → ^{87}Sr	4.88×10^{10} yr	Ancient continental crust

6 6. Geological Time and Evolution Timeline

The radiometric dates above anchor the geological timescale, which in turn calibrates NCERT's "Brief Account of Evolution" (Sec. 6.6). Memorising the numerical anchors helps with two-mark NEET questions.

Key evolutionary timeline anchors

$t_{\text{Big Bang}} \approx 13.7$ Gya

$t_{\text{Earth formed}} \approx 4.5$ Gya

$t_{\text{First cells}} \approx 3.8$–$4.0$ Gya

$t_{\text{First multicellular life}} \approx 1.5$ Gya

$t_{\text{Dinosaurs extinct}} \approx 65$ Mya

$t_{\text{Homo habilis}} \approx 2$ Mya ; $t_{\text{Homo sapiens}} \approx 0.2$ Mya

1 Gya $= 10^9$ years ago; 1 Mya $= 10^6$ years ago. **Earth is roughly one-third the age of the universe**; cellular life appeared within the first billion years of Earth's existence.

Reading the NCERT "Brief Account" (Sec. 6.6)

The chapter sequence of major events — **first invertebrates** (Cambrian, ~ 540 Mya) $\rightarrow$ **jawless fish** (~ 500 Mya) $\rightarrow$ **first land plants** (~ 450 Mya) $\rightarrow$ **amphibians** (~ 370 Mya, e.g. *Ichthyostega*) $\rightarrow$ **reptiles** (~ 300 Mya) $\rightarrow$ **mammals/dinosaurs split** (~ 200 Mya) $\rightarrow$ **birds** (~ 150 Mya, *Archaeopteryx*) $\rightarrow$ **mammal radiation after K-Pg** (~ 65 Mya) $\rightarrow$ **flowering plants dominate** $\rightarrow$ **primates** (~ 15 Mya) $\rightarrow$ **hominids** (~ 7 Mya).

7 7. Non-formula NCERT Concepts (Coverage Map)

Evolution is a concept-heavy chapter where most NCERT sections carry no algebra. They are summarised here so the formula sheet covers *every* numbered subsection without gaps.

Theories of origin of life (NCERT 6.1)

Panspermia: life arrived as spores from space. **Spontaneous generation**: life from decaying matter — disproved by **Louis Pasteur** (swan-neck flask). **Chemical (abiogenic) evolution**: **Oparin & Haldane** hypothesis — inorganic molecules $\rightarrow$ organic $\rightarrow$ macromolecules. **Miller-Urey (1953) experiment**: spark discharge through CH_4, NH_3, H_2, water vapour $\rightarrow$ amino acids formed, proving abiotic synthesis is feasible.

Evidence for evolution (NCERT 6.3)

Paleontological: fossils in successive rock layers show progressive change. **Comparative anatomy**: **homologous organs** (same origin, different function; forelimbs of vertebrates) $\Rightarrow$ *divergent evolution*; **analogous organs** (different origin, same function; wing of bird vs. butterfly) $\Rightarrow$ *convergent evolution*. **Embryological** (now downplayed by NCERT): von Baer's observations of common embryonic features. **Biogeographical**: Darwin's finches, Australian marsupials. **Molecular**: similarities in DNA/protein sequences across species.

Theories of biological evolution (NCERT 6.4–6.5)

Lamarckism: inheritance of acquired characters; "use and disuse" (e.g. giraffe's neck) — now **discredited**. **Darwinism (1859)**: descent with modification by **natural selection**; based on Galapagos finches and Malthusian population logic. **Modern synthesis (neo-Darwinism)**: Darwinian selection + Mendelian genetics + population genetics + mutation as source of variation. **Branching descent**: all extant species share common ancestors.

Adaptive radiation (NCERT 6.3.1)

Process by which one ancestral species **diversifies rapidly into many forms** occupying different ecological niches. Examples: **Darwin's finches** on Galapagos (13 species from one ancestor, varied beak shapes for different foods); **Australian marsupials** (one ancestral marsupial $\rightarrow$ many forms paralleling placental mammals). **Convergent evolution** occurs when two such radiations on different continents produce similar-looking organisms (e.g. marsupial vs. placental wolf).

Human evolution (NCERT 6.7) — key hominins

Dryopithecus (15 Mya, ape-like) $\rightarrow$ **Ramapithecus** (more man-like) $\rightarrow$ **Australopithecus** (~ 3.5 Mya, Africa, bipedal) $\rightarrow$ **Homo habilis** (~ 2 Mya, brain ≈ 650–800 cc, first stone tools, did not eat meat) $\rightarrow$ **Homo erectus** (~ 1.5 Mya, brain ≈ 900 cc, ate meat) $\rightarrow$ **Neanderthal man** ($\sim 100{,}000$–$40{,}000$ ya, brain ≈ 1400 cc, buried dead) $\rightarrow$ **Homo sapiens** ($\sim 200{,}000$ ya, modern humans).

Memory hook — the five HW disturbers

"**MS-GMN**" — **M**utation, **S**election, **G**ene flow (migration), Genetic drift (= small-**N**), **N**on-random mating. Each one breaks one of the five HW conditions; together they are the operational **mechanisms of evolution**.

8 8. Quick Reference — Formula Index

Quantity	Formula	When to use
Allele frequencies sum	$p + q = 1$	Two-allele locus, always
Genotype frequencies (HW)	$p^2 + 2pq + q^2 = 1$	Equilibrium population
p from counts	$p = (2N_{AA} + N_{Aa})/2N$	Empirical estimation
Carrier frequency (rare q)	$2pq \approx 2q$ when $q \ll 1$	Genetic counselling
Gene-flow change	$\Delta p = m(p_M - p)$	Migration into population
Mutation balance	$\Delta q = \mu p - \nu q$	Mutation-only model
Drift variance	$\sigma^2_{\Delta p} = pq/2N_e$	Small populations
Drift fixation prob.	$P_{\text{fix}} = p_0$	Neutral allele fate
Fitness	w (range 0–1)	Reproductive success
Selection coefficient	$s = 1 - w$	Strength of selection
Selection-mutation eqm.	$\hat{q} \approx \sqrt{\mu/s}$	Recessive deleterious
F_{ST}	$(H_T - H_S)/H_T$	Population structure
Inbreeding F	$(H_{\text{exp}} - H_{\text{obs}})/H_{\text{exp}}$	Heterozygote deficit
Decay law	$N = N_0 e^{-\lambda t}$	Any radioisotope
Half-life	$T_{1/2} = 0.693/\lambda$	Convert $\lambda \leftrightarrow T_{1/2}$
Age formula	$t = (T_{1/2}/\ln 2)\ln(N_0/N)$	Radiometric dating
n-half-life form	$N/N_0 = (1/2)^n$	Quick mental arithmetic
Carbon-14 age	$t = (5730/0.693)\ln(A_0/A)$	Fossils < 50 kyr

End of Formula Sheet — Class 12 Biology Chapter 6 Evolution.
Continue with Chapter 7 (Human Health & Disease) or revisit Chapter 5 (Principles of Inheritance) for the Mendelian basis of p and q.