IB Diploma Programme

Chuyên luyện thi IELTS/SAT → AP / IB / A-levels

8020 ENGLISH

IB Diploma Programme Biology

Giáo trình luyện thi chuyên sâu

Song ngữ Anh–Việt

8020 ENGLISH

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Lời mở đầu · Foreword

Cuốn sách này thuộc bộ giáo trình luyện thi chương trình quốc tế của **8020 English (8020 Education)** — trung tâm luyện thi trọng điểm **IELTS · SAT · AP · IB · A-level · IGCSE** và săn học bổng du học. Toàn bộ nội dung được biên soạn bởi đội ngũ **Giáo sư · Tiến sĩ · Thạc sĩ** tốt nghiệp các trường top đầu thế giới, bám sát khung chương trình chính thức, trình bày đầy đủ lý thuyết, ví dụ mẫu, hình minh hoạ và hệ thống bài tập có lời giải chi tiết.

This book is part of the 8020 English international exam-prep series: complete English theory with Vietnamese explanations, worked examples, illustrations and fully-solved practice, aligned to the official framework.

Thành tích 8020 English

9.0 IELTS cao nhất	**1570** SAT cao nhất
5/5 AP — điểm tuyệt đối	**90/100** IB Diploma
100% GV $\geq$ 8.0 IELTS / 1500 SAT	**CMU** Tiến sĩ ĐH #1 Hoa Kỳ về CS

Đội ngũ tiêu biểu: Thầy Châu Cát Tường (Academic Head, ThS Western Sydney, top 1% IELTS 8.5) · TS Nguyễn Anh Huy (Carnegie Mellon, cựu kỹ sư Amazon) · TS Nguyễn Phước Trường (Toán, ĐH Klagenfurt) · cùng đội ngũ giảng viên SAT 1500–1600, IELTS 8.0–8.5.

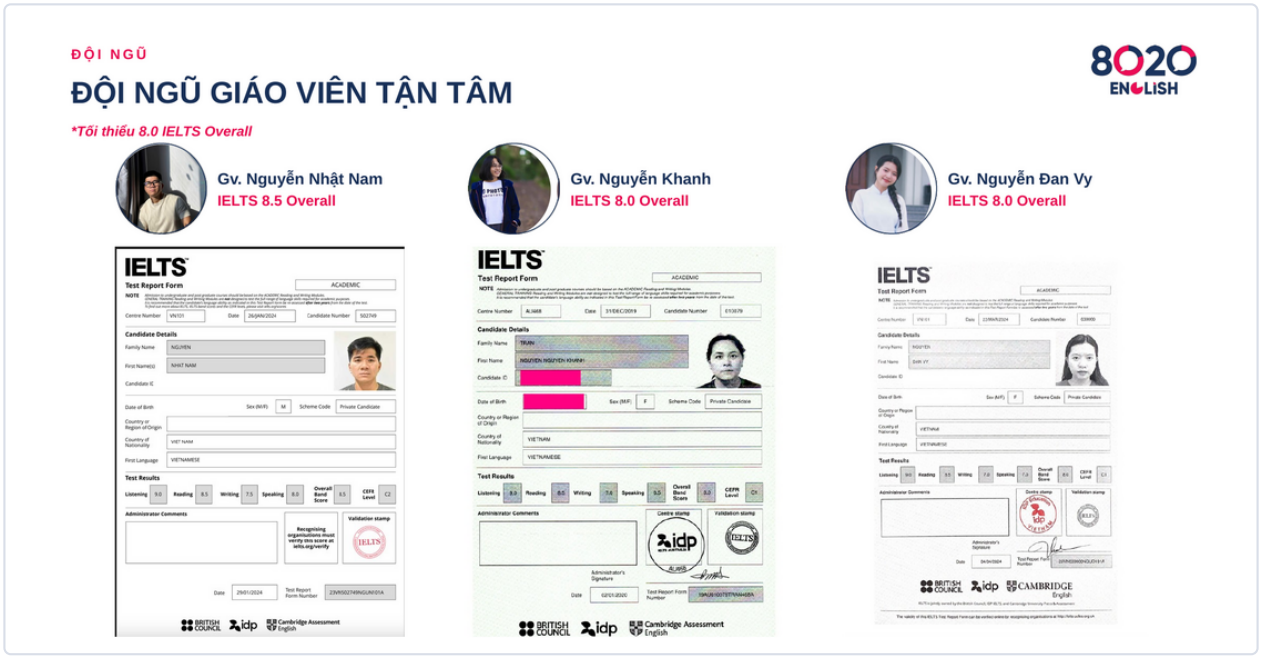
Kết quả học viên — điểm thi thật: IELTS 8.0–9.0 · SAT 1550 / 1570 / 1590 · AP 5/5 (Calculus BC, Microeconomics) · IB 90/100 (Economics) · Duolingo 110 · PTE 90 · TOEFL 120. **Bảng vàng SAT:** Khánh Đăng 1510 · Thảo Nguyên 1520 · Tâm Anh 1530.

"Cuối cùng đã đậu vào trường top như mong muốn." — Phan Thị Thanh Hằng, IELTS Overall 8.5.

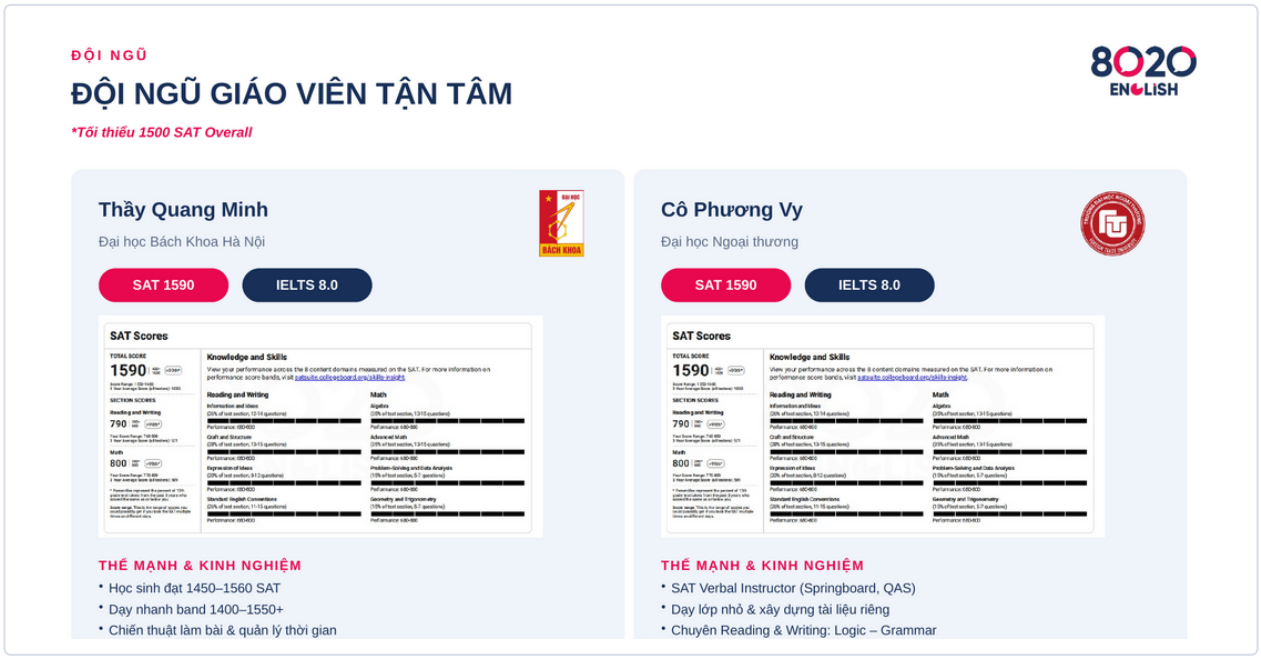
Cách dùng sách hiệu quả: mỗi Unit gồm (1) **Lý thuyết trọng tâm** tiếng Anh kèm **giải thích tiếng Việt**; (2) **Ví dụ mẫu** có lời giải; (3) **Hệ thống bài tập** kèm **lời giải chi tiết**. Hãy tự làm bài trước khi xem lời giải để đạt hiệu quả tối đa.

THÀNH TÍCH THỰC TẾ · 8020 ENGLISH

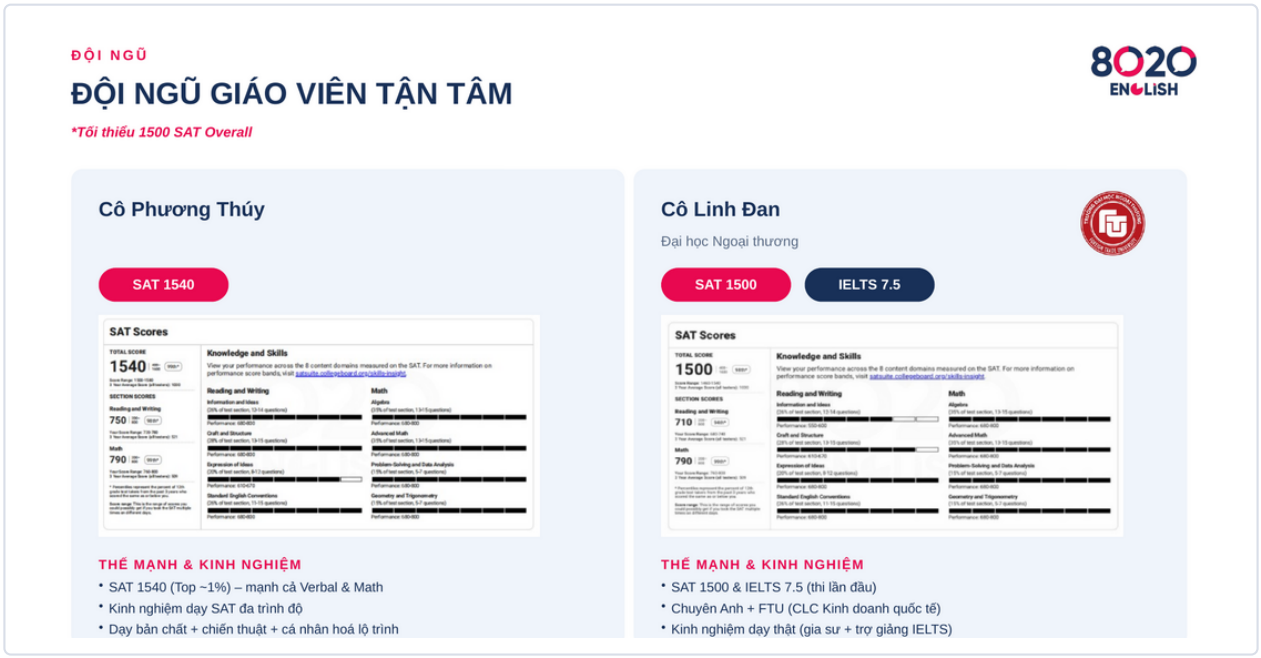
Điểm thi thật · Bằng & bảng điểm thật của giảng viên và học viên 8020 English — **Điểm thật · Thầy thật · Kết quả thật**



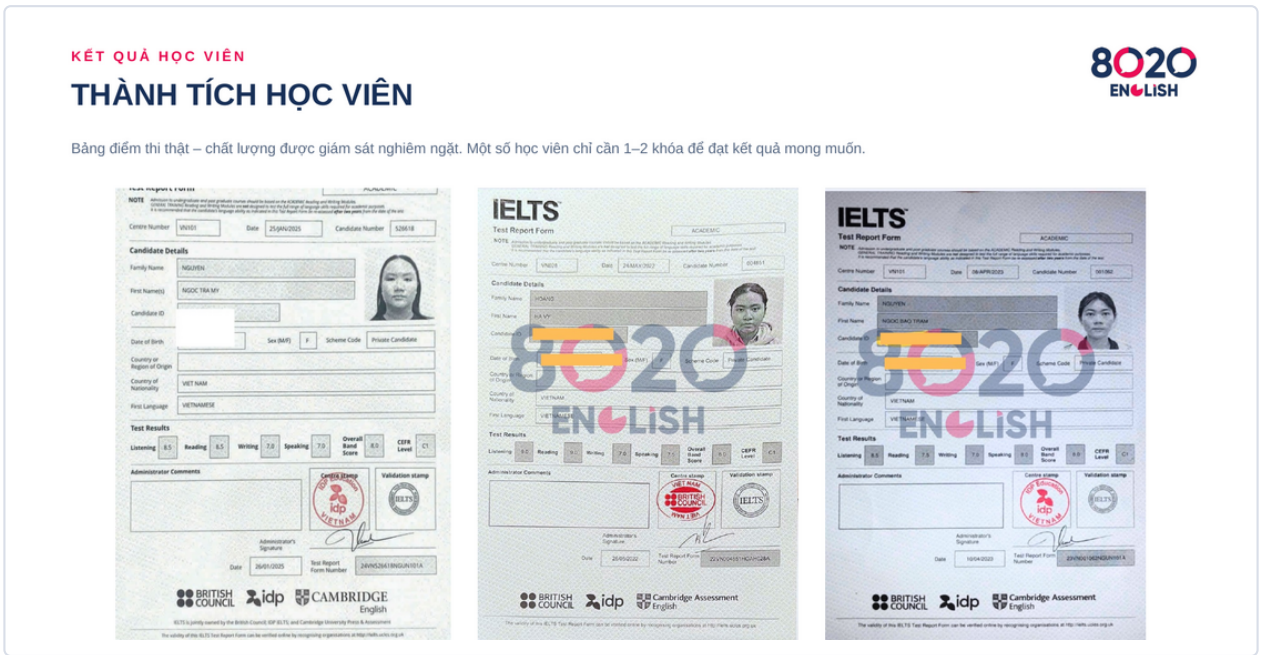
Đội ngũ giảng viên — IELTS 8.5 & 8.0 Overall (British Council · IDP · Cambridge)



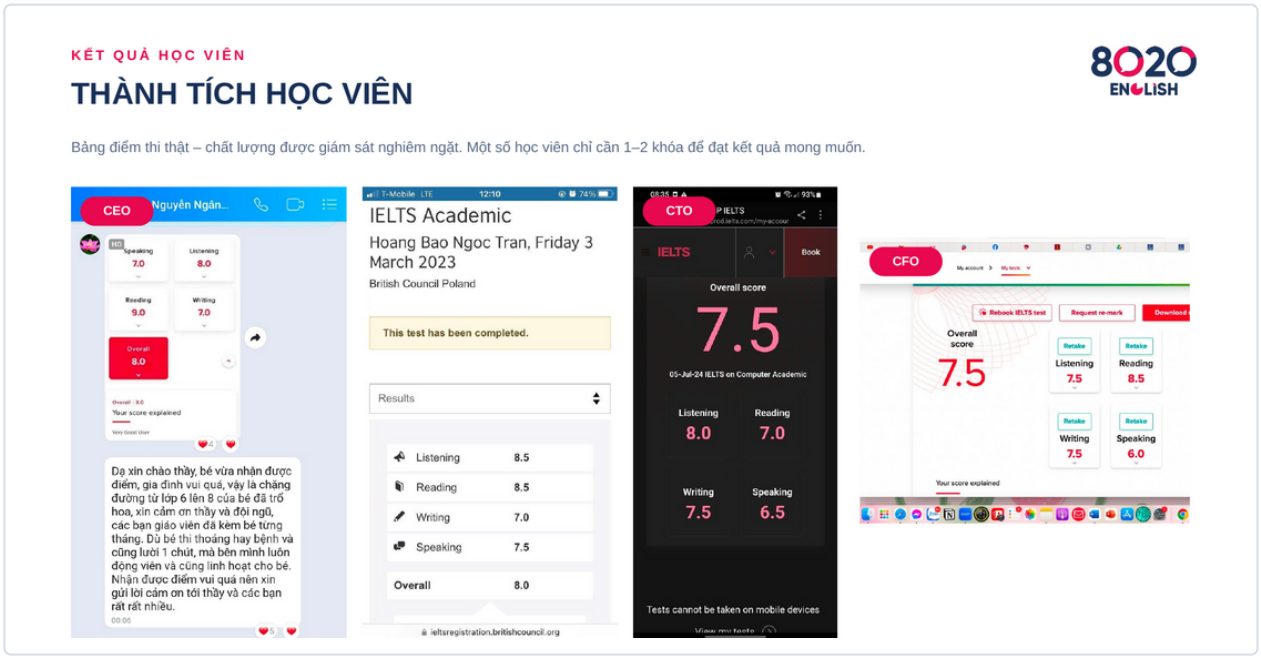
Giảng viên SAT 1590 — ĐH Bách Khoa Hà Nội & ĐH Ngoại thương



Giảng viên SAT 1540 & 1500 Overall



Học viên 8020 — IELTS 8.0 Overall (bảng điểm thật)



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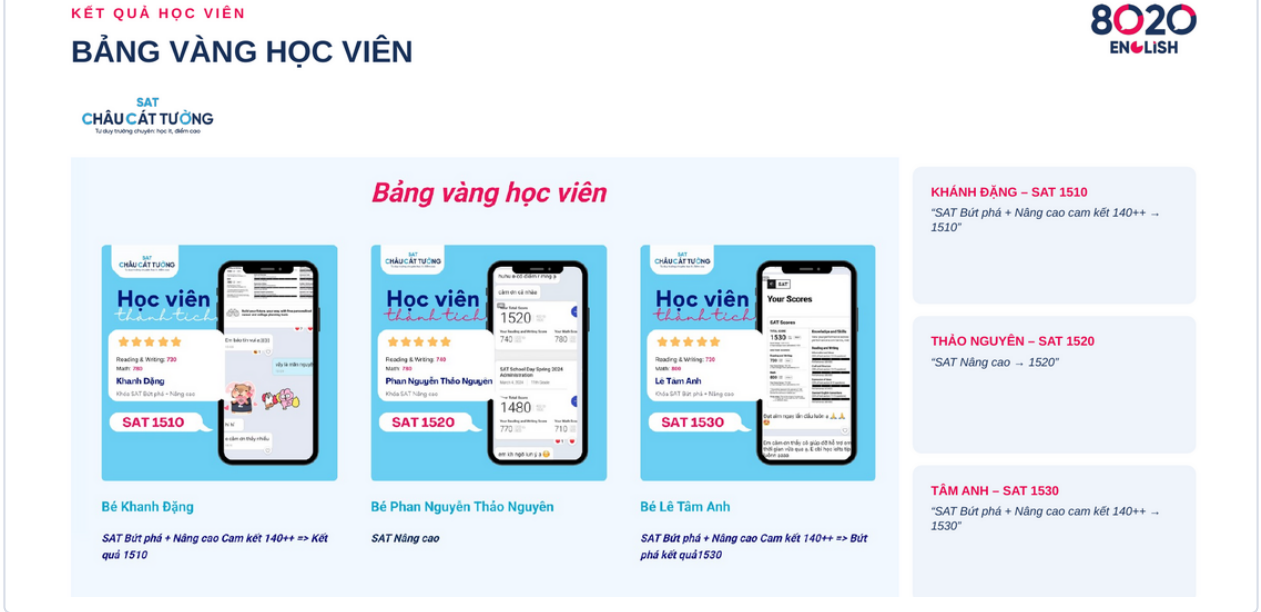
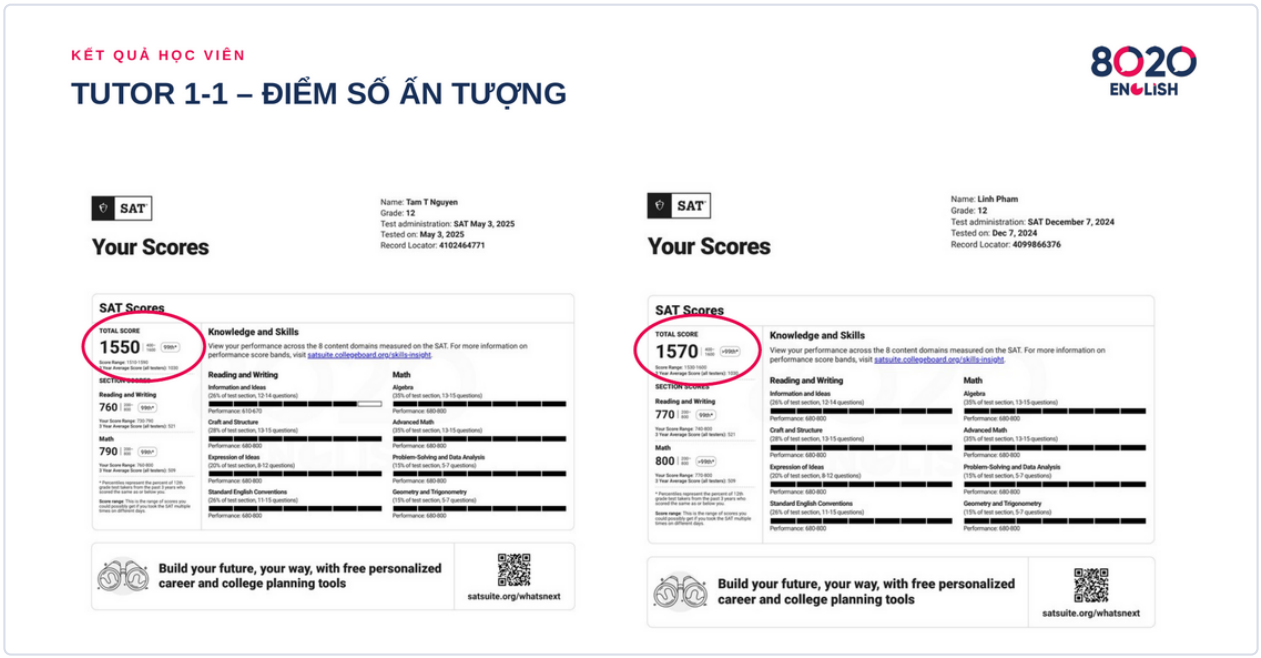
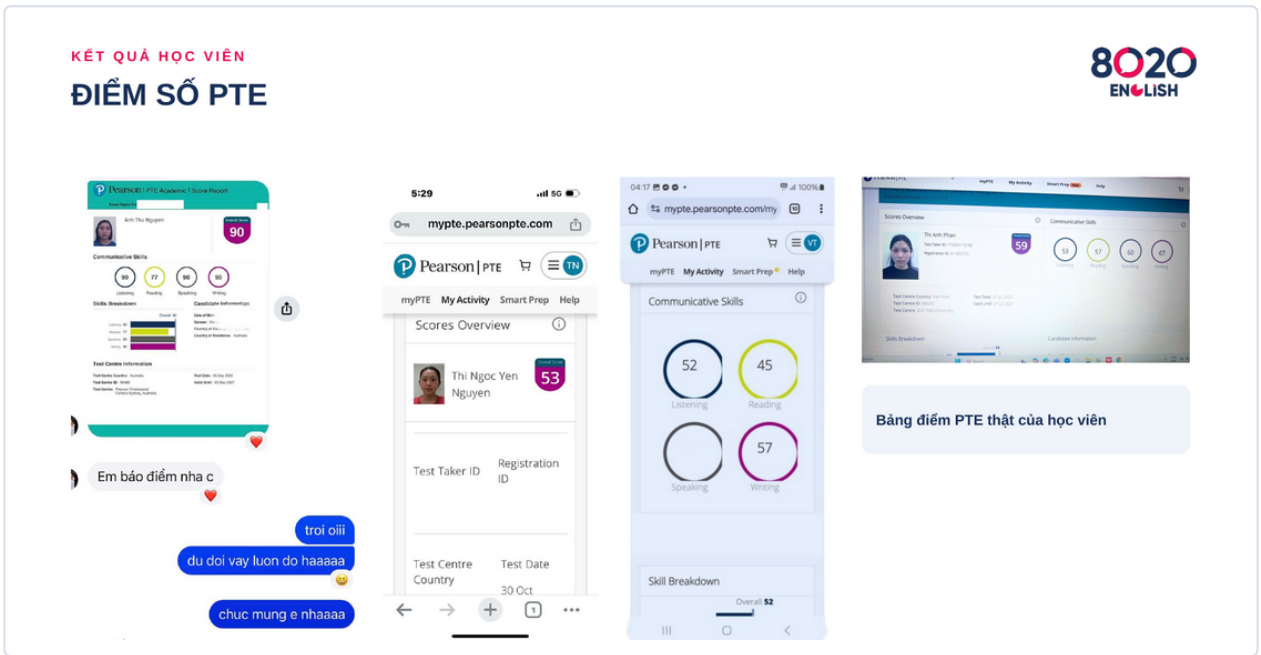


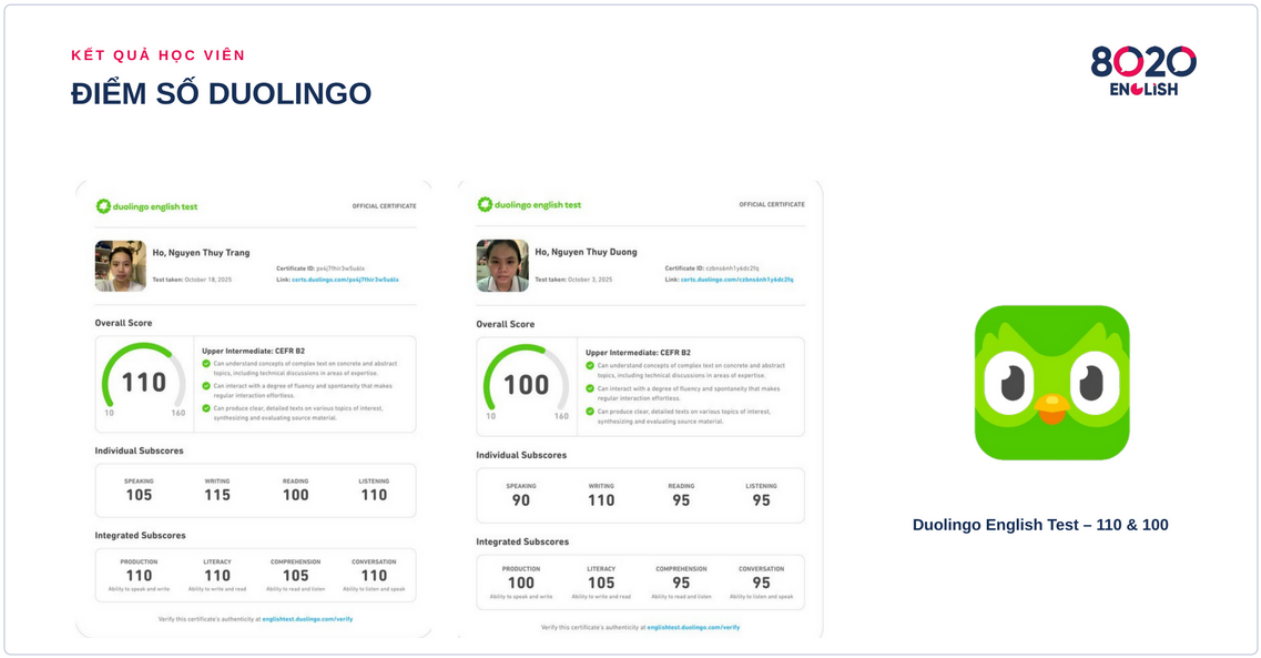
Bảng vàng SAT — Học viên đạt 1510 · 1520 · 1530



Học viên 8020 — SAT 1550 & 1570 (College Board)



Học viên 8020 — PTE Academic 90



Học viên 8020 — Duolingo English Test 110 & 100

Mục lục · Contents

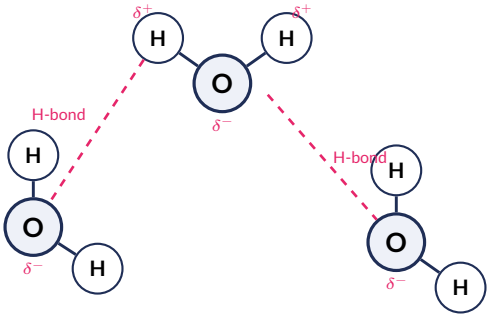
Theme A: Unity and Diversity

Mục tiêu Unit: Sau khi hoàn thành Theme A, học sinh có thể: giải thích tính phân cực và các tính chất đặc biệt của nước (liên kết hydro, sức căng bề mặt, mao dẫn, nhiệt dung riêng cao, nhiệt hoá hơi cao, băng nổi, tính dung môi vạn năng) và vai trò của nước như môi trường cho phản ứng chuyển hoá và vận chuyển trong cơ thể sống; mô tả cấu trúc nucleotide, phân biệt DNA với RNA, áp dụng nguyên tắc bắt cặp base bổ sung và quy tắc Chargaff, hiểu tính định hướng $5' \rightarrow 3'$; trình bày các giả thuyết về nguồn gốc sự sống và tế bào (hình thành túi màng từ phân tử lưỡng tính, giả thuyết thế giới RNA, bằng chứng về tổ tiên chung, thuyết nội cộng sinh về ty thể và lục lạp); phát biểu học thuyết tế bào và các ngoại lệ của nó; so sánh cấu trúc — kích thước tế bào nhân sơ và nhân thực, mô tả cấu tạo tế bào động vật, thực vật và vi khuẩn; tính toán độ phóng đại kính hiển vi và chuyển đổi đơn vị đo (mm, µm, nm); phân tích cấu trúc virus, phân biệt chu trình tan và chu trình tiềm tan, giải thích vì sao virus không được xem là sinh vật sống và cơ chế tiến hoá nhanh của virus (biến đổi kháng nguyên); áp dụng danh pháp hai từ La-tinh, khái niệm loài và hệ thống ba vực; xây dựng và diễn giải khoá phân loại lưỡng phân cùng cây phát sinh chủng loại dựa trên bằng chứng phân tử; giải thích cơ chế chọn lọc tự nhiên, hai kiểu hình thành loài (dị vực và đồng vực), bức xạ thích nghi; và phân tích tính đa dạng sinh học, bao gồm cách tính chỉ số đa dạng Simpson, các chiến lược bảo tồn tại chỗ và chuyển vị trí, cùng hệ thống phân hạng của IUCN.

1.1 A1 Molecules: Water and Nucleic Acids

1.1.1 A1.1 Water

Polarity and hydrogen bonding. A water molecule, H_2O, consists of one oxygen atom covalently bonded to two hydrogen atoms at a bond angle of approximately $104.5°$. Oxygen is considerably more electronegative than hydrogen, so the shared electrons in each O–H bond are pulled closer to the oxygen nucleus. This produces a **polar molecule**: the oxygen atom carries a partial negative charge (δ^-) and each hydrogen atom carries a partial positive charge (δ^+). Because the molecule is bent rather than linear, these partial charges do not cancel out, giving water a permanent dipole. The δ^+ hydrogen of one water molecule is weakly attracted to the δ^- oxygen of a neighboring molecule, forming a **hydrogen bond** — a weak, non-covalent interaction that is individually far weaker than a covalent bond, but immensely important collectively because each water molecule can form up to four hydrogen bonds at once (two donated through its hydrogens, two accepted through the lone pairs on oxygen). This extensive, constantly re-forming hydrogen-bonded network is the single underlying cause of nearly every distinctive property of water described below.



Three water molecules linked by hydrogen bonds (dashed). Each δ^+ hydrogen of one molecule is attracted to a δ^- oxygen lone pair of a neighbor; in liquid water each molecule hydrogen-bonds to about four neighbors on average, and

the bonds continuously break and re-form.

VN **GIẢI THÍCH TIẾNG VIỆT**

Phân tử nước có dạng hình chữ V (góc liên kết $\approx 104.5^\circ$). Vì oxy có độ âm điện lớn hơn hydro nên cặp electron dùng chung bị lệch về phía oxy, tạo ra **điện tích một phần**: oxy mang δ^-, mỗi hydro mang δ^+. Do phân tử không đối xứng thẳng hàng nên các điện tích này không triệt tiêu — nước là phân tử **phân cực**. **Liên kết hydro** hình thành giữa H mang δ^+ của phân tử này với O mang δ^- của phân tử bên cạnh; mỗi phân tử nước có thể tạo tối đa 4 liên kết hydro cùng lúc. Mạng lưới liên kết hydro rộng lớn, liên tục đứt gãy và tái tạo này là nguồn gốc của toàn bộ các tính chất đặc biệt của nước.

Cohesion, adhesion, capillary action, and surface tension. Hydrogen bonds hold water molecules to one another — this mutual attraction between like molecules is **cohesion**, and it is responsible for the unbroken columns of water that can be pulled continuously upward through the narrow vessels of plant xylem as water evaporates from the leaves. Water molecules also hydrogen-bond to other polar surfaces, such as the cellulose walls of a xylem vessel; attraction between unlike substances is **adhesion**. Acting together, cohesion and adhesion allow water to rise against gravity in narrow tubes, a phenomenon called **capillary action**. At the boundary between liquid water and air, surface molecules are pulled inward and sideways by their neighbors (with no water molecules above them to balance the pull), creating an elastic, film-like **surface tension** strong enough to support small, dense objects such as a water strider's legs or a carefully placed steel paperclip.

VN **GIẢI THÍCH TIẾNG VIỆT**

Cố kết (cohesion): nước hút nước (liên kết hydro giữa các phân tử nước với nhau) — giúp cột nước trong mạch gỗ (xylem) không bị đứt gãy khi bị kéo lên cao. **Bám dính (adhesion)**: nước hút bề mặt phân cực khác (ví dụ thành cellulose của mạch gỗ). Kết hợp cả hai tạo ra **hiện tượng mao dẫn (capillary action)** — nước dâng lên trong ống hẹp ngược chiều trọng lực. **Sức căng bề mặt (surface tension)** là hệ quả của cố kết tại bề mặt tiếp xúc nước–không khí, đủ mạnh để nâng đỡ những vật nhỏ, nhẹ như chân của loài nhện nước.

High specific heat capacity and high latent heat of vaporization. Raising the temperature of liquid water requires breaking a large number of hydrogen bonds before the added thermal energy can go into increasing the kinetic energy (temperature) of the molecules; correspondingly, cooling water releases a large amount of energy as those bonds re-form. Water's **specific heat capacity** (about 4.18 J/(g $\cdot^\circ$ C)) is unusually high compared to most other common liquids, so large bodies of water — and the water inside living organisms — resist rapid temperature change, buffering the internal and external thermal environment of life. The same hydrogen-bond network gives water an unusually high **latent heat of vaporization**: converting liquid water to vapor requires breaking essentially *all* the hydrogen bonds holding a molecule to its neighbors, which demands a very large energy input (roughly 2260 J/g at 100°C, and even more, about 2400–2450 J/g, at body-surface temperature, since molecules starting with less thermal energy require proportionally more added heat to escape the liquid). This is why evaporative cooling — sweating in mammals, panting in birds and reptiles, transpiration in plants — is such an effective way to lose heat: a comparatively small mass of evaporated water removes a very large quantity of heat energy from the body.

Ví dụ mẫu · Evaporative cooling and latent heat

During a marathon, a runner loses 1.5 L of sweat (density ≈ 1 g/mL, so mass ≈ 1500 g), essentially all of which evaporates from the skin. Using a latent heat of vaporization for water at body-surface temperature of $L \approx 2430$ J/g, calculate the total heat energy removed from the runner's body by evaporative cooling.

Apply $q = mL$:

$$q = (1500\ \text{g})(2430\ \text{J/g}) = 3\,645\,000\ \text{J} \approx 3.6 \times 10^6\ \text{J}\ (\approx 3.6\ \text{MJ}).$$

This is a substantial quantity of heat (equivalent to roughly 870 kcal) removed purely by the phase change of water from liquid to vapor — illustrating why evaporative cooling is metabolically "cheap" compared to other cooling mechanisms and why dehydration (running out of water to sweat) severely compromises an athlete's ability to thermoregulate.

VN **GIẢI THÍCH TIẾNG VIỆT**

Vì phần lớn nhiệt năng đưa vào nước bị dùng để **bẻ gãy liên kết hydro** thay vì làm tăng nhiệt độ, nước có **nhiệt dung riêng cao** (4.18 J/(g $\cdot^\circ$ C)) — cơ thể sống và các vực nước lớn nhờ đó ổn định nhiệt độ tốt hơn. Tương tự, để bốc hơi (chuyển từ lỏng sang khí), gần như toàn bộ liên kết hydro giữ một phân tử với các phân tử lân cận phải bị phá vỡ, đòi hỏi năng lượng rất lớn — đây là **nhiệt hoá hơi cao** của nước, và là lý do vì sao đổ mồ hôi, thở hổn hển, hay thoát hơi nước ở thực vật đều là cơ chế làm mát hiệu quả: chỉ cần bốc hơi một lượng nước nhỏ đã lấy đi một lượng nhiệt rất lớn khỏi cơ thể.

Ice is less dense than liquid water. In ice, each water molecule is locked into exactly four hydrogen bonds arranged in a rigid, open hexagonal lattice. This crystal structure holds molecules farther apart, on average, than in liquid water, where hydrogen bonds are constantly breaking and re-forming and molecules can pack more closely and randomly. As a result, ice is about 9% less dense than liquid water and floats. This is biologically critical: a layer of floating ice insulates the liquid water beneath it, allowing aquatic organisms to survive through winter instead of a pond or lake freezing solid from the bottom up.

(!) Lỗi thường gặp: Học sinh thường mặc định "chất rắn luôn đặc hơn chất lỏng cùng loại" — điều này *sai* với nước. Trong nước đá, mỗi phân tử bị khoá cố định trong đúng **4** liên kết hydro, tạo mạng tinh thể lục giác cồng kềnh khiến các phân tử cách xa nhau hơn so với nước lỏng (nơi liên kết hydro liên tục đứt và tái tạo, cho phép các phân tử xếp gần nhau hơn tại một thời điểm bất kỳ). Vì vậy băng *nổi* trên nước lỏng — một ngoại lệ quan trọng, không phải một lỗi ghi nhớ.

Water as a solvent, and as a medium for metabolism and transport. Water's polarity allows it to surround and dissolve other polar or ionic substances, forming hydration shells around ions (e.g., Na^+, Cl^-) and polar molecules (e.g., glucose, amino acids). Substances that dissolve readily in water because they are polar or charged are described as **hydrophilic** ("water-loving"); nonpolar substances such as fats and oils, which cannot form favorable hydrogen bonds with water and are excluded from the hydrogen-bonded network, are **hydrophobic** ("water-fearing"). Because it is such a versatile solvent, water is the medium in which the overwhelming majority of biochemical reactions of metabolism take place: enzymes, substrates, and products are typically dissolved or suspended in the aqueous cytosol or extracellular fluid, and reactions such as hydrolysis directly consume a water molecule as a reactant. Water is equally central to **transport**: it is the solvent of blood plasma, lymph, and the cytosol, and the medium through which xylem and phloem move dissolved substances through plants; its cohesive and adhesive properties directly enable long-distance transport of water and minerals through plants via the transpiration stream.

Water's key emergent properties (all traceable to hydrogen bonding): cohesion & adhesion → capillary action; surface tension; high specific heat capacity (thermal buffering); high latent heat of vaporization (evaporative cooling); lower density of ice than liquid water (floating ice insulates); versatile solvent for polar/ionic (hydrophilic) substances, medium for metabolism and transport.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tính **phân cực** của nước cho phép nó bao quanh và hoà tan các chất phân cực hoặc mang điện tích (ion), tạo thành **dung môi vạn năng**. Chất tan tốt trong nước gọi là **ưa nước (hydrophilic)**; chất không phân cực (như chất béo) không hoà tan được gọi là **kỵ nước (hydrophobic)**. Vì hầu hết phản ứng chuyển hoá trong tế bào xảy ra trong môi trường nước (bào tương, dịch ngoại bào), và vì tính cố kết/bám dính của nước cho phép vận chuyển đường dài qua mạch gỗ ở thực vật, nước không chỉ là "thành phần" mà còn là **môi trường thiết yếu** cho cả chuyển hoá lẫn vận chuyển trong cơ thể sống.

1.1.2 A1.2 Nucleic Acids

Nucleotide structure. Nucleic acids — DNA and RNA — are polymers built from repeating monomers called **nucleotides**. Every nucleotide has three components: (1) a five-carbon (**pentose**) sugar, (2) a **phosphate group** attached to the sugar's $5'$ carbon, and (3) a nitrogen-containing **nitrogenous base** attached to the sugar's $1'$ carbon. Nitrogenous bases fall into two structural families based on ring number: **purines** — **adenine (A)** and **guanine (G)** — have a double-ring structure, while **pyrimidines** — **cytosine (C)**, **thymine (T)**, and **uracil (U)** — have a single-ring structure.

Feature	DNA	RNA
Pentose sugar	Deoxyribose (no $-$OH at the $2'$ carbon)	Ribose (has $-$OH at the $2'$ carbon)
Nitrogenous bases	A, T, G, C	A, U, G, C (uracil replaces thymine)
Strandedness	Almost always double-stranded (double helix)	Almost always single-stranded (often folds back on itself)
Chemical stability	More stable — lacks reactive $2'$-OH	Less stable — the $2'$-OH makes RNA more chemically reactive and prone to hydrolysis
Primary biological role	Long-term, stable storage of genetic information	Diverse: carries genetic messages (mRNA), assembles proteins (tRNA, rRNA), catalysis, gene regulation

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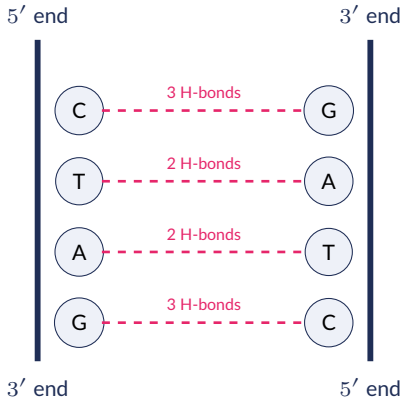
Nucleotide gồm 3 thành phần: **đường pentose**, **nhóm phosphate**, và **base nitơ**. Base nitơ chia thành **purine** (vòng đôi: Adenine A, Guanine G) và **pyrimidine** (vòng đơn: Cytosine C, Thymine T, Uracil U). DNA dùng đường **deoxyribose** (thiếu $-$OH ở carbon $2'$) và base T; RNA dùng đường **ribose** (có $-$OH ở $2'$) và base U thay cho T. Nhóm $-$OH ở vị trí $2'$ khiến RNA kém bền hoá học hơn DNA — đây là lý do DNA phù hợp để **lưu trữ lâu dài** thông tin di truyền, còn RNA linh hoạt hơn cho các vai trò tạm thời (truyền tin, tổng hợp protein).

Phosphodiester bonds, directionality, and the antiparallel double helix. Successive nucleotides within a single strand are joined by **phosphodiester bonds**: the phosphate group attached to one nucleotide's $5'$ carbon bonds to the free $3'$-hydroxyl of the sugar on the next nucleotide. This creates a repeating sugar–phosphate **backbone** with bases projecting out to the side, and it gives every

single strand an inherent chemical direction: one end has a free phosphate on the $5'$ carbon (the "$5'$ end"), the other has a free hydroxyl on the $3'$ carbon (the "$3'$ end"). In double-stranded DNA, two complementary strands wind around each other into a **double helix**, running **antiparallel** to one another — one strand $5' \to 3'$, the other $3' \to 5'$ — held together by hydrogen bonds between bases on opposite strands, following strict **Watson–Crick complementary base-pairing** rules: **adenine pairs with thymine** (A–T, or A–U in RNA) via **2** hydrogen bonds, and **guanine pairs with cytosine** (G–C) via **3** hydrogen bonds. Because a purine always pairs with a pyrimidine, the double helix has a uniform width along its entire length. This strict complementarity underlies **Chargaff's rule**: in any sample of double-stranded DNA, $\%\text{A} = \%\text{T}$ and $\%\text{G} = \%\text{C}$ — and therefore total purines always equal total pyrimidines — regardless of the species the DNA came from.



Schematic antiparallel DNA double helix, drawn as a ladder: the two sugar–phosphate backbones run in opposite $5' \to 3'$ directions. A pairs with T via 2 hydrogen bonds; G pairs with C via 3 hydrogen bonds — so G–C-rich DNA is more thermally stable (higher melting temperature) than A–T-rich DNA.

Base pairing: A–T (or A–U in RNA), 2 hydrogen bonds; G–C, 3 hydrogen bonds. **Chargaff's rule:** in double-stranded DNA, $\%\text{A} = \%\text{T}$ and $\%\text{G} = \%\text{C}$, so purines $=$ pyrimidines overall. **Directionality:** every strand runs $5' \to 3'$; the two strands of a double helix are always antiparallel.

Ví dụ mẫu · Applying Chargaff's rule

A sample of double-stranded viral DNA is analyzed and found to be 34% guanine. (a) Find the percentage of each of the other three bases. (b) State the ratio of total purines to total pyrimidines.

(a) By Chargaff's rule, $\%\text{C} = \%\text{G} = 34\%$. The two remaining bases (A and T) together make up $100\% - 34\% - 34\% = 32\%$ of all bases; since $\%\text{A} = \%\text{T}$ by Chargaff's rule, each is $32\% \div 2 = 16\%$. So $\%\text{A} = 16\%$, $\%\text{T} = 16\%$, $\%\text{C} = 34\%$.

(b) Purines $= \%\text{A} + \%\text{G} = 16\% + 34\% = 50\%$. Pyrimidines $= \%\text{T} + \%\text{C} = 16\% + 34\% = 50\%$. The ratio is **1 : 1** — as expected, since every purine on one strand pairs with exactly one pyrimidine on the other strand, this $1:1$ ratio holds for *any* double-stranded DNA sample, regardless of its overall base composition.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hai mạch DNA chạy **ngược chiều nhau (antiparallel)**: một mạch $5' \to 3'$, mạch còn lại $3' \to 5'$, nối với nhau qua **liên kết phosphodiester** giữa phosphate ở carbon $5'$ của nucleotide này với $-\text{OH}$ ở carbon $3'$ của nucleotide kế tiếp. Base bắt cặp bổ sung: **A–T** (2 liên kết hydro), **G–C** (3 liên kết hydro) — luôn là purine bắt cặp với pyrimidine nên chuỗi xoắn kép có bề rộng đồng nhất. **Quy tắc Chargaff**: $\%\text{A} = \%\text{T}$ và $\%\text{G} = \%\text{C}$ ở mọi loài — vùng DNA giàu G–C có nhiều

liên kết hydro hơn trên mỗi đơn vị chiều dài nên bền nhiệt hơn vùng giàu A–T.

Ví dụ mẫu · Reconstructing a complementary DNA strand

A short single strand of DNA has the sequence $5'$-ATGCCGTACGGT-$3'$. (a) Write the sequence of its complementary strand, showing correct antiparallel directionality. (b) Calculate the %GC content of the original strand. (c) State the %GC content of the complementary strand, and explain your reasoning without repeating the full calculation. (d) Calculate the total number of hydrogen bonds holding this 12-base-pair double-stranded segment together.

(a) Pair each base with its complement (A↔T, G↔C), remembering the second strand runs in the opposite direction:

$$5'\text{-A T G C C G T A C G G T-}3'$$
$$3'\text{-T A C G G C A T G C C A-}5'$$

Written conventionally in the standard $5' \to 3'$ direction, the complementary strand is $5'$-ACCGTACGGCAT-$3'$.

(b) Count bases in the original strand (A, T, G, C, C, G, T, A, C, G, G, T): A$= 2$, T$= 3$, G$= 4$, C$= 3$, total $= 12$. $\%\text{GC} = \dfrac{G + C}{\text{total}} \times 100\% = \dfrac{4 + 3}{12} \times 100\% \approx 58.3\%$.

(c) The complementary strand also has $\%\text{GC} \approx 58.3\%$. Every G on the original strand pairs with a C on the complementary strand, and every C pairs with a G, so the *total* count of G's plus C's is identical on both strands (only *which* base, G or C, sits at each position swaps) — %GC content is therefore always equal on both strands of any double-stranded DNA molecule, exactly as Chargaff's rule requires.

(d) Each base pair contributes 2 hydrogen bonds if it is an A–T pair, or 3 if it is a G–C pair. In the original strand, A and T together occur at $2 + 3 = 5$ positions (each an A–T pair), and G and C together occur at $4 + 3 = 7$ positions (each a G–C pair). Total hydrogen bonds $= (5 \times 2) + (7 \times 3) = 10 + 21 = \mathbf{31}$.

VN **GIẢI THÍCH TIẾNG VIỆT**

Để xây dựng mạch bổ sung: ghép từng base theo quy tắc A↔T, G↔C, sau đó viết mạch mới theo chiều $5' \to 3'$ (ngược hướng với mạch gốc). %GC được tính bằng $\dfrac{\text{số G} + \text{số C}}{\text{tổng số base}} \times 100\%$ — và luôn **bằng nhau** ở cả hai mạch của một phân tử DNA mạch đôi, vì mỗi G ở mạch này ứng với một C ở mạch kia. Tổng số liên kết hydro của cả đoạn có thể tính bằng cách đếm số cặp A–T (mỗi cặp 2 liên kết) và số cặp G–C (mỗi cặp 3 liên kết) rồi cộng lại.

Ví dụ mẫu · Chargaff's rule with a base ratio

A double-stranded DNA sample is analyzed, and the ratio of adenine to guanine is found to be $1 : 3$. Determine the percentage of each of the four bases, and confirm that purines equal pyrimidines overall.

Set up variables. Let $\%\text{A} = x$. Since the ratio of A to G is $1 : 3$, $\%\text{G} = 3x$. By Chargaff's rule, $\%\text{T} = \%\text{A} = x$ and $\%\text{C} = \%\text{G} = 3x$.

Solve. All four percentages must sum to 100%:

$$x + x + 3x + 3x = 100\% \;\Rightarrow\; 8x = 100\% \;\Rightarrow\; x = 12.5\%.$$

So $\%\text{A} = 12.5\%$, $\%\text{T} = 12.5\%$, $\%\text{G} = 37.5\%$, $\%\text{C} = 37.5\%$.

Check. Purines $= \%\text{A} + \%\text{G} = 12.5\% + 37.5\% = 50\%$; pyrimidines $= \%\text{T} + \%\text{C} = 12.5\% + 37.5\% = 50\%$ — the $1:1$ purine-to-pyrimidine ratio holds exactly, as it must for any double-stranded DNA sample regardless of its overall base composition.

VN **GIẢI THÍCH TIẾNG VIỆT**

Khi đề bài cho **tỉ lệ** giữa hai base thay vì phần trăm trực tiếp (ví dụ A:G $= 1:3$), hãy đặt ẩn cho một base ($\%\text{A} = x$), suy ra base còn lại theo tỉ lệ ($\%\text{G} = 3x$), rồi áp dụng quy tắc Chargaff để suy ra $\%\text{T} = \%\text{A} = x$ và $\%\text{C} = \%\text{G} = 3x$. Vì tổng bốn base luôn bằng 100%, ta lập phương trình $8x = 100\%$ để giải ra x. Luôn kiểm tra lại bằng cách tính tổng purine và tổng pyrimidine — hai giá trị này phải bằng nhau (50%–50%) ở bất kỳ mẫu DNA mạch đôi nào.

DNA as the universal information molecule. With only trivial, well-documented exceptions, every known living organism — from bacteria to humans — stores its heritable genetic information in DNA and uses essentially the same genetic code (the correspondence between nucleotide triplets and amino acids) to translate that information into proteins. This universality is one of the strongest pieces of evidence for the common ancestry of all life, and it is also what makes modern biotechnology possible: a gene taken from one species can be inserted into, and correctly read by, the completely different molecular machinery of another species (as in the bacterial production of human insulin). DNA's stability — a direct consequence of its double-stranded, deoxyribose-based structure lacking the reactive $2'$-OH of RNA — makes it well suited to serve as a durable, faithfully-copyable long-term information store, while RNA's structural versatility and greater reactivity suit its more transient roles in reading out and acting on that information.

(!) Lỗi thường gặp: Hai lỗi thường gặp khi so sánh DNA và RNA: (1) nhầm đường — DNA dùng **deoxyribose** (không có $-$OH ở $2'$), RNA dùng **ribose** (có $-$OH ở $2'$) — chính nhóm $-$OH này khiến RNA kém bền hơn về mặt hoá học; (2) nhầm base — RNA có **uracil (U)** thay cho **thymine (T)**, còn ba base A, G, C giống nhau ở cả hai loại. Ngoài ra, đừng nhầm "ít bền hơn" với "kém quan trọng hơn" — chính sự linh hoạt và kém bền của RNA lại phù hợp với vai trò tạm thời của nó trong biểu hiện gene.

1.2 A2 Cells: Origins, Structure and Viruses

1.2.1 A2.1 Origins of Cells

HIGHER LEVEL (HL) ONLY

Prebiotic chemistry and the formation of protocells. Under the conditions thought to have existed on early Earth — an atmosphere very different from today's, with sources of energy such as lightning, ultraviolet radiation, and volcanic heat — simple organic monomers (amino acids, simple sugars, nucleotide bases) could plausibly have formed spontaneously from inorganic precursor molecules through purely chemical processes, without the involvement of any pre-existing life. A separate but equally essential step was the enclosure of such molecules inside a boundary that could concentrate them and separate an internal chemical environment from the surroundings. **Amphipathic molecules** — molecules with both a hydrophilic and a hydrophobic region, similar to phospholipids — spontaneously self-assemble into hollow spherical **vesicles** when mixed with water, because this arrangement lets hydrophobic tails cluster away from water while hydrophilic heads face the surrounding water on both sides. Such self-assembling vesicles are proposed as a plausible chemical precursor to the plasma membrane, producing simple "protocells": bounded compartments capable of concentrating and protecting prebiotic reactions from the wider environment.

VN **GIẢI THÍCH TIẾNG VIỆT**

Trong điều kiện Trái Đất nguyên thuỷ (khí quyển khác ngày nay, có sẵn năng lượng từ sét, tia UV, núi lửa), các phân tử hữu cơ đơn giản (amino acid, đường đơn, base nitơ) có thể hình thành một cách tự phát từ các chất vô cơ mà không cần sự sống có sẵn. Các phân tử **lưỡng tính (amphipathic)** — vừa có phần ưa nước vừa có phần kỵ nước — khi gặp nước sẽ tự sắp xếp thành các **túi màng (vesicle)** hình cầu rỗng, tương tự cách phospholipid tạo lớp kép. Đây được xem là bước hoá học tiền thân hợp lý của màng sinh chất, tạo ra "tế bào nguyên thuỷ" — những khoang kín đầu tiên có thể cô đặc và bảo vệ các phản ứng hoá học tiền sinh học khỏi môi trường xung quanh.

The RNA world hypothesis. A central puzzle in origin-of-life chemistry is the "chicken-and-egg" problem: modern cells use DNA to store information and proteins (enzymes) to catalyze reactions, but replicating DNA requires protein enzymes, while building proteins requires information encoded in DNA (via RNA). The **RNA world hypothesis** proposes a solution: RNA molecules can act as *both* a carrier of genetic information (like DNA) *and* a catalyst of chemical reactions (like an enzyme). Catalytic RNA molecules are called **ribozymes**; a compelling piece of supporting evidence is that the ribosome itself — the molecular machine that builds every protein in every living cell — uses ribosomal RNA (rRNA), not a protein, to catalyze the formation of the peptide bond. If early self-replicating systems relied on RNA alone to both store information and catalyze its own replication, this would remove the need for the two functions to have evolved separately and simultaneously, and would explain why RNA sits at the functional center of the machinery (transcription, translation) that still links DNA and protein in every living cell today.

VN **GIẢI THÍCH TIẾNG VIỆT**

Giả thuyết thế giới RNA giải quyết nghịch lý "con gà và quả trứng": DNA cần enzyme protein để sao chép, còn protein cần thông tin di truyền để tổng hợp — vậy cái nào có trước? Giả thuyết cho rằng RNA từng đóng cả hai vai trò cùng lúc: vừa **lưu trữ thông tin** (như DNA) vừa **xúc tác phản ứng** (như enzyme, gọi là **ribozyme**). Bằng chứng thuyết phục: ribosome — bộ máy tổng hợp protein của mọi tế bào sống — dùng chính rRNA (không phải protein) để xúc tác hình thành liên kết peptide, cho thấy RNA vẫn giữ vai trò trung tâm trong bộ máy di truyền hiện đại.

Evidence for a single common origin of life. Several deep, universal features shared by essentially all known living organisms are best explained by descent from a single common ancestral lineage (often called LUCA, the "last universal common ancestor"), rather than by life having originated independently many separate times: the **genetic code** is (with only minor, well-understood exceptions) identical across bacteria, archaea, and eukaryotes, so the same codon specifies the same amino acid almost universally; the same 20 amino acids are used to build proteins across all domains of life; DNA replication, transcription, and translation follow the same basic chemical logic in every organism; and a common set of core metabolic pathways (such as glycolysis) and the universal use of ATP as the immediate energy currency of the cell are shared broadly across life. The near-universality — rather than the arbitrary diversity one would expect from many independent chemical origins — is itself the evidence.

VN **GIẢI THÍCH TIẾNG VIỆT**

Sự sống ngày nay chia sẻ nhiều đặc điểm sâu sắc và **gần như phổ quát**: cùng một **mã di truyền** (bộ ba mã hoá cùng loại amino acid ở hầu hết mọi loài), cùng 20 loại amino acid tiêu chuẩn, cùng cơ chế sao chép — phiên mã — dịch mã, và cùng dùng **ATP** làm đơn vị năng lượng tức thời. Tính phổ quát này — thay vì sự đa dạng ngẫu nhiên ta mong đợi nếu sự sống hình thành độc lập nhiều lần — chính là bằng chứng mạnh mẽ cho **một tổ tiên chung duy nhất** của mọi sinh vật sống.

Endosymbiotic theory. Mitochondria (found in nearly all eukaryotic cells) and chloroplasts (found in plant and algal cells) are proposed to have originated as free-living prokaryotes that were engulfed by a larger host cell and, instead of being digested, survived and entered into a stable mutualistic relationship — the host provided protection and raw materials, while the engulfed prokaryote provided efficient ATP production (mitochondria) or photosynthesis (chloroplasts). Over evolutionary time this relationship became permanent and obligate, with the engulfed prokaryotes becoming true organelles. Multiple independent lines of structural and molecular evidence support this **endosymbiotic theory**.

Ví dụ mẫu · Weighing the evidence for endosymbiotic theory

The table below compares features of mitochondria with features of a typical free-living, aerobic bacterium. Explain how each observation supports the hypothesis that mitochondria originated as engulfed free-living prokaryotes.

Feature	Mitochondrion	Free-living bacterium
Membranes	Double membrane	Single plasma membrane
Genome	Small circular DNA, not associated with histones	Circular DNA, not associated with histones
Ribosomes	$70S$	$70S$
Division	Independent binary fission, on its own schedule	Binary fission
rRNA sequence	Most similar to alpha-proteobacteria	—

Double membrane: best explained if the inner membrane is the original plasma membrane of the engulfed bacterium, while the outer membrane is derived from the host cell's engulfing (phagocytic) vesicle membrane during the original engulfment event — a eukaryotic organelle built by simply folding in the host's own plasma membrane would be expected to have only one membrane, not two.

Circular, histone-free DNA and $70S$ ribosomes: these match bacterial genomes and bacterial ribosomes exactly, and are strikingly different from the eukaryotic host's own linear, histone-bound nuclear DNA and $80S$ cytoplasmic ribosomes — mitochondria have retained the genetic "fingerprint" of a bacterial ancestor rather than acquiring the host's own genome architecture.

Independent binary fission: mitochondria replicate on their own schedule by splitting in two, largely independently of when the host cell itself divides — consistent with having once been an independently-reproducing organism, not merely a folded piece of host membrane.

rRNA sequence similarity to alpha-proteobacteria: molecular sequence comparison directly pinpoints the specific bacterial lineage from which mitochondria are descended (chloroplasts show a corresponding similarity to cyanobacteria), providing the most direct, quantitative evidence of shared ancestry.

VN **GIẢI THÍCH TIẾNG VIỆT**

Thuyết nội cộng sinh (endosymbiotic theory) cho rằng ty thể và lục lạp từng là vi khuẩn sống tự do bị một tế bào lớn hơn "nuốt" vào nhưng không bị tiêu hoá, dần trở thành bào quan cố định qua quá trình cộng sinh. Bằng chứng: (1) **màng kép** — màng trong là màng sinh chất gốc của vi khuẩn, màng ngoài hình thành từ túi thực bào của tế bào chủ; (2) **DNA dạng vòng, không có histone** và **ribosome 70S** — giống vi khuẩn, khác hẳn DNA dạng thẳng có histone và ribosome 80S trong nhân/bào tương tế bào chủ; (3) **tự phân đôi độc lập**, không đồng bộ với chu kỳ tế bào chủ; (4) trình tự **rRNA** của ty thể giống vi khuẩn alpha-proteobacteria, của lục

lạp giống vi khuẩn lam (cyanobacteria).

1.2.2 A2.2 Cell Structure

Cell theory. The **cell theory** is one of the unifying principles of biology, stated in three parts: (1) all living organisms are composed of one or more cells; (2) the cell is the smallest unit of life — the basic structural and functional unit of every organism; (3) all cells arise only from pre-existing cells (*omnis cellula e cellula*), by cell division. Although overwhelmingly well-supported, a small number of biological structures are commonly cited as apparent exceptions worth understanding precisely: **striated (skeletal) muscle fibres** are long, multinucleate structures formed by the fusion of many individual muscle cell precursors (myoblasts) into one continuous fibre, so a single "fibre" does not correspond to one discrete cell in the usual sense; **aseptate fungal hyphae** (found in some fungal groups) are long tubular filaments containing many nuclei sharing one continuous cytoplasm, without the cross-walls (septa) that would divide them into separate cellular compartments; and **giant algae** such as *Acetabularia*, which can grow several centimetres long as a single cell containing one nucleus, stretch the intuitive notion that a "cell" must be microscopic.

Cell theory: (1) all organisms are made of cells; (2) the cell is the smallest unit of life; (3) all cells come from pre-existing cells. Recognized exceptions: striated muscle fibres (multinucleate, from fused myoblasts), aseptate fungal hyphae (multinucleate, no dividing septa), and giant algae (very large single cells, e.g. *Acetabularia*).

VN GIẢI THÍCH TIẾNG VIỆT

Học thuyết tế bào gồm 3 luận điểm: mọi sinh vật đều cấu tạo từ tế bào; tế bào là đơn vị nhỏ nhất của sự sống; mọi tế bào sinh ra từ tế bào có trước. Ba "ngoại lệ" thường gặp: **sợi cơ vân** (nhiều nhân, hình thành từ sự hợp nhất nhiều tế bào tiền thân — không phải một tế bào đơn lẻ theo đúng nghĩa); **sợi nấm không vách ngăn (aseptate hyphae)** (nhiều nhân chia sẻ chung một khối bào tương liên tục, không có vách ngăn giữa các "tế bào"); và **tảo khổng lồ** như *Acetabularia* (một tế bào đơn lẻ dài tới vài centimet, thách thức trực giác rằng tế bào phải rất nhỏ).

Prokaryotic versus eukaryotic cells. All cellular life is divided into two broad structural categories. **Prokaryotic cells** (bacteria and archaea) are small (typically 1–$5\ \mu$m), lack a membrane-bound nucleus (their DNA is a single circular chromosome condensed in a region called the **nucleoid**, not enclosed by a membrane), and lack membrane-bound organelles; they have $70S$ ribosomes and divide by binary fission. **Eukaryotic cells** (protists, fungi, plants, animals) are typically much larger (10–$100\ \mu$m), possess a true membrane-bound **nucleus** enclosing linear, histone-associated DNA, and contain a variety of membrane-bound organelles that compartmentalize different metabolic functions; they have larger $80S$ ribosomes (though their mitochondria and chloroplasts retain bacterial-type $70S$ ribosomes, consistent with endosymbiotic theory) and divide by mitosis or meiosis.

Feature	Prokaryotic cell	Eukaryotic cell
Typical size	1–$5\ \mu$m	10–$100\ \mu$m
Nucleus	Absent (DNA in nucleoid region)	Present, membrane-bound
DNA	Single circular chromosome, no histones	Multiple linear chromosomes, wound around histones
Membrane-bound organelles	Absent	Present (mitochondria, ER, Golgi, etc.)
Ribosomes	$70S$	$80S$ (cytoplasmic); $70S$ in mitochondria/chloroplasts
Cell division	Binary fission	Mitosis or meiosis
Examples	Bacteria, archaea	Protists, fungi, plants, animals

Ví dụ mẫu · Comparing prokaryotic and eukaryotic cell sizes

A typical bacterium (*E. coli*) has a diameter of about $1\ \mu$m; a typical eukaryotic cell has a diameter of about $20\ \mu$m. Approximating both as spheres, estimate how many bacteria-sized cells could fit, by volume, inside one eukaryotic-sized cell.

The volume of a sphere is $V = \frac{4}{3}\pi r^3$, which is proportional to the *cube* of the radius (or diameter). Taking the ratio of the two volumes, the constant $\frac{4}{3}\pi$ cancels:

$$\frac{V_{\text{eukaryotic}}}{V_{\text{prokaryotic}}} = \left(\frac{d_{\text{eukaryotic}}}{d_{\text{prokaryotic}}}\right)^3 = \left(\frac{20\ \mu\text{m}}{1\ \mu\text{m}}\right)^3 = 20^3 = 8000.$$

Despite the linear size difference looking modest (only 20-fold), the *volume* difference is roughly 8000**-fold**, because volume scales with the cube of linear dimension. This dramatic scaling is also central to why prokaryotic cells, being so much smaller, maintain a far higher surface-area-to-volume ratio than large eukaryotic cells — allowing efficient diffusion of nutrients and waste across the plasma membrane without requiring internal compartmentalization.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tế bào nhân sơ (**prokaryotic**, vi khuẩn/cổ khuẩn) nhỏ (1–$5\ \mu$m), không có nhân thật (DNA nằm ở vùng **nucleoid**, không có màng bao), không có bào quan có màng, ribosome $70S$. Tế bào nhân thực (**eukaryotic**) lớn hơn nhiều (10–$100\ \mu$m), có **nhân thật** (DNA dạng thẳng, cuộn quanh histone, có màng nhân bao bọc), có nhiều bào quan có màng, ribosome $80S$ (riêng ty thể/lục lạp vẫn giữ ribosome $70S$ — bằng chứng thuyết nội cộng sinh). Vì thể tích tỉ lệ với luỹ thừa 3 của kích thước dài, chênh lệch kích thước dù không lớn cũng dẫn đến chênh lệch thể tích rất lớn — đây là lý do tế bào nhân sơ có tỉ lệ diện tích bề mặt/thể tích cao, thuận lợi cho trao đổi chất qua khuếch tán trực tiếp.

Ví dụ mẫu · Surface area-to-volume ratio and the limit on cell size

Model a cell as a cube. For a cube of side length s, surface area $SA = 6s^2$ and volume $V = s^3$, so the surface-area-to-volume ratio is $SA : V = 6s^2/s^3 = 6/s$. Calculate the $SA : V$ ratio for a small cell with $s = 10\ \mu$m and a larger cell with $s = 20\ \mu$m, and explain the biological significance of the result.

Small cell ($s = 10\ \mu$m): $SA = 6(10)^2 = 600\ \mu\text{m}^2$; $V = (10)^3 = 1000\ \mu\text{m}^3$; $SA : V = 600/1000 =$ **0.6** $\square\text{m}^{-1}$ (matches $6/10 = 0.6$ directly).

Large cell ($s = 20\ \mu$m): $SA = 6(20)^2 = 2400\ \mu\text{m}^2$; $V = (20)^3 = 8000\ \mu\text{m}^3$; $SA : V = 2400/8000 =$ **0.3** $\square\text{m}^{-1}$ (matches $6/20 = 0.3$).

Significance. Doubling the linear size of a cell *halves* its surface-area-to-volume ratio, because volume (and therefore the cell's metabolic demand for nutrient uptake, waste removal, and gas exchange) grows with the *cube* of linear size, while the plasma membrane's surface area (the interface across which all that exchange must occur) grows only with the *square*. Past a certain size, the membrane surface simply cannot supply and remove material fast enough to service the volume inside by diffusion alone — a fundamental physical constraint on how large a single cell can become, and a key reason why large organisms are built from many small cells rather than one greatly enlarged cell.

Why cells are small: for a cell modeled as a simple solid, surface area scales with (linear size)^2 while volume scales with (linear size)^3. As a cell grows larger, its $SA : V$ ratio falls, so eventually the membrane surface cannot keep pace with the volume's metabolic demands by diffusion alone — this sets an upper limit on efficient single-cell size and explains why large multicellular organisms consist of many small cells (collectively providing far more total membrane surface area) rather than one large cell.

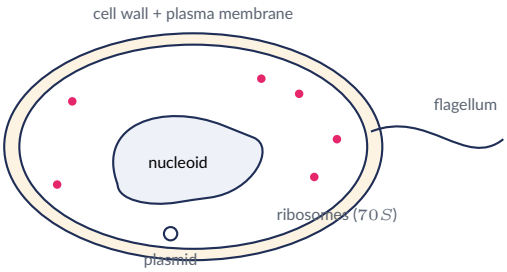
VN **GIẢI THÍCH TIẾNG VIỆT**

Xem tế bào như một khối lập phương cạnh s: diện tích bề mặt $SA = 6s^2$, thể tích $V = s^3$, nên tỉ lệ $SA : V = 6/s$. Khi kích thước dài tăng gấp đôi, tỉ lệ $SA : V$ giảm còn một nửa — vì thể tích (nhu cầu trao đổi chất) tăng theo luỹ thừa 3 trong khi diện tích bề mặt (nơi diễn ra trao đổi chất qua khuếch tán) chỉ tăng theo luỹ thừa 2. Đây là lý do vật lý cơ bản giới hạn kích thước tối đa của một tế bào đơn lẻ, và là lý do sinh vật lớn cấu tạo từ **nhiều tế bào nhỏ** thay vì một tế bào khổng lồ duy nhất.

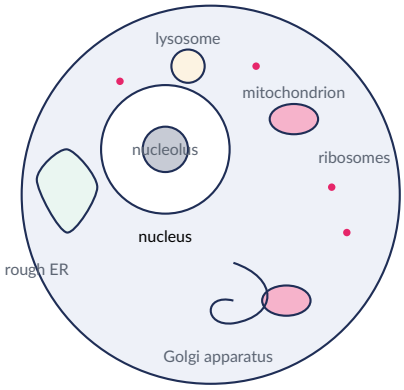
Generalized animal cell. A typical animal cell is enclosed by a **plasma membrane** and contains a membrane-bound **nucleus** (housing the linear chromosomes and a **nucleolus**, where ribosomal subunits are assembled), a network of **rough endoplasmic reticulum** (studded with ribosomes; folds and modifies proteins destined for secretion or membranes) continuous with **smooth endoplasmic reticulum** (synthesizes lipids, detoxifies harmful substances, stores calcium ions), a **Golgi apparatus** (further modifies, sorts, and packages proteins and lipids into vesicles for their final destinations), numerous **mitochondria** (generate ATP via aerobic cellular respiration), **lysosomes** (membrane-bound sacs of digestive enzymes that break down worn-out organelles and ingested material), free and membrane-bound **ribosomes** (sites of protein synthesis), a **cytoskeleton** of protein filaments (maintains cell shape, enables movement and intracellular transport), and **centrioles** (organize the mitotic spindle during cell division).

Generalized plant cell. A plant cell shares the core eukaryotic organelles above, but differs in several important respects: it is surrounded by a rigid **cell wall** made of cellulose, external to the plasma membrane, which provides structural support and limits cell expansion; it typically contains a single large **central vacuole**, which stores water, ions, and waste products and generates **turgor pressure** against the cell wall to keep the plant firm; it contains **chloroplasts**, the site of photosynthesis; and adjacent plant cells are connected through channels in their cell walls called **plasmodesmata**, which allow direct cytoplasmic communication between cells. Most plant cells lack centrioles.

Generalized prokaryotic (bacterial) cell. A typical bacterial cell has a **plasma membrane** surrounded by a rigid **cell wall** (built from peptidoglycan in most bacteria), enclosing **cytoplasm** in which the single circular chromosome is condensed into the **nucleoid** region (no membrane boundary); many bacteria also carry one or more small circular **plasmids**, extra-chromosomal DNA that can carry genes such as antibiotic resistance and can be exchanged between cells. Bacterial cytoplasm contains numerous $70S$ **ribosomes** but no membrane-bound organelles. Some bacteria have external structures: a **flagellum** (a rotating filament for motility, structurally distinct from a eukaryotic flagellum), **pili** (short hair-like projections used for attachment to surfaces or for DNA transfer during conjugation), and in some species a protective outer **capsule**.



Prokaryotic cell



Eukaryotic (animal) cell

Left: generalized prokaryotic cell — nucleoid (no membrane), $70S$ ribosomes, plasmid, cell wall, flagellum. Right: generalized eukaryotic (animal) cell — membrane-bound nucleus with nucleolus, mitochondria, rough ER, Golgi apparatus, lysosome, free ribosomes. A plant cell would add a cellulose cell wall, chloroplasts, a large central vacuole, and plasmodesmata.

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Tế bào động vật: có nhân (chứa nhân con — nơi lắp ráp ribosome), lưới nội chất hạt (tổng hợp/gấp protein), lưới nội chất trơn (tổng hợp lipid, khử độc), bộ máy Golgi (chỉnh sửa, đóng gói protein), ty thể (tạo ATP), lysosome (tiêu hoá nội bào), ribosome, khung xương tế bào, trung thể. **Tế bào thực vật** có thêm: vách tế bào cellulose, không bào trung tâm lớn (tạo áp suất trương nước — turgor), lục lạp (quang hợp), cầu sinh chất (plasmodesmata) nối các tế bào; thường không có trung thể. **Tế bào vi khuẩn**: màng sinh chất + vách tế bào (peptidoglycan), vùng nucleoid chứa DNA vòng (không có màng bao), ribosome $70S$, có thể có plasmid, tiêm mao (pili), roi (flagellum) và vỏ nang (capsule).

Microscopy: magnification and resolution. Two distinct concepts describe the performance of a microscope. **Magnification** is how many times larger an image appears compared to the actual size of the object — it is purely a matter of optical or digital enlargement. **Resolution** (resolving power) is the ability to distinguish two objects that are very close together as two separate points, rather than one single blur — it depends fundamentally on the wavelength of the radiation used to form the image, not simply on how much the image is enlarged. A **light microscope** uses visible light (wavelength ≈ 400–700 nm), giving a maximum resolution of about 200 nm (0.2 μm) and typical maximum useful magnification around $1500\times$; it can image living cells and preserves natural color, but cannot resolve structures smaller than roughly 200 nm (below this, simply zooming in further — increasing magnification without improving resolution — only produces a larger but no clearer, blurrier image; this is called **empty magnification**). An **electron microscope** uses a beam of electrons, whose much shorter effective wavelength gives vastly superior resolution — down to about 0.1–2 nm — and allows far higher useful magnifications, up to roughly $2\,000\,000\times$ for transmission electron microscopy (TEM); however, samples must typically be fixed, dehydrated, and often sectioned into extremely thin slices in a vacuum, killing the cell and introducing possible preparation artefacts, and images are inherently in grayscale (any color seen in electron micrographs is added artificially afterward).

(!) Lỗi thường gặp: Đừng đánh đồng **độ phóng đại (magnification)** với **độ phân giải (resolution)**. Độ phóng đại chỉ đơn thuần là ảnh được phóng to bao nhiêu lần; độ phân giải là khả năng *phân biệt* hai điểm rất gần nhau thành hai điểm riêng biệt, phụ thuộc vào bước sóng của bức xạ dùng để tạo ảnh. Phóng to một ảnh đã bị mờ (dưới giới hạn phân giải) chỉ tạo ra ảnh to hơn nhưng *không* rõ hơn — hiện tượng này gọi là **phóng đại rỗng (empty magnification)**. Kính hiển vi điện tử vượt trội kính hiển vi quang học chủ yếu vì *độ phân giải* cao hơn hẳn (do bước sóng electron ngắn hơn ánh sáng khả kiến rất nhiều), chứ không chỉ vì phóng to được nhiều hơn.

VN **GIẢI THÍCH TIẾNG VIỆT**

Độ phóng đại là ảnh được phóng to gấp bao nhiêu lần so với vật thật; **độ phân giải** là khả năng phân biệt hai điểm gần nhau thành hai điểm riêng biệt (phụ thuộc bước sóng). **Kính hiển vi quang học**: dùng ánh sáng khả kiến, độ phân giải ≈ 200 nm, phóng đại tối đa $\approx 1500\times$, quan sát được tế bào sống, giữ màu tự nhiên. **Kính hiển vi điện tử**: dùng chùm electron, độ phân giải cao hơn nhiều (0.1–2 nm), phóng đại tới hàng triệu lần, nhưng mẫu vật phải cố định, khử nước, cắt lát mỏng trong chân không — tế bào bị giết chết, ảnh chỉ có thang xám (màu sắc nếu có là tô thêm sau).

The magnification formula and unit conversions. Magnification, image size, and actual (real) size are related by a simple formula that can be rearranged to solve for any one of the three quantities given the other two:

$$\text{Magnification} = \frac{\text{Image size}}{\text{Actual size}} \quad \Longleftrightarrow \quad \text{Image size} = M \times A \quad \Longleftrightarrow \quad \text{Actual size} = \frac{I}{M}$$

Image size and actual size must be expressed in the *same* unit before dividing (magnification itself has no units). Useful conversions: 1 mm $= 1000$ μm $= 1\,000\,000$ nm; 1 μm $= 1000$ nm $= 10^{-3}$ mm; 1 nm $= 10^{-3}$ μm $= 10^{-6}$ mm.

Ví dụ mẫu · Magnification, image size, and actual size

An electron micrograph shows the image of a mitochondrion measuring 40 mm in length. If the micrograph was produced at a magnification of $\times 20\,000$, calculate the actual length of the mitochondrion in micrometres (μm).

Rearrange the magnification formula to solve for actual size: $A = \dfrac{I}{M}$.

Convert image size to a convenient unit first: $I = 40$ mm $= 40\,000$ μm.

$$A = \frac{I}{M} = \frac{40\,000\ \mu\text{m}}{20\,000} = 2\ \mu\text{m}.$$

The actual length of the mitochondrion is **2 □m** — consistent with the known typical size range of mitochondria (1–2 μm in length), which is a useful check on the arithmetic.

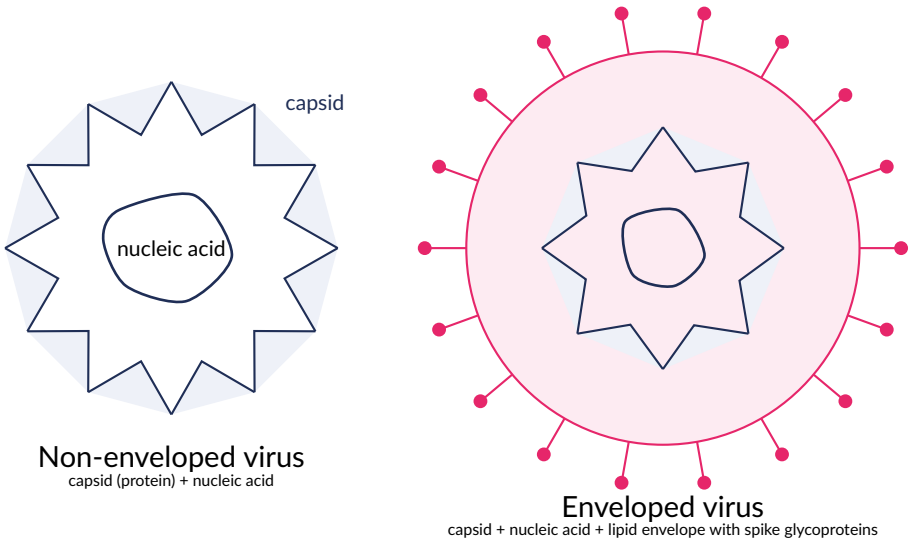
VN **GIẢI THÍCH TIẾNG VIỆT**

Công thức độ phóng đại: $M = I/A$ (Image/Actual), có thể biến đổi để tìm bất kỳ đại lượng nào trong ba đại lượng: kích thước ảnh I, kích thước thật A, và độ phóng đại M. **Lưu ý quan trọng**: I và A phải cùng đơn vị trước khi chia — đây là lỗi tính toán phổ biến nhất trong dạng bài này. Cần thuộc các quy đổi: 1 mm $= 1000$ μm $= 10^6$ nm.

1.2.3 A2.3 Viruses

HIGHER LEVEL (HL) ONLY

Virus structure. A **virus** is a small infectious particle consisting, at minimum, of a **nucleic acid genome** (DNA or RNA, which may be single- or double-stranded) enclosed within a protective protein coat called a **capsid**, built from repeating protein subunits. Many viruses — particularly those that infect animal cells, such as influenza, HIV, and SARS-CoV-2 — additionally acquire a lipid **envelope** derived from a membrane of the host cell as they exit it, studded with viral glycoproteins ("spikes") used to recognize and bind specific host-cell receptors. Non-enveloped ("naked") viruses, lacking this lipid coat, tend to be more resistant to drying, detergents, and environmental degradation.

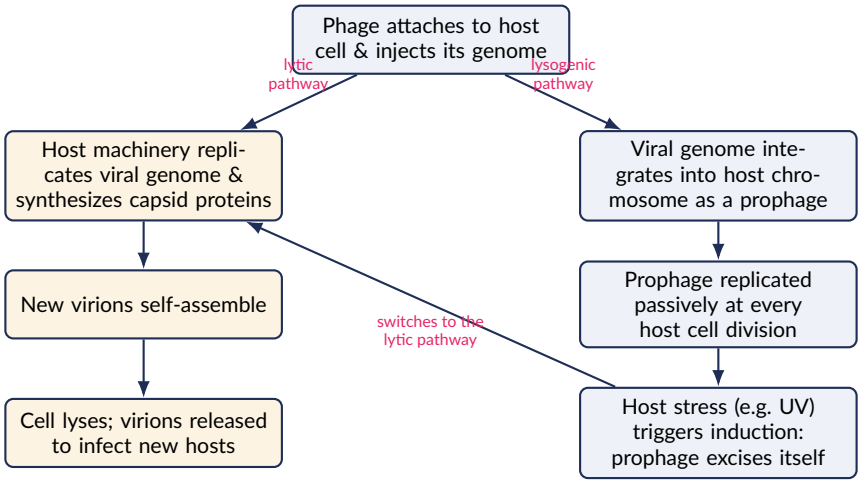


Left: a non-enveloped virus — nucleic acid genome enclosed directly by a protein capsid (e.g., many bacteriophages). Right: an enveloped virus (e.g., influenza, HIV, SARS-CoV-2) — the capsid is further wrapped in a lipid envelope studded with glycoprotein spikes used for host-receptor recognition.

VN **GIẢI THÍCH TIẾNG VIỆT**

Virus là một hạt lây nhiễm nhỏ gồm tối thiểu: **bộ gene acid nucleic** (DNA hoặc RNA, mạch đơn hoặc mạch đôi) được bao bọc bởi **vỏ capsid** (protein). Nhiều virus gây bệnh ở người (cúm, HIV, SARS-CoV-2) còn có thêm **lớp vỏ ngoài (envelope)** bằng lipid lấy từ màng tế bào chủ khi virus thoát ra, gắn các **gai glycoprotein** dùng để nhận diện và bám vào thụ thể đặc hiệu trên tế bào chủ. Virus không có vỏ ngoài thường bền hơn với môi trường bên ngoài (khô, chất tẩy rửa) so với virus có vỏ ngoài.

The lytic and lysogenic cycles. Because viruses have no ribosomes, no metabolic enzymes of their own, and no means of generating ATP, they are **obligate intracellular parasites**: they can only replicate by hijacking the molecular machinery of a living host cell. In the **lytic cycle**, a virus attaches to a host cell, injects (or is taken up with) its genetic material, and immediately redirects the host's own ribosomes, enzymes, and energy supply to replicate the viral genome and manufacture new capsid proteins; these self-assemble into many new virus particles, which are released by **lysis** — rupture and destruction of the host cell — to go on and infect further host cells. Some viruses (called **temperate** phages when they infect bacteria, e.g. **bacteriophage lambda**) can instead enter the **lysogenic cycle**: the viral genome integrates into the host chromosome as a **prophage**, where it is replicated passively along with the host's own DNA every time the host cell divides, without producing new viral particles or harming the host. A prophage can remain dormant for many host-cell generations, but environmental stress on the host (such as UV damage, starvation, or chemical damage to host DNA) can trigger **induction** — the prophage excises itself from the host chromosome and switches into the lytic cycle, producing new virions and lysing the cell.



The lytic cycle (left, amber) immediately replicates the viral genome, assembles new virions, and lyses the host cell. The lysogenic cycle (right, navy) instead integrates the viral genome as a dormant prophage, copied passively alongside the host's own DNA at every division, until host-cell stress triggers induction and a switch into the lytic pathway.

Ví dụ mẫu · Deciding between the lytic and lysogenic cycles

Bacteriophage lambda infects an *E. coli* population. Under favorable, nutrient-rich conditions, most infected cells enter lysogeny (the prophage is maintained silently); under conditions of severe host-cell stress (e.g., DNA-damaging UV exposure), lysogenic cells switch to the lytic cycle and are destroyed, releasing new phage particles.

(a) Name the two cycles described. (b) Explain why switching from lysogeny to the lytic cycle in response to host-cell stress is adaptive for the phage.

(a) Silent integration and passive replication with the host genome describes the **lysogenic cycle**; active replication, assembly of new virions, and host-cell destruction describes the **lytic cycle**.

(b) While the host is healthy and dividing normally, remaining lysogenic lets the phage genome be copied and passed on "for free" every time the host divides, spreading through the bacterial population at essentially no cost and without triggering any destructive immune or defensive response from the host. However, if the host cell is already badly damaged and likely to die regardless, continuing to wait would mean losing the viral genome along with the dying cell. Switching to the lytic cycle at that point lets the phage rapidly produce and release many new infectious particles before the host (and the prophage within it) is lost — maximizing the chance that at least some offspring virus particles find a new, healthy host. This flexible strategy — passive persistence when conditions are good, rapid reproduction and escape when conditions turn bad — is a form of evolutionary bet-hedging.

GIẢI THÍCH TIẾNG VIỆT

VN

Virus không có ribosome, enzyme chuyển hoá hay khả năng tạo ATP riêng — chúng là **ký sinh nội bào bắt buộc**, chỉ nhân lên được bằng cách chiếm dụng bộ máy của tế bào chủ. **Chu trình tan (lytic cycle)**: virus xâm nhập, chiếm quyền điều khiển tế bào chủ để nhân bản bộ gene và vỏ capsid, lắp ráp thành virus mới rồi phá huỷ (làm tan) tế bào chủ để giải phóng chúng. **Chu trình tiềm tan (lysogenic cycle)**: bộ gene virus (ví dụ thể thực khuẩn lambda) chèn vào nhiễm sắc thể tế bào chủ thành **prophage**, được sao chép thụ động theo mỗi lần tế bào chủ phân chia mà không gây hại; khi tế bào chủ bị stress (tia UV, tổn thương DNA), prophage có thể tách ra và chuyển sang chu trình tan.

Ví dụ mẫu · Exponential growth during a lytic infection

A bacteriophage has a **burst size** of 100 (lysis of one infected bacterium releases 100 new phage particles). Assume every released phage immediately and successfully infects a new bacterium, and that each infection-to-lysis cycle takes the same fixed amount of time. (a) Starting from a single infected bacterium, calculate the number of free phage particles released after 1, 2, and 3 complete lytic cycles. (b) Write a general formula for the number of phage particles after n cycles. (c) Explain why this pattern allows a lytic infection to overwhelm a host so quickly.

(a) Cycle 1: the single infected cell lyses, releasing 100 phage, each of which infects a new cell: 100 particles. Cycle 2: those 100 newly infected cells each lyse and release 100 phage: $100 \times 100 = 10\,000$ particles. Cycle 3: those $10\,000$ infected cells each release 100 phage: $10\,000 \times 100 = \mathbf{1\,000\,000}$ particles.

(b) After n complete cycles, starting from one infected cell: $N = 100^{n}$.

(c) Because each cycle multiplies the existing phage population by a constant factor (the burst size) rather than adding a fixed number, growth is **exponential**, not linear. Here, just 3 cycles turn a single infected cell into a million virus particles. This is why an unchecked lytic infection can progress from a handful of infected cells to overwhelming, tissue-wide viral loads within a very short time, and why interrupting replication even one cycle earlier (e.g., with an antiviral drug, or the host's early immune response) has a disproportionately large effect on the total number of virus particles produced.

VN **GIẢI THÍCH TIẾNG VIỆT**

Kích thước bùng nổ (burst size) là số hạt virus mới giải phóng ra khi một tế bào chủ bị tan. Vì mỗi chu kỳ nhân lên nhân số lượng virus hiện có lên gấp **burst size** lần (thay vì cộng thêm một số cố định), sự tăng trưởng có dạng **luỹ thừa (exponential)**: chỉ sau vài chu kỳ, số lượng virus có thể tăng lên hàng triệu lần từ một tế bào nhiễm ban đầu. Đây là lý do nhiễm virus theo chu trình tan có thể áp đảo vật chủ rất nhanh, và vì sao việc ngăn chặn virus nhân lên sớm (thuốc kháng virus, đáp ứng miễn dịch sớm) có tác động rất lớn đến tổng số lượng virus tạo ra về sau.

Examples of medically important viruses. **HIV** (human immunodeficiency virus) is an enveloped **retrovirus**: its genome is single-stranded RNA, which the virus's own enzyme **reverse transcriptase** copies into DNA once inside a host cell; this viral DNA then integrates into the genome of the host T-helper lymphocyte, from which new viral RNA and proteins are later produced, progressively destroying the immune system's helper T-cell population. **SARS-CoV-2** (the cause of COVID-19) is an enveloped virus with a single-stranded, positive-sense RNA genome; its surface **spike protein** binds specifically to the ACE2 receptor on human respiratory epithelial cells to gain entry. **Influenza virus** is an enveloped virus with a segmented, single-stranded, negative-sense RNA genome, carrying two key surface glycoproteins, **haemagglutinin (H)** (mediates attachment to host cells) and **neuraminidase (N)** (helps release newly-formed virus particles from the host cell surface) — the basis of strain names such as "H1N1."

Why viruses are not classified as living organisms. Viruses fail several of the criteria typically used to define life: they cannot reproduce independently (they possess no ribosomes or metabolic machinery of their own and are entirely dependent on hijacking a host cell's machinery to replicate); they carry out no independent metabolism (no respiration, no biosynthesis outside a host); they do not grow or maintain homeostasis as an individual particle; and outside a host cell, a virus particle is metabolically completely inert — it can persist for long periods as an essentially non-living particle, in stark contrast to the continuous metabolic activity of even the simplest living cell. Because they nonetheless carry genetic information, undergo mutation, and evolve, viruses occupy a genuinely ambiguous position at the conceptual boundary between the living and the non-living.

Rapid viral evolution. Viruses, and especially RNA viruses, evolve extremely rapidly, for three

compounding reasons: RNA-dependent RNA polymerases (used to replicate RNA viral genomes) generally lack the proofreading ability of DNA polymerases, producing a high mutation rate; viral generation times are extremely short (new virus particles can be produced within hours); and viral population sizes within an infected host can be enormous. Two specific mechanisms are especially important in influenza: **antigenic drift** is the gradual, continuous accumulation of small point mutations in the genes encoding haemagglutinin and neuraminidase, slowly changing their shape enough to partially evade antibodies raised against previous strains — this is why seasonal influenza vaccines must be reformulated most years. **Antigenic shift** is a sudden, much larger change: when two genetically distinct influenza strains infect the same host cell simultaneously (a host such as a pig, capable of being infected by both avian and human strains, can act as a "mixing vessel"), their segmented genomes can reassort, producing an entirely new strain with a novel combination of surface proteins to which the human population has little or no pre-existing immunity — historically the trigger for major influenza pandemics. The implication for vaccination is that surveillance of circulating viral strains must be ongoing and vaccines periodically redesigned, since immunity (whether from prior infection or vaccination) to one viral variant may confer little protection against a substantially drifted or shifted new variant.

VN **GIẢI THÍCH TIẾNG VIỆT**

Virus không được coi là sinh vật sống vì: không tự nhân lên độc lập (không có ribosome/bộ máy chuyển hoá riêng), không có quá trình chuyển hoá độc lập, không tự lớn lên hay duy trì cân bằng nội môi — bên ngoài tế bào chủ, hạt virus hoàn toàn trơ về mặt chuyển hoá. Virus (đặc biệt virus RNA) tiến hoá rất nhanh vì enzyme sao chép RNA thường không có khả năng "đọc sửa lỗi", thời gian thế hệ ngắn, và số lượng cá thể rất lớn. **Biến đổi kháng nguyên từ từ (antigenic drift)** — tích luỹ đột biến điểm nhỏ dần theo thời gian — là lý do vắc-xin cúm mùa cần cập nhật hàng năm; **biến đổi kháng nguyên đột ngột (antigenic shift)** — tái tổ hợp bộ gene phân đoạn khi hai chủng cúm khác nhau cùng nhiễm một vật chủ — có thể tạo ra chủng hoàn toàn mới, nguy cơ gây đại dịch vì cộng đồng chưa có miễn dịch từ trước.

1.3 A3 Organisms: Diversity and Classification

1.3.1 A3.1 Diversity of Organisms

Binomial nomenclature. To communicate unambiguously about species across languages and countries, biologists use **binomial nomenclature**: every species is given a two-part Latin (or Latinized) name consisting of its **genus** (capitalized) followed by its **specific epithet** (lowercase), with both parts italicized (or underlined when handwritten) — for example, *Homo sapiens* (humans) or *Panthera leo* (lion). This system, formalized by Carl Linnaeus, avoids the confusion of common names, which vary by language and region and sometimes refer to entirely different organisms in different places.

VN **GIẢI THÍCH TIẾNG VIỆT**

Danh pháp hai từ (binomial nomenclature): mỗi loài có tên khoa học gồm hai phần bằng tiếng La-tinh — **tên chi (genus)** viết hoa chữ đầu và **tên loài (species)** viết thường, cả hai đều in nghiêng — ví dụ *Homo sapiens* (người), *Panthera leo* (sư tử). Hệ thống này (do Linnaeus đề xuất) tránh được sự nhầm lẫn của tên gọi thông thường vốn khác nhau theo ngôn ngữ và vùng miền.

Defining a species, and the difficulty of doing so. The most widely used working definition is the **biological species concept**: a species is a group of organisms capable of interbreeding in nature to produce fertile, viable offspring, and which is reproductively isolated from other such groups. This definition works well for many familiar sexually-reproducing organisms, but it runs into serious difficulties in several common situations: it cannot be applied at all to **asexually reproducing organisms** (most bacteria and archaea, and some plants and protists), which do not interbreed in the relevant sense; it cannot be tested directly on **fossil organisms**, since interbreeding cannot be observed; it is complicated by **hybridization** between otherwise-distinct species (e.g., lions and tigers can mate in

captivity, and horses and donkeys produce mules), which are usually — but not always — infertile; and **ring species** and continuous geographic variation can produce populations where neighboring groups can interbreed but the two ends of the chain cannot, making any single dividing line between "one species" and "two species" somewhat arbitrary. For these reasons, biologists also use complementary approaches — morphological similarity, ecological niche, and increasingly DNA/molecular sequence comparison — alongside the biological species concept.

Ví dụ mẫu · Testing the limits of the biological species concept

Lions and tigers can be induced to mate in captivity, producing offspring called ligers or tigons; male ligers are essentially always sterile. Horses (with 64 chromosomes) and donkeys (with 62 chromosomes) can interbreed to produce mules (with an odd number, 63, chromosomes), which are almost always sterile. Explain why these observations do *not* violate the biological species concept, and explain what these examples reveal about the concept's limitations.

The biological species concept requires not merely successful mating, but production of **fertile** offspring capable of sustaining ongoing gene flow between the two groups. Because ligers/tigons and mules are (almost always) infertile — largely because their two parent species' chromosomes cannot pair up correctly during meiosis (an odd, mismatched chromosome number in the mule prevents normal chromosome pairing) — no meaningful, sustained gene flow occurs between lions and tigers, or between horses and donkeys, despite occasional successful mating. Both pairs therefore remain distinct species under the biological species concept: hybrid **sterility** is itself a (post-zygotic) reproductive isolating mechanism, not evidence against the two parent groups being separate species. At the same time, this shows the concept has fuzzy edges: because *some* interbreeding and *occasional* viable offspring do occur, the boundary between "one species" and "two closely related species" is not always a clean, binary line — which is exactly why the biological species concept alone cannot handle every real-world case.

VN **GIẢI THÍCH TIẾNG VIỆT**

Khái niệm loài sinh học: một loài là nhóm sinh vật có thể giao phối với nhau trong tự nhiên và sinh ra con cái **hữu thụ** (fertile), đồng thời cách ly sinh sản với các nhóm khác. Khái niệm này gặp khó khăn với: sinh vật sinh sản **vô tính** (không giao phối), hoá thạch (không thể kiểm chứng khả năng giao phối), **lai giữa hai loài** (ví dụ la — con lai ngựa và lừa — thường vô sinh do số nhiễm sắc thể lẻ, không bắt cặp được khi giảm phân), và **loài vòng (ring species)** nơi các quần thể liền kề giao phối được nhưng hai đầu chuỗi thì không. Vì vậy, sinh vật vô sinh (lai) không phủ nhận khái niệm loài, mà là một minh chứng cho **cơ chế cách ly sau hợp tử**.

Natural classification and the three-domain system. A **natural classification system** groups organisms according to their evolutionary relationships (phylogeny) — reflecting shared descent from common ancestors — rather than by convenient but arbitrary shared features (an **artificial classification**, such as grouping organisms simply by habitat, size, or color). A natural system has genuine predictive and explanatory power: organisms grouped by evolutionary relatedness tend to share many unmeasured features (biochemistry, genetics, development) beyond whichever traits were originally used to classify them. The modern natural classification of life at its highest level is the **three-domain system**, proposed by Carl Woese in 1990: **Bacteria**, **Archaea**, and **Eukarya**. Although both Bacteria and Archaea are prokaryotic (lacking a membrane-bound nucleus) and were historically lumped together, molecular evidence shows Archaea are at least as different from Bacteria as either is from Eukarya. Key evidence for treating Archaea as a separate domain includes: comparison of ribosomal RNA (**rRNA**) gene sequences, which showed archaeal rRNA sequences to be as distinct from bacterial rRNA as from eukaryotic rRNA; differences in **membrane lipids** — archaeal membranes are built from lipids with **ether linkages** and branched isoprenoid hydrocarbon chains, while bacterial

and eukaryotic membranes use lipids with **ester linkages** and straight fatty-acid chains; differences in cell-wall chemistry (archaea lack the peptidoglycan found in bacterial cell walls); and differences in RNA polymerase structure and other details of the transcription and translation machinery, some of which are actually more similar between Archaea and Eukarya than between Archaea and Bacteria.

> **Three-domain system (Woese, 1990):** Bacteria, Archaea, Eukarya. Evidence Archaea is a distinct domain (not simply another bacterium): divergent rRNA sequences; ether-linked, branched-chain membrane lipids (vs. ester-linked, straight-chain in Bacteria/Eukarya); absence of peptidoglycan in the cell wall; distinct RNA polymerase and transcription/translation machinery, in some respects closer to Eukarya than to Bacteria.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hệ thống phân loại tự nhiên nhóm sinh vật theo **quan hệ tiến hoá** (huyết thống chung) thay vì theo đặc điểm tiện lợi nhưng tuỳ tiện (phân loại nhân tạo). **Hệ thống ba vực** (Woese, 1990) chia sự sống thành **Bacteria**, **Archaea**, **Eukarya**. Dù Bacteria và Archaea đều là sinh vật nhân sơ, bằng chứng phân tử cho thấy chúng khác biệt nhau không kém gì so với Eukarya: trình tự **rRNA** khác biệt, **lipid màng** khác nhau (Archaea dùng liên kết ether, mạch nhánh; Bacteria/Eukarya dùng liên kết ester, mạch thẳng), Archaea không có peptidoglycan trong vách tế bào, và một số đặc điểm bộ máy phiên mã của Archaea lại giống Eukarya hơn là giống Bacteria.

Kingdoms within domain Eukarya. Within the domain Eukarya, organisms are traditionally grouped (with modern molecular phylogenetics continuing to refine finer relationships) into broad kingdoms based on nutrition, cell-wall composition, and body organization: **Protista** — a diverse, largely unicellular (or simple multicellular) grouping including algae, amoebae, and other single-celled eukaryotes, historically a convenient "catch-all" rather than a single natural (monophyletic) group; **Fungi** — heterotrophic, mostly multicellular organisms with cell walls made of **chitin**, which feed by secreting digestive enzymes onto their food and absorbing the products (absorptive heterotrophic nutrition); **Plantae** — autotrophic, multicellular organisms with cell walls made of **cellulose** and chlorophyll-containing chloroplasts, obtaining energy by photosynthesis; and **Animalia** — heterotrophic, multicellular organisms lacking cell walls, typically obtaining nutrients by ingestion (eating and internally digesting food).

Diversity of body plans as evidence of evolution. The immense variety of body plans and adaptations across living organisms — radial versus bilateral symmetry, segmented versus unsegmented bodies, exoskeletons versus endoskeletons, the independent evolution of wings for flight in insects, birds, and bats — reflects both deep evolutionary divergence from different ancestral lineages and repeated, independent evolutionary solutions (**convergent evolution**) to similar ecological challenges. This diversity of structural solutions to the shared problems all organisms face (movement, feeding, gas exchange, reproduction) is itself strong evidence that evolution is an ongoing, branching, and often repeatedly-converging process, rather than organisms having been created independently, once, in a fixed and unchanging form.

VN **GIẢI THÍCH TIẾNG VIỆT**

Trong vực Eukarya, sinh vật thường được chia thành các giới: **Protista** (chủ yếu đơn bào, đa dạng, không phải một nhóm tiến hoá thống nhất thực sự), **Fungi/Nấm** (dị dưỡng, vách tế bào chitin, tiết enzyme tiêu hoá ra ngoài rồi hấp thụ), **Plantae/Thực vật** (tự dưỡng, vách cellulose, quang hợp), **Animalia/Động vật** (dị dưỡng, không vách tế bào, ăn và tiêu hoá nội bào). Sự đa dạng cực lớn về hình thái và kiểu cơ thể (đối xứng toả tròn/hai bên, có/không phân đốt, bộ xương ngoài/trong, cánh tiến hoá độc lập ở côn trùng — chim — dơi) chính là bằng chứng cho thấy tiến hoá là quá trình phân nhánh liên tục, đôi khi hội tụ nhiều lần về cùng một giải pháp thích nghi.

1.3.2 A3.2 Classification and Cladistics

HIGHER LEVEL (HL) ONLY

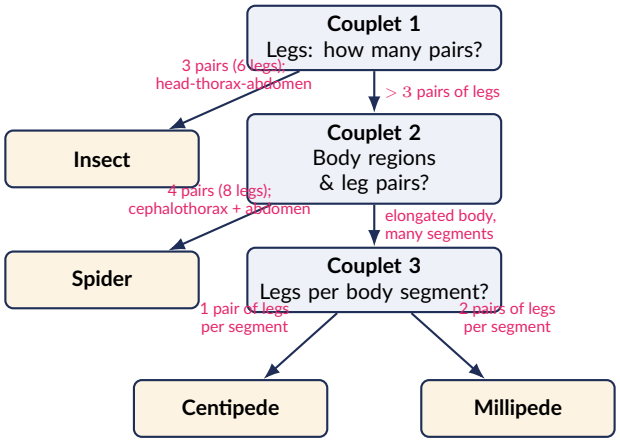
The taxonomic hierarchy. Below the level of domain, biologists organize species into a nested hierarchy of increasingly specific groups (taxa), from broadest to narrowest: **Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species**. Each level contains one or more groups from the level below it (e.g., a class contains one or more orders), and every organism belongs to exactly one group at each level.

> **Taxonomic hierarchy (broadest to narrowest):** Domain → Kingdom → Phylum → Class → Order → Family → Genus → Species. Mnemonic: *"**D**ear **K**ing **P**hilip **C**ame **O**ver **F**or **G**ood **S**oup."*

VN **GIẢI THÍCH TIẾNG VIỆT**

Thứ bậc phân loại từ rộng đến hẹp: **Vực (Domain)** → **Giới (Kingdom)** → **Ngành (Phylum)** → **Lớp (Class)** → **Bộ (Order)** → **Họ (Family)** → **Chi (Genus)** → **Loài (Species)**. Mỗi bậc chứa một hoặc nhiều nhóm ở bậc thấp hơn liền kề; mỗi sinh vật thuộc đúng một nhóm ở mỗi bậc.

Dichotomous keys. A **dichotomous key** is a tool for identifying an unknown organism through a series of paired statements ("couplets"), each offering exactly two mutually exclusive choices based on an observable characteristic; each choice either identifies the organism directly or directs the user to another couplet, until a single named organism is reached.

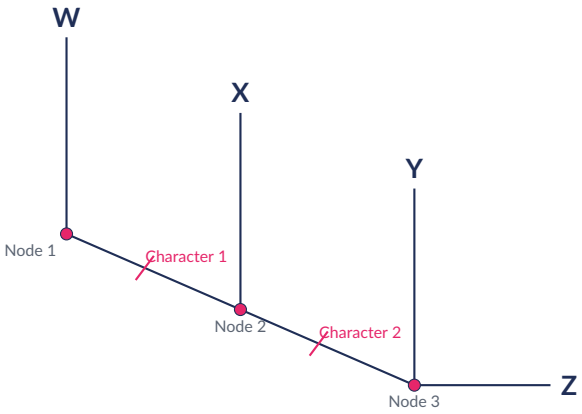


A dichotomous key for four arthropod groups, drawn as a flowchart. Each couplet offers exactly two choices based on an observable feature; following the correct branch at each step leads either to another couplet or to a final identification.

VN **GIẢI THÍCH TIẾNG VIỆT**

Khoá phân loại lưỡng phân (dichotomous key) là chuỗi các cặp phát biểu, mỗi cặp đưa ra đúng hai lựa chọn loại trừ lẫn nhau dựa trên đặc điểm quan sát được, dẫn tới cặp phát biểu tiếp theo hoặc tới tên loài cần xác định. Sơ đồ trên minh hoạ khoá phân biệt côn trùng, nhện, rết và cuốn chiếu dựa trên số đôi chân và cách chia đốt cơ thể.

Cladograms and phylogenetic trees. A **cladogram** (or phylogenetic tree) is a branching diagram that represents hypothesized evolutionary relationships among a set of taxa. Each branch point (**node**) represents a hypothetical **common ancestor**, at which one ancestral lineage is inferred to have split into two descendant lineages. A **clade** is a group consisting of an ancestor *and all* of its descendants — such a group is called **monophyletic**. Taxa that share a more recent common ancestor (i.e., whose lineages diverged from each other more recently) are considered more closely related than taxa whose most recent shared node lies further back (deeper) in the tree; two taxa that share their most recent common ancestor with each other, and with no other taxon on the tree, are called **sister taxa**.



A cladogram for four taxa (W, X, Y, Z). Node 1 is the common ancestor of all four; Node 2 is the common ancestor of X, Y, Z only; Node 3 is the most recent common ancestor of Y and Z, making Y and Z sister taxa. Tick marks show where a derived character (Character 1, shared by X, Y, Z; Character 2, shared by Y, Z) is inferred to have evolved. $\{X, Y, Z\}$ together with Node 2 is a valid clade (monophyletic: the ancestor plus *all* its descendants); $\{W, X\}$ is *not* a valid clade, because it excludes Y and Z, which also descend from Node 1.

Ví dụ mẫu · Interpreting a cladogram

Using the cladogram of taxa W, X, Y, and Z above: (a) Which two taxa are most closely related, and how do you know? (b) Is $\{W, X, Y, Z\}$ a valid clade? Is $\{W, X\}$ a valid clade? Justify each answer. (c) A newly discovered fifth taxon is found to share Character 1 but not Character 2. At which node would its lineage most plausibly attach to this tree?

(a) Y and Z are most closely related — they are sister taxa, sharing the most recent common ancestor on the tree (Node 3), meaning their lineages diverged from each other more recently than any other pair.

(b) $\{W, X, Y, Z\}$ **is** a valid clade: it consists of the ancestor at Node 1 together with *every one* of its descendants (W, X, Y, and Z) — nothing is left out, so it is monophyletic. $\{W, X\}$ is **not** a valid clade: Node 1 is the most recent common ancestor shared by W and X together, but Node 1 is also the ancestor of Y and Z, which are excluded from the group $\{W, X\}$ — a clade must include *all* descendants of the relevant ancestor, so any grouping that leaves some descendants out (a **paraphyletic** grouping) is not a true clade.

(c) Since it shares Character 1 (present in the lineage leading to X, Y, Z) but not Character 2 (present only in the lineage leading to Y and Z), the new taxon's lineage must have branched off *after* Character 1 evolved but *before* Character 2 evolved — that is, its lineage attaches at **Node 2**, as a sister lineage to the branch that leads on to Node 3 (and hence to Y and Z).

(!) Lỗi thường gặp: Lỗi đọc cây phát sinh chủng loại thường gặp nhất: cho rằng **vị trí trái–phải hoặc trên–dưới** của một nhánh trên trang giấy thể hiện mức độ "tiến hoá cao hơn" hay quan hệ họ hàng gần hơn. *Sai*: mức độ quan hệ họ hàng chỉ được xác định bởi **vị trí của điểm nút chung gần nhất (most recent common ancestor)**, không phải bởi khoảng cách hình học trên trang giấy — hai nhánh có thể vẽ cách xa nhau nhưng vẫn là hai đơn vị phân loại chị em (sister taxa) nếu ta xoay cây tại một điểm nút mà không đổi cấu trúc phân nhánh. Một lỗi khác: nhầm nhóm **cận ngành (paraphyletic)** — nhóm bỏ sót một số hậu duệ — với một **nhánh (clade)** thực sự, vốn luôn phải bao gồm tổ tiên *và toàn bộ* hậu duệ của nó.

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Cây phát sinh chủng loại (cladogram): mỗi **điểm nút (node)** là một tổ tiên chung giả định; một

nhánh (clade) gồm tổ tiên và *toàn bộ* hậu duệ của nó (nhóm **đơn ngành/monophyletic**). Hai đơn vị phân loại có tổ tiên chung gần nhất (node gần ngọn cây nhất) là họ hàng gần nhất — gọi là **đơn vị chị em (sister taxa)**. Lỗi phổ biến: nhầm vị trí hình học trên trang giấy với mức độ họ hàng thực sự, hoặc coi một nhóm bỏ sót hậu duệ (**cận ngành, paraphyletic**) là một nhánh hợp lệ.

The principle of parsimony. When more than one possible cladogram is consistent with a given set of character data, systematists prefer the tree that requires the **fewest independent evolutionary changes** (character-state origins or reversals) to explain the observed distribution of characters — this is the **principle of parsimony** (sometimes called maximum parsimony). The underlying reasoning is that convergent evolution (the same character state arising independently more than once) and evolutionary reversal are both treated as comparatively uncommon events; a cladogram that requires many separate, independent origins of the identical character is considered a less likely hypothesis than a simpler one requiring only a single origin, all else being equal. Parsimony is not a guarantee of the true evolutionary history — evolution has no obligation to follow the simplest path — but among competing cladograms consistent with the same data, it gives systematists an objective, repeatable criterion for choosing which hypothesis to prefer, which becomes indispensable once many characters and taxa make it impractical to judge every possible tree by inspection alone.

VN GIẢI THÍCH TIẾNG VIỆT

Nguyên tắc tiết kiệm tối đa (parsimony): khi nhiều cây phát sinh chủng loại khác nhau đều phù hợp với cùng một bộ dữ liệu đặc điểm, các nhà phân loại học ưu tiên chọn cây đòi hỏi **số lần thay đổi tiến hoá độc lập ít nhất** để giải thích dữ liệu quan sát được — vì tiến hoá hội tụ (một đặc điểm xuất hiện độc lập nhiều lần) và đảo ngược tiến hoá được xem là hiếm gặp hơn. Nguyên tắc này không đảm bảo phản ánh đúng lịch sử tiến hoá thực sự (tiến hoá không nhất thiết đi theo con đường đơn giản nhất), nhưng cung cấp một tiêu chí khách quan, có thể lặp lại để lựa chọn giữa nhiều giả thuyết cây khả dĩ — đặc biệt hữu ích khi số lượng đặc điểm và đơn vị phân loại quá lớn để so sánh từng cây bằng mắt thường.

Molecular evidence and its role in revising classification. Beyond anatomical (morphological) features, cladograms are increasingly constructed and tested using **molecular evidence**: the degree of similarity between DNA sequences or the amino acid sequences of shared proteins between two species. Because mutations accumulate roughly steadily over time, species whose DNA or protein sequences differ by *fewer* changes are inferred to share a *more recent* common ancestor than species whose sequences differ by many more changes; molecular data can be collected for genes present across a very wide range of organisms (such as rRNA genes), allowing comparisons even between very distantly related groups where morphology gives few useful clues. Because molecular evidence is more directly quantifiable and less subject to the confounding effects of convergent evolution (which can make unrelated organisms look anatomically similar), it has substantially revised classifications that were originally based on morphology alone. Two well-established examples: molecular and detailed fossil evidence place **birds firmly within the dinosaur lineage** (specifically, nested among theropod dinosaurs), rather than as a separate, coordinate group; and molecular sequence comparison shows that **Fungi are more closely related to Animalia than either is to Plantae** (both Fungi and Animalia fall within a clade sometimes called Opisthokonta), overturning the older, morphology-based grouping of fungi with plants, which had been based on superficial similarities such as immobility and the presence of a cell wall.

VN GIẢI THÍCH TIẾNG VIỆT

Bằng chứng phân tử (so sánh trình tự DNA/protein) ngày càng được dùng để xây dựng và kiểm định cây phát sinh chủng loại: hai loài càng ít khác biệt trình tự thì càng có tổ tiên chung gần đây, và bằng chứng này ít bị ảnh hưởng bởi tiến hoá hội tụ (vốn khiến các loài không họ

hàng trông giống nhau về hình thái) hơn so với bằng chứng hình thái đơn thuần. Nhờ đó, phân loại học đã được điều chỉnh đáng kể: **chim** nay được xếp *trong* chính dòng khủng long chân thú (theropoda), và **nấm** được xác định có quan hệ họ hàng gần với **động vật** hơn là với thực vật — trái với phân loại cũ dựa trên đặc điểm hình thái bề ngoài (bất động, có vách tế bào).

Ví dụ mẫu · Constructing and using a dichotomous key

Using the arthropod dichotomous-key flowchart above, identify the organism described: *"An elongated, worm-like animal with a long, segmented body; each body segment bears two pairs of jointed legs."* Show which couplet choice is made at each step. Then write a single new couplet (in the standard 1a/1b format) that could be added to distinguish adult insects from insect larvae (maggots/caterpillars), which have no jointed legs on the abdomen at all.

Identification: At Couplet 1, the organism has clearly more than 3 pairs of legs (it is described as having many segments, each with legs), so we proceed to Couplet 2. At Couplet 2, the body is elongated with many similar segments rather than divided into a cephalothorax and abdomen, so we proceed to Couplet 3. At Couplet 3, each segment bears *two* pairs of legs (not one), matching the millipede branch. The organism is a **millipede**.

New couplet (for use before the existing Couplet 1, to separate adult insects from larval insect forms):
1a. Body has 3 pairs of jointed legs attached to a thorax .....go to next couplet (adult form)
1b. Body has no jointed legs (or only soft, unjointed prolegs), body divided into many similar soft segments .....Insect larva

Ví dụ mẫu · Constructing a cladogram from a character-state matrix

The table below records the presence (1) or absence (0) of four derived characters in five vertebrate taxa. Lamprey is included as an **outgroup** — a taxon known, from independent evidence, to have branched off before the others and to lack all four derived characters.

Character	Lamprey	Shark	Salmon	Lizard	Rabbit
Jaws	0	1	1	1	1
Bony skeleton	0	0	1	1	1
Amniotic egg	0	0	0	1	1
Hair	0	0	0	0	1

Using the principle of parsimony, construct a cladogram for these five taxa, identifying the character (synapomorphy) that defines each branch point.

Step 1 — root the tree with the outgroup. Lamprey lacks all four characters, so it is designated the outgroup and placed as the first branch off the base of the tree.

Step 2 — find the character shared by the most taxa. Jaws are present in Shark, Salmon, Lizard, and Rabbit, but absent in Lamprey — the broadest shared derived character. Shark, Salmon, Lizard, and Rabbit therefore form a clade to the exclusion of Lamprey.

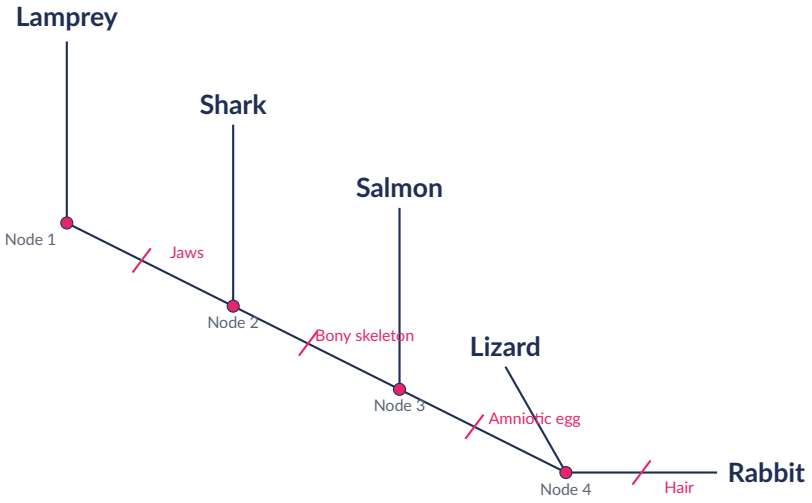
Step 3 — nest the next most broadly shared character. Bony skeleton is present in Salmon, Lizard, and Rabbit, but absent in Shark (whose skeleton is cartilaginous) — so Salmon, Lizard, and Rabbit form a more deeply nested clade, with Shark branching off first among the jawed taxa.

Step 4 — continue nesting by shared derived characters. Amniotic egg is present only in Lizard and Rabbit — so these two form a still more nested clade, with Salmon branching off

first among the bony-skeleton taxa.

Step 5 — the most restricted character is the final branch point. Hair is present in Rabbit alone, distinguishing Rabbit from Lizard at the final split.

This nested arrangement requires only four independent character origins (one per character, each arising exactly once) — the minimum possible — so it is the most parsimonious tree consistent with the data.



The resulting cladogram for the five vertebrate taxa. Node 1 is the ancestor of all jawed vertebrates (Gnathostomata); Node 2 marks the origin of a bony skeleton; Node 3 marks the origin of the amniotic egg (Amniota); the branch leading to Rabbit alone shows the origin of hair. Lizard and Rabbit are the most recently diverged pair in this data set.

VN **GIẢI THÍCH TIẾNG VIỆT**

Để dựng cây phát sinh chủng loại từ bảng đặc điểm: (1) xác định nhóm ngoại (outgroup) — đơn vị thiếu tất cả đặc điểm phái sinh, dùng làm gốc cây; (2) tìm đặc điểm được chia sẻ bởi nhiều đơn vị phân loại nhất — đây là điểm phân nhánh sâu nhất (gần gốc nhất); (3) tiếp tục lồng các đặc điểm hẹp dần vào bên trong, mỗi đặc điểm mới xác định một điểm nút nông hơn. Cây được chọn phải là cây đòi hỏi **ít lần xuất hiện tiến hoá độc lập nhất** cho toàn bộ dữ liệu — đúng theo **nguyên tắc tiết kiệm tối đa (parsimony)**.

1.4 A4 Ecosystems: Evolution and Conservation

1.4.1 A4.1 Evolution and Speciation

Evidence for evolution. Multiple independent lines of evidence converge to support the theory that all living species have descended, with modification, from common ancestors over immense spans of time. **Fossils** document a chronological sequence of organisms in rock strata, including transitional forms that show intermediate combinations of ancestral and derived features (such as fossils linking early tetrapods to their fish-like ancestors), and dating techniques allow this sequence to be placed on an absolute timescale. **Comparative anatomy** reveals **homologous structures** — structures that are anatomically similar because they were inherited from a shared common ancestor, even when they now serve very different functions (for example, the same basic bone pattern — humerus, radius/ulna, carpals, digits — underlies the human arm, the whale flipper, and the bat wing, each modified for a different function) — as well as **analogous structures**, which perform a similar function but evolved independently in unrelated lineages and show no shared underlying structure (**convergent evolution**), such as the wings of insects and birds. **Molecular biology** shows that the

degree of similarity in DNA and protein sequences between species correlates closely with their evolutionary relatedness as established by other evidence, and the near-universality of the genetic code itself points to common ancestry. **Biogeography** — the geographic distribution of species — is best explained by evolutionary history combined with continental drift and dispersal barriers (for example, Australia's unique marsupial fauna, isolated for tens of millions of years, and the distinctive endemic species that evolve on remote islands). Finally, **selective (artificial) breeding** demonstrates, on human timescales, that heritable variation combined with consistent selection can produce substantial change within a population or species — from the enormous range of dog breeds selectively bred from a wolf ancestor, to crop varieties bred for yield or disease resistance — directly illustrating the raw mechanism (heritable variation plus differential selection) that drives natural selection in the wild.

(!) Lỗi thường gặp: Đừng nhầm **cấu trúc tương đồng (homologous)** với **cấu trúc tương tự (analogous)**. Cấu trúc tương đồng có *cùng nguồn gốc cấu trúc* (thừa hưởng từ tổ tiên chung) dù chức năng hiện tại có thể khác nhau — ví dụ chi trước của người, cá voi, dơi đều theo cùng một khuôn xương (xương cánh tay–xương trụ/quay–xương cổ tay–ngón) dù dùng để cầm nắm, bơi, hay bay. Cấu trúc tương tự có *chức năng giống nhau* nhưng *cấu trúc nền tảng hoàn toàn khác nhau* vì tiến hoá độc lập (tiến hoá hội tụ) — ví dụ cánh côn trùng (mở rộng từ lớp vỏ kitin, không có xương) và cánh chim (chi trước biến đổi, có xương) đều dùng để bay nhưng không có quan hệ họ hàng trực tiếp về mặt cấu trúc đó. Quy tắc ghi nhớ: *tương đồng → so sánh cấu trúc/nguồn gốc; tương tự → so sánh chức năng*.

Ví dụ mẫu · Homologous or analogous?

Classify each pair of structures as homologous or analogous, and justify your answer: (a) the arm of a human and the flipper of a whale; (b) the wing of a bird and the wing of a butterfly; (c) the tail fin of a shark and the tail fluke of a dolphin.

(a) Homologous. Both are built on the same underlying pentadactyl-limb skeletal plan (humerus → radius/ulna → carpals → digits), inherited from a shared mammalian (tetrapod) ancestor, but subsequently modified for very different functions — grasping and manipulation versus swimming.

(b) Analogous. Both serve the same function (powered flight), but the underlying structures share no common evolutionary origin: a bird wing is a modified, feathered bony forelimb, while a butterfly wing is a thin membrane extended from the chitinous exoskeleton, containing no bones at all. Flight evolved completely independently in these very distantly related lineages — convergent evolution.

(c) Analogous. Both provide thrust for aquatic locomotion and have converged on a similar external streamlined shape, but a shark's tail fin is supported internally by cartilage and fin rays (a fish structure), while a dolphin's fluke is a modification of mammalian connective tissue attached to a horizontally-oriented tail vertebral column, with no equivalent fin-ray skeleton — dolphins are secondarily aquatic mammals whose ancestors had legs, not fins. The superficially similar shape reflects a shared selection pressure (efficient swimming), not shared ancestry of that specific structure.

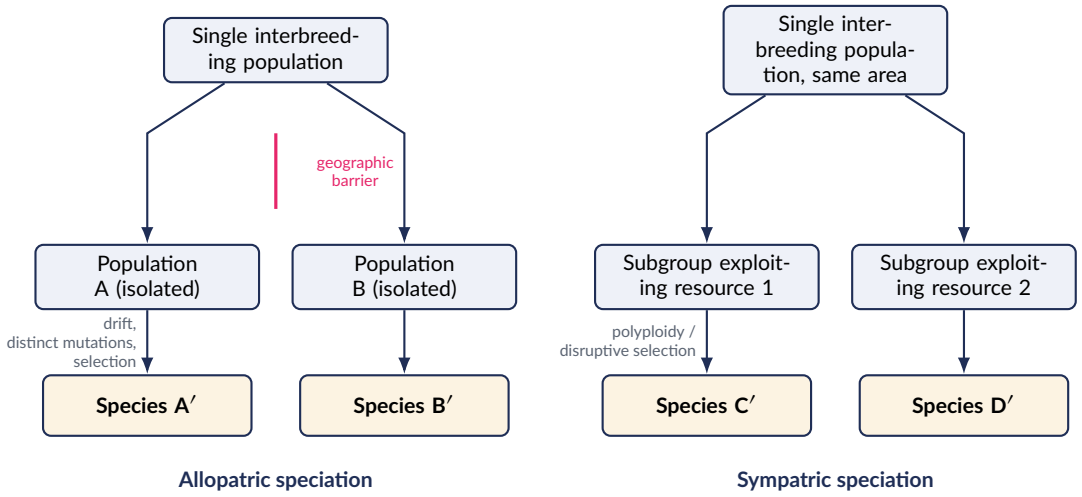
VN GIẢI THÍCH TIẾNG VIỆT

Nhiều bằng chứng độc lập ủng hộ thuyết tiến hoá: **hoá thạch** (trình tự thời gian, dạng chuyển tiếp), **giải phẫu so sánh** (cấu trúc tương đồng do tổ tiên chung, cấu trúc tương tự do tiến hoá hội tụ), **sinh học phân tử** (mức độ giống nhau của trình tự DNA/protein tương quan với quan hệ họ hàng), **địa sinh học** (phân bố địa lý phản ánh lịch sử tiến hoá và sự trôi dạt lục địa — ví

dụ hệ thú có túi đặc hữu ở Úc), và **chọn lọc nhân tạo** (lai tạo giống vật nuôi/cây trồng chứng minh biến dị di truyền kết hợp chọn lọc có thể tạo ra thay đổi lớn trong thời gian ngắn — cùng cơ chế với chọn lọc tự nhiên).

Natural selection — a recap. Evolution by **natural selection** requires four conditions to operate on a population: (1) **variation** — individuals within a population differ in their heritable traits, arising ultimately from mutation and (in sexually reproducing species) genetic recombination; (2) **overproduction / a selection pressure** — populations tend to produce more offspring than the environment can support, and factors such as predation, competition, disease, or a changing climate act as **selection pressures** that not all individuals survive or reproduce equally well under; (3) **differential survival and reproduction** — individuals whose heritable traits happen to be better suited to the current selection pressures are, on average, more likely to survive and produce offspring than individuals with less-suited traits; (4) **heritability** — because the advantageous traits are heritable, they are passed disproportionately to the next generation. Repeated over many generations, this process shifts the frequency of alleles within the population, which *is* evolution at the population level.

Allopatric and sympatric speciation. Speciation is the evolutionary process by which one species gives rise to two or more descendant species, ultimately through the accumulation of enough genetic difference and **reproductive isolation** that the resulting populations can no longer interbreed. **Allopatric speciation** occurs when a population is split by a physical geographic barrier (a mountain range, a river changing course, a new island forming, long-distance dispersal) that prevents gene flow between the two resulting populations; isolated from one another, the populations accumulate different mutations and experience different selection pressures and genetic drift, and over enough time diverge so much that even if the geographic barrier were later removed, the two populations could no longer successfully interbreed — they have become separate species. **Sympatric speciation** occurs without any geographic separation, while the diverging populations remain in the same physical area; mechanisms include **polyploidy** (a sudden change in chromosome number, especially common in plants, which can instantly create reproductive isolation from the parent population because hybrids between the polyploid and the original diploid population are usually sterile), strong **disruptive selection** on a trait combined with non-random (assortative) mating, and distinct temporal or behavioral differences (e.g., shifting to breed at a different time of year, or specializing on a different host/food resource) that progressively reduce interbreeding even without any physical barrier.



Left: allopatric speciation — a physical barrier splits one population into two, which diverge independently (through genetic drift, distinct new mutations, and different local selection pressures) until they can no longer interbreed. Right: sympatric speciation — divergence occurs within the same shared area, without any geographic separation, driven instead by mechanisms such as polyploidy or strong disruptive selection combined with assortative mating.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hình thành loài dị vực (allopatric) (trái): một rào cản địa lý chia quần thể thành hai, mỗi nhóm tích luỹ đột biến, chịu áp lực chọn lọc và trôi dạt di truyền khác nhau một cách độc lập, dần dần không thể giao phối trở lại được nữa dù rào cản có biến mất. **Hình thành loài đồng vực (sympatric)** (phải): sự phân hoá xảy ra ngay trong cùng khu vực địa lý, không có rào cản vật lý — thường qua cơ chế đa bội hoá (polyploidy) ở thực vật hoặc chọn lọc phân hoá mạnh kết hợp giao phối chọn lọc (assortative mating) theo nguồn thức ăn hoặc nơi ở khác nhau.

Reproductive isolation mechanisms. Reproductive isolation can act before or after mating/fertilization is attempted. **Prezygotic** mechanisms prevent mating or fertilization from occurring at all: **geographic isolation** (populations never encounter each other), **temporal isolation** (breeding at different times of day, season, or year), **behavioral isolation** (different courtship displays or mating signals fail to attract a mate from the other population), **mechanical isolation** (physical incompatibility of reproductive structures), and **gametic isolation** (sperm and egg are incompatible and fail to fuse even if mating is attempted). **Postzygotic** mechanisms act after a hybrid zygote has actually formed: **hybrid inviability** (the hybrid embryo fails to develop or dies before reproductive age), **hybrid sterility** (the hybrid survives but cannot itself produce viable offspring, e.g., mules), and **hybrid breakdown** (first-generation hybrids are viable and fertile, but their own offspring in later generations have reduced viability or fertility).

Adaptive radiation. Adaptive radiation is the relatively rapid diversification of a single ancestral lineage into many descendant species, each adapted to a different ecological niche — typically triggered by colonization of a new environment with many unoccupied niches (such as a newly-formed volcanic island) or by the extinction of former competitors that opens up previously unavailable ecological opportunities.

Darwin's finches: a case study. The finches of the Galápagos Islands, studied by Charles Darwin and, in exhaustive long-term detail, by Peter and Rosemary Grant, are a classic case study of adaptive radiation. All of the roughly 13–15 recognized species are believed to descend from a single ancestral finch species that colonized the islands from mainland South America. As descendants spread to different islands and exploited different food sources — large hard seeds, small soft seeds, insects, cactus flowers and pulp — natural selection favored different beak sizes and shapes on different islands and in different ecological niches, producing today's striking diversity of finch beak morphology from one common ancestor. The Grants' long-term field studies on the island of Daphne Major directly documented natural selection acting on beak depth in real time: during a severe drought that greatly reduced the supply of small, soft seeds, birds with deeper, stronger beaks (better able to crack the larger, tougher seeds that remained available) survived at substantially higher rates, and the average beak depth of the surviving population's offspring increased in the following generation — a directly observed, quantifiable episode of natural selection.

Ví dụ mẫu · Natural selection in a Darwin's finch population

The table below illustrates the type of pattern documented in long-term field studies of Galápagos finches during a severe drought, when small, soft seeds became scarce and birds depended more heavily on larger, tougher seeds.

Beak depth class (mm)	Number before drought	Number surviving after drought
6–8	20	2
8–10	45	20
10–12	15	12
12–14	5	5

(a) Which beak-depth class suffered the highest proportional mortality, and which the low-

est? (b) Explain how this drought event could shift the mean beak depth of the population in the next generation. (c) Explain why this observation counts as evidence of natural selection, rather than merely evidence that beak depth varies within the population.

(a) Survival rate by class: 6–8 mm: $2/20 = 10\%$; 8–10 mm: $20/45 \approx 44\%$; 10–12 mm: $12/15 = 80\%$; 12–14 mm: $5/5 = 100\%$. The 6–8 mm class suffered the **highest** proportional mortality (90% died); the 12–14 mm class suffered the **lowest** (none died).

(b) Since beak depth is heritable and the drought caused strongly non-random (differential) survival favoring deeper-beaked birds, the survivors — who disproportionately have deep beaks — become the parents of the next generation. Assuming beak depth is passed on to offspring, the **mean beak depth of the population is expected to increase** in the next generation.

(c) This is evidence of natural selection specifically because survival was non-random with respect to a *heritable* trait, under an identifiable *selection pressure* (scarcity of small, soft seeds forcing reliance on larger, tougher seeds that only deep-beaked birds could crack efficiently). Variation in beak depth alone, without a plausible selective mechanism and a link to differential, heritable reproductive success, would not by itself demonstrate that natural selection had occurred.

VN **GIẢI THÍCH TIẾNG VIỆT**

Chọn lọc tự nhiên cần 4 điều kiện: **biến dị** di truyền trong quần thể, **áp lực chọn lọc** từ môi trường, **sống sót và sinh sản khác biệt** có lợi cho cá thể mang tính trạng phù hợp, và tính trạng đó phải **di truyền được**. **Hình thành loài dị vực (allopatric)** xảy ra khi có rào cản địa lý ngăn cách dòng gene; **hình thành loài đồng vực (sympatric)** xảy ra không cần cách ly địa lý (ví dụ đa bội hoá ở thực vật). Cách ly sinh sản chia thành **trước hợp tử** (ngăn giao phối/thụ tinh: địa lý, thời gian, tập tính, cơ học, giao tử) và **sau hợp tử** (con lai kém sống/vô sinh/suy thoái con lai). **Bức xạ thích nghi (adaptive radiation)** — như chim sẻ Darwin ở Galápagos — là sự đa dạng hoá nhanh từ một tổ tiên chung thành nhiều loài thích nghi với các ổ sinh thái khác nhau.

1.4.2 A4.2 Conservation of Biodiversity

Reasons for biodiversity loss. Human activity is currently driving a rate of species loss far above natural background rates, through several interacting mechanisms: **habitat destruction and fragmentation** (deforestation, conversion of land to agriculture, urban expansion) removes or divides the space species need to survive and reduces the size of populations that fragments can support; **climate change** shifts temperature and precipitation patterns faster than many species can migrate or adapt, and drives ocean warming/acidification and coral bleaching; **invasive species** introduced (deliberately or accidentally) to new regions can outcompete, prey upon, or bring novel diseases to native species that have no evolved defenses against them; **overharvesting** (overfishing, poaching, unsustainable logging) removes individuals faster than populations can reproduce to replace them; and **pollution** (plastic waste, industrial chemicals, agricultural runoff causing eutrophication, oil spills) directly poisons organisms or degrades the habitats and food webs they depend on.

Measuring biodiversity: richness, diversity, and Simpson's Index. Species richness is simply the number of different species present in a given area — a straightforward count that ignores how common or rare each species is. **Species diversity** is a more informative measure that accounts for *both* richness *and* the relative abundance (**evenness**) of each species: a community with 5 species present in roughly equal numbers is considered more diverse than a community with the same 5 species where one species makes up 96% of all individuals and the other four are rare, even though both have identical species richness. **Simpson's Diversity Index** is a widely used quantitative measure that combines richness and evenness into a single value.

Simpson's Diversity Index:

$$D = 1 - \frac{\sum n(n-1)}{N(N-1)}$$

where n = the number of individuals of a particular species, and N = the total number of individuals of *all* species in the sample. D ranges from 0 (no diversity — a single species dominates completely) up to just under 1 (very high diversity — many species, evenly represented). A higher D value indicates greater biodiversity.

Ví dụ mẫu · Calculating Simpson's Diversity Index

A student surveys a 1 m^2 quadrat in a meadow and records the following counts:

Species	Count (n)	$n(n-1)$
Daisy	8	$8 \times 7 = 56$
Buttercup	5	$5 \times 4 = 20$
Clover	3	$3 \times 2 = 6$
Grass tuft	4	$4 \times 3 = 12$

Calculate Simpson's Diversity Index for this quadrat.

Step 1 — total individuals: $N = 8 + 5 + 3 + 4 = 20$.

Step 2 — sum of $n(n-1)$: $\sum n(n-1) = 56 + 20 + 6 + 12 = 94$.

Step 3 — $N(N-1)$: $N(N-1) = 20 \times 19 = 380$.

Step 4 — apply the formula:

$$D = 1 - \frac{94}{380} = 1 - 0.247 = \mathbf{0.75} \text{ (to 2 s.f.)}.$$

A value of $D \approx 0.75$, fairly close to 1, indicates a reasonably diverse plant community in this quadrat, with no single species overwhelmingly dominant — daisies are the most common species but still make up less than half of all individuals sampled.

VN **GIẢI THÍCH TIẾNG VIỆT**

Độ phong phú loài (species richness) chỉ đếm số loài khác nhau; **độ đa dạng loài (species diversity)** còn tính đến **độ đồng đều (evenness)** — số lượng cá thể tương đối giữa các loài. **Chỉ số đa dạng Simpson**: $D = 1 - \frac{\sum n(n-1)}{N(N-1)}$, với n là số cá thể của một loài, N là tổng số cá thể mọi loài. D càng gần 1, quần xã càng đa dạng (nhiều loài, phân bố đồng đều); D càng gần 0, một loài càng chiếm ưu thế áp đảo. Lưu ý: công thức dùng $n(n-1)$ và $N(N-1)$ — chứ không phải n^2 và N^2 — đây là lỗi tính toán học sinh hay mắc phải.

Ví dụ mẫu · Simpson's Index before and after a pollution event

A stream invertebrate community is surveyed by the same team both before and after an industrial spill.

Species	Count before spill (n)	Count after spill (n)
Species A	15	38
Species B	12	6
Species C	10	4
Species D	8	1
Species E	5	1

Calculate Simpson's Diversity Index before and after the spill, and interpret the ecological meaning of the change.

Before the spill: $N = 15 + 12 + 10 + 8 + 5 = 50$; $N(N-1) = 50 \times 49 = 2450$.

$$\sum n(n-1) = (15)(14) + (12)(11) + (10)(9) + (8)(7) + (5)(4) = 210 + 132 + 90 + 56 + 20 = 508.$$

$$D_{\text{before}} = 1 - \frac{508}{2450} = 1 - 0.207 = \mathbf{0.79} \text{ (to 2 s.f.)}.$$

After the spill: $N = 38 + 6 + 4 + 1 + 1 = 50$; $N(N-1) = 2450$ (same total).

$$\sum n(n-1) = (38)(37) + (6)(5) + (4)(3) + (1)(0) + (1)(0) = 1406 + 30 + 12 + 0 + 0 = 1448.$$

$$D_{\text{after}} = 1 - \frac{1448}{2450} = 1 - 0.591 = \mathbf{0.41} \text{ (to 2 s.f.)}.$$

Interpretation: although the *total* number of individuals sampled is identical before and after ($N = 50$ in both), diversity fell sharply, from $D \approx 0.79$ to $D \approx 0.41$. Species A — likely a pollution-tolerant species — came to dominate the post-spill community (from 15 to 38 individuals, or 30% to 76% of the sample), while the other, more pollution-sensitive species declined sharply. This is a common real-world signature of pollution: total abundance may recover or even increase, but community **evenness** collapses as tolerant species outcompete sensitive ones, which Simpson's Index — unlike a simple species count or total abundance count — correctly detects.

VN **GIẢI THÍCH TIẾNG VIỆT**

Chỉ số Simpson có thể dùng để so sánh cùng một địa điểm ở hai thời điểm khác nhau (trước và sau một sự kiện ô nhiễm), không chỉ để so sánh hai địa điểm khác nhau. Trong ví dụ trên, tổng số cá thể không đổi ($N = 50$ ở cả hai lần khảo sát), nhưng chỉ số D giảm mạnh vì một loài chịu được ô nhiễm (Loài A) trở nên áp đảo, còn các loài nhạy cảm hơn suy giảm số lượng — minh hoạ vì sao chỉ đếm tổng số cá thể hoặc số loài hiện diện là chưa đủ để đánh giá tác động sinh thái của ô nhiễm; cần đo cả **độ đồng đều**.

In-situ versus ex-situ conservation. **In-situ conservation** protects species within their natural habitat — national parks, marine protected areas, wildlife corridors connecting fragmented habitat. Its advantages include preserving the full web of natural ecological interactions and ongoing co-evolution between species, allowing populations to continue adapting through natural selection, and generally being more cost-effective for protecting large numbers of species and large populations at once; its main vulnerability is that threats affecting the whole habitat (wildfire, disease outbreak, regional climate change) can still affect the entire protected population. **Ex-situ conservation** protects species outside their natural habitat — zoos, botanic gardens, seed banks (such as the Svalbard Global Seed Vault), captive breeding programs, and gene/cryopreservation banks. It can be a critical last resort for critically endangered species with very small remaining wild populations, allows carefully managed and monitored breeding programs and later reintroduction to the wild (e.g.,

the California condor, the giant panda), but is typically far more expensive per individual protected, often involves small founder populations at risk of inbreeding and reduced genetic diversity, may lead to loss of natural behaviors needed for survival in the wild, and — unlike in-situ conservation — does nothing by itself to address the original cause of the species' decline.

The importance of biodiversity. Biodiversity underpins a wide range of **ecosystem services**: provisioning services (food, timber, fresh water, medicinal compounds derived from wild species), regulating services (climate regulation, water purification, pollination of crops, natural pest control), cultural services (recreation, aesthetic and spiritual value, ecotourism), and supporting services (nutrient cycling, soil formation, primary production that underlies every other service). Biodiversity also contributes directly to **ecosystem resilience and stability**: more diverse ecosystems generally show greater **functional redundancy** (several different species capable of performing a similar ecological role), so that if one species declines or is lost, others can partly compensate for its ecological function, making the overall ecosystem more resistant to and quicker to recover from disturbance. Biodiversity is additionally a vast, largely untapped genetic and biochemical resource for future medicine, agriculture, and biotechnology, beyond its recognized intrinsic and existence value.

IUCN Red List categories. The International Union for Conservation of Nature (IUCN) maintains the **Red List**, which classifies species according to their risk of extinction, from lowest to highest concern: **Least Concern (LC)**, **Near Threatened (NT)**, **Vulnerable (VU)**, **Endangered (EN)**, **Critically Endangered (CR)**, **Extinct in the Wild (EW)** (survives only in captivity or cultivation), and **Extinct (EX)** (no individuals remain anywhere). Species assessed as Vulnerable, Endangered, or Critically Endangered are collectively described as **threatened**. A separate category, **Data Deficient (DD)**, is used when there is not enough information to assess a species' risk at all.

IUCN Red List categories (increasing extinction risk): Least Concern → Near Threatened → Vulnerable → Endangered → Critically Endangered → Extinct in the Wild → Extinct. Vulnerable, Endangered, and Critically Endangered together are the "threatened" categories.

VN GIẢI THÍCH TIẾNG VIỆT

Bảo tồn tại chỗ (in-situ): bảo vệ loài ngay trong môi trường sống tự nhiên (vườn quốc gia, khu bảo tồn biển) — giữ được tương tác sinh thái tự nhiên, chi phí thường thấp hơn cho quy mô lớn, nhưng dễ bị ảnh hưởng bởi thảm hoạ trên diện rộng. **Bảo tồn chuyển vị trí (ex-situ)**: bảo vệ loài bên ngoài môi trường tự nhiên (sở thú, ngân hàng hạt giống, nhân giống trong điều kiện nuôi nhốt) — là giải pháp cuối cùng cho loài cực kỳ nguy cấp nhưng tốn kém, dễ suy giảm đa dạng di truyền do quần thể nhỏ, và không giải quyết nguyên nhân gốc rễ gây suy giảm. Đa dạng sinh học quan trọng vì cung cấp **dịch vụ hệ sinh thái** (cung cấp, điều tiết, văn hoá, hỗ trợ) và tăng **khả năng phục hồi** của hệ sinh thái trước biến động. **Danh sách Đỏ IUCN** xếp hạng nguy cơ tuyệt chủng từ thấp đến cao: Ít lo ngại → Sắp bị đe doạ → Sẽ nguy cấp → Nguy cấp → Cực kỳ nguy cấp → Tuyệt chủng trong tự nhiên → Tuyệt chủng.

1.5 Theme A Practice Bank

Bài tập luyện tập

A single water molecule can donate hydrogen bonds through its hydrogen atoms and accept hydrogen bonds through the lone pairs on its oxygen atom. What is the *maximum* number of hydrogen bonds one water molecule can form with its neighbors at a given instant?

(A) 1
(B) 2
(C) 4
(D) 8

Lời giải chi tiết

Each water molecule has 2 hydrogen atoms (each can donate one hydrogen bond) and 2 lone electron pairs on oxygen (each can accept one hydrogen bond): $2 + 2 = 4$ hydrogen bonds maximum. **(C)**.

Bài tập luyện tập

Explain, in terms of hydrogen bonding, why ice floats on liquid water even though most solids are denser than their corresponding liquid.

Lời giải chi tiết

In ice, each water molecule is locked into exactly 4 fixed hydrogen bonds, arranged in an open, rigid hexagonal lattice that holds molecules farther apart on average than in liquid water. In liquid water, hydrogen bonds are continually breaking and re-forming, allowing molecules to pack more closely and randomly. Because ice's crystal structure keeps molecules further apart, ice is about 9% less dense than liquid water and therefore floats.

Bài tập luyện tập

Water rises up the narrow xylem vessels of a tall tree against gravity through a combination of water molecules adhering to the polar vessel walls and cohering to one another. This combined phenomenon is called:

(A) Surface tension
(B) Capillary action
(C) Osmosis
(D) Specific heat capacity

Lời giải chi tiết

Capillary action is exactly the combined effect of adhesion (water–wall attraction) and cohesion (water–water attraction) that allows water to rise in a narrow tube against gravity. **(B)**.

Bài tập luyện tập

A small aquarium containing 2.0×10^4 g of water absorbs 8.4×10^5 J of heat from a nearby lamp over an afternoon. Using a specific heat capacity of water of 4.18 J/(g $\cdot^\circ$ C), calculate the resulting temperature increase, ignoring heat loss.

Lời giải chi tiết

Apply $q = mc\Delta T \Rightarrow \Delta T = \dfrac{q}{mc}$:

$$\Delta T = \frac{8.4 \times 10^5 \text{ J}}{(2.0 \times 10^4 \text{ g})(4.18 \text{ J/(g} \cdot^\circ \text{C)})} = \frac{8.4 \times 10^5}{8.36 \times 10^4} \approx 10.0^\circ\text{C}.$$

Water's high specific heat capacity means a comparatively large heat input produces only a modest temperature rise — the same reason large bodies of water buffer the temperature of the surrounding environment.

Bài tập luyện tập

Which base-pairing statement is correct for double-stranded DNA?

(A) Adenine pairs with guanine via 2 hydrogen bonds

(B) Adenine pairs with thymine via 3 hydrogen bonds

(C) Guanine pairs with cytosine via 3 hydrogen bonds

(D) Cytosine pairs with thymine via 2 hydrogen bonds

Lời giải chi tiết

Guanine (a purine) pairs with cytosine (a pyrimidine) via 3 hydrogen bonds; adenine pairs with thymine via 2 hydrogen bonds. A purine never pairs with another purine, and a pyrimidine never pairs with another pyrimidine. **(C)**.

Bài tập luyện tập

A double-stranded DNA sample is found to be 21% cytosine. Using Chargaff's rule, determine the percentage of adenine, thymine, and guanine in the sample.

Lời giải chi tiết

By Chargaff's rule, $\%\text{G} = \%\text{C} = 21\%$. The remaining bases (A and T) together make up $100\% - 21\% - 21\% = 58\%$; since $\%\text{A} = \%\text{T}$, each is $58\% \div 2 = 29\%$. So $\%\text{A} = 29\%$, $\%\text{T} = 29\%$, $\%\text{G} = 21\%$.

Bài tập luyện tập

State two structural differences between DNA and RNA, and one functional consequence of each difference.

Lời giải chi tiết

(1) DNA uses **deoxyribose** (no $-$OH at the $2'$ carbon); RNA uses **ribose** (has a $2'$-OH). Consequence: the extra $-$OH makes RNA more chemically reactive and less stable, suiting RNA's more temporary functional roles, while DNA's greater stability suits its role as a long-term information store. (2) DNA is typically **double-stranded**; RNA is typically **single-stranded**. Consequence: DNA's double-stranded structure protects the genetic information (each strand can be used to check/repair the other) and allows semi-conservative replication; RNA's single strand allows it to fold into varied three-dimensional shapes needed for its diverse roles (e.g., tRNA cloverleaf structure, ribozyme catalysis).

Bài tập luyện tập

The table below shows the melting temperature (T_m, the temperature at which the two strands of a DNA sample separate) for four different double-stranded DNA samples with different base compositions.

Sample	1	2	3	4
%GC content	30%	45%	60%	75%
T_m (°C)	79	86	93	100

(a) Describe the relationship shown between %GC content and melting temperature. (b) Ex-

plain this relationship in terms of hydrogen bonding. (c) Predict, with reasoning, whether a DNA sample with 90% GC content would have a higher or lower T_m than Sample 4.

Lời giải chi tiết

(a) As %GC content increases, melting temperature (T_m) increases — a positive, roughly linear relationship in this data (each 15 percentage-point increase in GC content corresponds to about a 7°C rise in T_m).

(b) G–C base pairs are held together by 3 hydrogen bonds, while A–T base pairs have only 2. DNA with a higher %GC content therefore has more hydrogen bonds per unit length holding the two strands together (and correspondingly stronger base-stacking interactions), requiring more thermal energy — a higher temperature — to separate the strands.

(c) Higher than Sample 4. Following the trend, a sample with an even higher %GC content (90%, compared to Sample 4's 75%) would have proportionally more G–C pairs and hence more hydrogen bonds per unit length, requiring an even higher temperature to melt — likely above 100°C.

Bài tập luyện tập

The RNA world hypothesis is supported by the observation that:

(A) DNA polymerase can replicate RNA directly

(B) Ribosomal RNA (rRNA), not a protein, catalyzes peptide bond formation during translation

(C) RNA is more chemically stable than DNA

(D) All modern viruses use RNA as their genome

Lời giải chi tiết

The ribosome's catalytic activity resides in its rRNA component (a ribozyme), not in any of its protein subunits — direct evidence that RNA can act as a catalyst as well as an information carrier, supporting the idea that early life may have relied on RNA alone for both roles. **(B)**.

Bài tập luyện tập

Chloroplast rRNA sequences most closely resemble those of which group of free-living prokaryotes, supporting the endosymbiotic origin of chloroplasts?

(A) Alpha-proteobacteria

(B) Cyanobacteria

(C) Archaea

(D) Spirochaetes

Lời giải chi tiết

Chloroplast rRNA sequences most closely resemble those of cyanobacteria (photosynthetic bacteria), consistent with chloroplasts having originated from an engulfed cyanobacterium; mitochondria, by contrast, most closely resemble alpha-proteobacteria. **(B)**.

Bài tập luyện tập

Which of the following is a recognized exception to the cell theory, and why?

(A) Red blood cells, because they lack a nucleus

(B) Striated muscle fibres, because they are multinucleate structures formed by the fusion of many cell precursors

(C) Bacteria, because they lack membrane-bound organelles

(D) Neurons, because they can be very long

Lời giải chi tiết

Striated (skeletal) muscle fibres form when many individual myoblasts fuse into one continuous, multinucleate structure — so a single "fibre" does not correspond to one discrete cell in the usual sense, making it a commonly cited exception to the cell theory. **(B)**.

Bài tập luyện tập

A student measures the images of four different structures in a set of micrographs, along with the magnification used for each. Complete the missing value in each row.

Structure	Image size	Magnification	Actual size
(a) Chloroplast	25 mm	$\times 5000$	?
(b) Nucleus	?	$\times 2000$	6 μm
(c) Bacterium (*E. coli*)	6 mm	?	2 μm

Lời giải chi tiết

(a) $A = I/M$. Convert: 25 mm $= 25\,000$ μm. $A = 25\,000/5000 =$ **5** □m (a realistic chloroplast length).

(b) $I = M \times A = 2000 \times 6$ μm $= 12\,000$ μm $=$ **12** mm.

(c) $M = I/A$. Convert: 6 mm $= 6000$ μm. $M = 6000/2 =$ $\times$**3000**.

Bài tập luyện tập

Compare light microscopy and electron microscopy in terms of (a) maximum resolution, (b) ability to observe living specimens, and (c) sample preparation required.

Lời giải chi tiết

(a) Light microscopes have a maximum resolution of about 200 nm (limited by the wavelength of visible light); electron microscopes achieve far higher resolution, down to about 0.1–2 nm (electrons have a much shorter effective wavelength). **(b)** Light microscopes can observe living, unstained specimens in real time; electron microscopy requires the sample to be fixed and placed in a vacuum, which kills it — living specimens cannot be observed. **(c)** Light microscopy requires minimal preparation (sometimes just staining); electron microscopy requires fixation, dehydration, and often ultrathin sectioning and coating of the sample, which is time-consuming and can introduce preparation artefacts.

Bài tập luyện tập

Which statement best explains why viruses are not classified as living organisms?

(A) Viruses are far too small to be seen with a light microscope

(B) Viruses cannot reproduce independently — they lack ribosomes and metabolic machinery and must hijack a host cell's machinery to replicate

(C) Viruses only infect eukaryotic cells

(D) Viruses do not contain any nucleic acid

Lời giải chi tiết

Viruses have no ribosomes, no metabolic enzymes, and no way to generate ATP of their own; they can only be replicated by hijacking a living host cell's machinery, and outside a host they are metabolically inert — this failure to independently reproduce or metabolize is the core reason they are not classified as living. **(B)**.

Bài tập luyện tập

Distinguish antigenic drift from antigenic shift in influenza virus, and explain why antigenic shift is more strongly associated with pandemics than antigenic drift.

Lời giải chi tiết

Antigenic drift is the slow, continuous accumulation of small point mutations in the genes for haemagglutinin and neuraminidase, gradually changing their shape; because the change at any one time is small, existing population immunity (from past infection or vaccination) still offers partial protection, which is why seasonal flu vaccines only need periodic updating. **Antigenic shift** is a sudden, large change caused by reassortment of genome segments when two different influenza strains co-infect the same host (e.g., a pig acting as a "mixing vessel"), producing an entirely novel combination of surface proteins. Because the change is so large and sudden, the human population may have *little or no* pre-existing immunity to the new strain at all — which is why antigenic shift, not drift, is associated with the emergence of major pandemics.

Bài tập luyện tập

HIV is classified as a retrovirus because:

(A) It has a DNA genome that is transcribed into RNA before packaging

(B) It has an RNA genome that is reverse-transcribed into DNA by the enzyme reverse transcriptase, which then integrates into the host genome

(C) It lacks an envelope

(D) It infects only bacterial cells

Lời giải chi tiết

Retroviruses carry an RNA genome and their own enzyme, reverse transcriptase, which converts that RNA into DNA once inside a host cell; this viral DNA then integrates into the host cell's genome (in HIV's case, a T-helper lymphocyte). **(B)**.

Bài tập luyện tập

Explain why binomial nomenclature is preferred over common names in biological classification.

Lời giải chi tiết

Common names vary across languages and even across regions speaking the same language, and the same common name can refer to different organisms in different places (or different common names to the same organism), creating ambiguity. Binomial nomenclature assigns every species a unique, standardized two-part Latin name (genus + specific epithet), understood consistently by scientists worldwide regardless of their native language, eliminating this confusion.

Bài tập luyện tập

Explain why bacteria and archaea, despite both being prokaryotic (lacking a membrane-bound nucleus), are placed in two separate domains rather than one.

Lời giải chi tiết

Molecular and biochemical evidence shows Bacteria and Archaea are at least as different from each other as either is from Eukarya, despite sharing the superficial prokaryotic trait of lacking a nucleus: their ribosomal RNA (rRNA) sequences diverge substantially; their membrane lipids differ fundamentally (ether-linked, branched lipids in Archaea versus ester-linked, straight-chain lipids in Bacteria); Archaea lack the peptidoglycan cell wall found in Bacteria; and several details of Archaea's transcription/translation machinery more closely resemble Eukarya than Bacteria. "Prokaryotic" describes a shared absence of a nucleus (a structural similarity), not a close evolutionary relationship — Woese's three-domain system reclassifies life based on the deeper evolutionary evidence rather than this one structural similarity.

Bài tập luyện tập

The table shows the percentage sequence similarity of a particular gene between four species, compared pairwise.

	Species P	**Species Q**	**Species R**	**Species S**
Species P	—	98%	82%	65%
Species Q	98%	—	81%	64%
Species R	82%	81%	—	63%
Species S	65%	64%	63%	—

(a) Which two species are most closely related, and how do you know? (b) Which species is most distantly related to the other three? (c) Sketch (in words) the branching order of a cladogram consistent with this data.

Lời giải chi tiết

(a) Species P and Q are most closely related — they show the highest pairwise sequence similarity (98%), meaning the fewest accumulated differences and therefore the most recent common ancestor.

(b) Species S is most distantly related to the other three — it shows the lowest sequence similarity to each of P, Q, and R (around 63–65%), indicating its lineage diverged from the others longest ago.

(c) Consistent branching order (root to tips): the lineage leading to S branches off first (most ancient split); next, the lineage leading to R branches off from the remaining lineage; finally, P and Q — the most similar pair — share the most recent common ancestor and are sister taxa.

Schematically: $(((\mathrm{P}, \mathrm{Q}), \mathrm{R}), \mathrm{S})$.

Bài tập luyện tập

Using the arthropod dichotomous key given earlier in this unit, identify an organism described as: "a small animal with 3 pairs of jointed legs, and a body clearly divided into a head, thorax, and abdomen."

Lời giải chi tiết

At Couplet 1, the organism has exactly 3 pairs of legs and the head–thorax–abdomen body plan described in the key — this directly matches the first branch of Couplet 1. The organism is an **insect**.

Bài tập luyện tập

In the taxonomic hierarchy, which level lies directly between Class and Family?

(A) Phylum
(B) Order
(C) Genus
(D) Kingdom

Lời giải chi tiết

The full hierarchy from broad to narrow is Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species — Order sits directly between Class and Family. **(B)**.

Bài tập luyện tập

Fungi were traditionally classified together with plants, largely because both are immobile and have cell walls. Explain, using molecular evidence, why this classification has since been revised.

Lời giải chi tiết

Comparison of DNA and protein sequences shows that Fungi share a more recent common ancestor with Animalia than with Plantae — both Fungi and Animalia fall within a clade sometimes called Opisthokonta. The older classification grouping Fungi with Plantae was based on superficial morphological similarities (immobility, presence of a cell wall) that arose independently in the two lineages rather than reflecting a close evolutionary relationship; molecular evidence, being less prone to this kind of confusion from convergent traits, revealed the true, more recent shared ancestry between Fungi and Animalia.

Bài tập luyện tập

A population of insects becomes divided by a newly-formed river into two groups that can no longer physically encounter one another. Over many generations, the two groups accumulate different mutations and adapt to slightly different local conditions, eventually becoming unable to interbreed even if reunited. This is an example of:

(A) Sympatric speciation
(B) Allopatric speciation
(C) Adaptive radiation without speciation
(D) Convergent evolution

Lời giải chi tiết

A physical geographic barrier (the river) separates the population, preventing gene flow and allowing the two groups to diverge independently until reproductive isolation results — this is the defining pattern of allopatric speciation. **(B)**.

Bài tập luyện tập

Two closely related cricket species live in the same field (no geographic separation) but breed at different times of night, and males of each species produce distinctly different mating calls that females of the other species do not respond to. Identify the reproductive isolation mechanism(s) described, classifying each as prezygotic or postzygotic.

Lời giải chi tiết

Breeding at different times of night is **temporal isolation** (prezygotic — prevents mating from occurring at all, since the two species are rarely active/receptive at the same time). Distinct mating calls that fail to attract females of the other species is **behavioral isolation** (also prezygotic — mate-recognition signals prevent mating attempts between the species). Both operate *before* fertilization could occur, so both are prezygotic mechanisms.

Bài tập luyện tập

Following a volcanic eruption, a new island forms with no established plant life. Over several million years, a single ancestral plant species that colonizes the island diversifies into over 20 descendant species, each specialized for a different microhabitat (cliff faces, forest floor, high-altitude bog, coastal scrub). This pattern is best described as:

(A) Sympatric speciation only
(B) Adaptive radiation
(C) Convergent evolution
(D) Artificial selection

Lời giải chi tiết

Rapid diversification of a single ancestral lineage into many descendant species, each adapted to a different available ecological niche following colonization of a new, largely unoccupied environment, is the defining pattern of adaptive radiation. **(B)**.

Bài tập luyện tập

Widespread use of a particular insecticide leads, within a few years, to a farm insect population in which most individuals carry an allele conferring resistance to that insecticide, whereas the allele was rare before spraying began. Explain this outcome in terms of the four requirements for natural selection.

Lời giải chi tiết

Variation: even before spraying began, the resistance allele already existed at low frequency in the population (from pre-existing mutation), alongside susceptible alleles. **Selection pressure:** the insecticide itself became a strong, new selection pressure. **Differential survival and reproduction:** insects carrying the resistance allele were far more likely to survive insecticide exposure and go on to reproduce than susceptible individuals, which were killed before reproducing. **Heritability:** because resistance is genetically determined, surviving resistant indi-

viduals passed the resistance allele to their offspring. Repeated over several generations, this shifted the allele frequency in the population sharply toward the resistance allele — evolution by natural selection, driven by a human-imposed selection pressure.

Bài tập luyện tập

A tropical rainforest is cleared and replaced with a single-species commercial timber plantation. Identify the primary cause of biodiversity loss illustrated, and explain one likely consequence for the resilience of the resulting ecosystem.

Lời giải chi tiết

The primary cause is **habitat destruction** (specifically, conversion of natural habitat to agricultural/forestry monoculture), which eliminates the structural and species diversity of the original rainforest. A likely consequence for ecosystem resilience: a single-species plantation has essentially no functional redundancy — if a pest, disease, or extreme weather event affects that one species, there are no other species available to buffer the loss or maintain ecosystem processes, making the resulting ecosystem far less resistant to and slower to recover from disturbance than the original, diverse rainforest.

Bài tập luyện tập

Classify each of the following as primarily in-situ or ex-situ conservation, and briefly justify: (a) a national marine park where fishing is banned; (b) a seed bank storing samples of wild crop relatives at -20°C; (c) a captive-breeding program for a critically endangered amphibian, with plans to reintroduce offspring to protected wetlands.

Lời giải chi tiết

(a) In-situ — the species are protected within their natural marine habitat, with human activity (fishing) restricted rather than the organisms being removed. **(b) Ex-situ** — the genetic material is stored completely outside the plants' natural habitat, in an artificial, controlled facility. **(c) Ex-situ (with an in-situ goal)** — breeding itself occurs outside the natural habitat (in captivity), though the ultimate aim is to restore individuals to an in-situ, natural (protected) setting; the breeding phase itself is the defining ex-situ component of the program.

Bài tập luyện tập

A species is officially assessed as having a very small, severely fragmented population that has declined by more than 80% over the last three generations, but wild individuals still exist. Which IUCN Red List category does this best match?

(A) Near Threatened
(B) Vulnerable
(C) Critically Endangered
(D) Extinct in the Wild

Lời giải chi tiết

An extremely severe population decline ($> 80\%$) combined with a small, severely fragmented remaining population matches the IUCN's most severe category for species that still survive in the wild: **Critically Endangered**. (Extinct in the Wild would require no wild individuals to remain at all.) **(C)**.

Bài tập luyện tập

Two woodland ponds are surveyed for aquatic invertebrates. Pond X: Species 1 $= 10$, Species 2 $= 6$, Species 3 $= 6$, Species 4 $= 2$. Pond Y: Species 1 $= 22$, Species 2 $= 1$, Species 3 $= 1$. Calculate Simpson's Diversity Index for each pond and state which pond is more diverse.

Lời giải chi tiết

Pond X: $N = 10 + 6 + 6 + 2 = 24$. $\sum n(n-1) = (10)(9) + (6)(5) + (6)(5) + (2)(1) = 90 + 30 + 30 + 2 = 152$. $N(N-1) = 24 \times 23 = 552$.

$$D_X = 1 - \frac{152}{552} = 1 - 0.275 = \mathbf{0.72} \text{ (to 2 s.f.)}.$$

Pond Y: $N = 22 + 1 + 1 = 24$. $\sum n(n-1) = (22)(21) + (1)(0) + (1)(0) = 462 + 0 + 0 = 462$. $N(N-1) = 24 \times 23 = 552$.

$$D_Y = 1 - \frac{462}{552} = 1 - 0.837 = \mathbf{0.16} \text{ (to 2 s.f.)}.$$

Pond X is far more diverse ($D_X \approx 0.72$ vs. $D_Y \approx 0.16$). Both ponds have the same total number of individuals ($N = 24$) — the key difference is **evenness**: Pond X's individuals are fairly evenly spread across 4 species, while Pond Y is overwhelmingly dominated by Species 1 (22 of 24 individuals), which Simpson's Index correctly penalizes even though both samples have the same total abundance and similar species richness.

Bài tập luyện tập

Glucose dissolves readily in water, while vegetable oil does not mix with water and instead forms a separate layer. Classify glucose and vegetable oil as hydrophilic or hydrophobic, and explain the molecular basis for the difference.

Lời giải chi tiết

Glucose is **hydrophilic**: it is a polar molecule with several $-$OH groups that can form hydrogen bonds with surrounding water molecules, allowing it to be surrounded and dissolved. **Vegetable oil** is **hydrophobic**: it is composed mainly of long nonpolar hydrocarbon chains that cannot form favorable hydrogen bonds with water; water molecules preferentially hydrogen-bond with each other, excluding the nonpolar oil and forcing it to separate into its own layer rather than dissolve.

Bài tập luyện tập

The table below gives approximate specific heat capacities. A 1000 g mass of water and a 1000 g mass of dry beach sand, both starting at the same temperature, each absorb 4200 J of solar energy during a sunny afternoon.

Material	Specific heat capacity
Water	4.18 J/(g $\cdot^\circ$ C)
Dry sand	0.84 J/(g $\cdot^\circ$ C)

(a) Calculate the temperature rise of each material. (b) Use your answer to explain why coastal regions typically experience milder, more stable daily temperature swings than inland regions far from large bodies of water.

Lời giải chi tiết

(a) Apply $\Delta T = q/(mc)$ to each material:

$$\Delta T_{\text{water}} = \frac{4200}{(1000)(4.18)} = \frac{4200}{4180} \approx 1.0^{\circ}\text{C}; \qquad \Delta T_{\text{sand}} = \frac{4200}{(1000)(0.84)} = \frac{4200}{840} = 5.0^{\circ}\text{C}.$$

(b) For the same energy input and mass, sand heats up (and by the same logic, cools down) about 5 times more than water, because water's much higher specific heat capacity means a large amount of energy is absorbed or released for only a small temperature change. Coastal land is close to a large thermal reservoir of water that warms and cools slowly, moderating the local air temperature; inland areas, dominated by land (which behaves more like the sand in this problem), heat up quickly by day and cool quickly by night, producing much larger daily temperature swings.

Bài tập luyện tập

Within a single strand of DNA, successive nucleotides are joined by phosphodiester bonds. This bond forms between:

(A) The $3'$ carbon of one nucleotide's sugar and the $5'$ carbon of the next nucleotide's sugar

(B) The phosphate group on one nucleotide's $5'$ carbon and the free $3'$-hydroxyl of the next nucleotide's sugar

(C) Two nitrogenous bases on opposite strands

(D) The $1'$ carbon of one sugar and the $1'$ carbon of the next sugar

Lời giải chi tiết

The phosphate group attached to one nucleotide's $5'$ carbon forms a phosphodiester bond with the free $3'$-hydroxyl group of the sugar on the next nucleotide in the chain, building the repeating sugar–phosphate backbone and giving the strand its $5' \to 3'$ directionality. **(B)**.

Bài tập luyện tập

Two viral DNA samples are analyzed for base composition:

Sample	%A	%T	%G	%C
Sample 1	24	24	26	26
Sample 2	32	18	22	28

Using Chargaff's rule, determine which sample is more likely to be double-stranded DNA and which is more likely to be single-stranded DNA. Justify your answer.

Lời giải chi tiết

Sample 1 satisfies Chargaff's rule almost exactly ($\%\text{A} = \%\text{T} = 24\%$ and $\%\text{G} = \%\text{C} = 26\%$), which is expected only when every A on one strand is paired with a T on a complementary strand (and every G with a C) — this pattern is strong evidence that Sample 1 is **double-stranded** DNA. **Sample 2** clearly violates Chargaff's rule ($\%\text{A} = 32\% \neq \%\text{T} = 18\%$, and $\%\text{G} = 22\% \neq \%\text{C} = 28\%$): with no complementary strand constraining base composition, a **single-stranded** DNA genome (as found in some small DNA viruses) is free to have any base composition, so it is not required to — and in this case does not — satisfy Chargaff's rule.

Bài tập luyện tập

State two functions of ribosomal RNA (rRNA) that support the idea, central to the RNA world hypothesis, that RNA can act as a catalyst as well as an information-related molecule.

Lời giải chi tiết

(1) rRNA forms the catalytic core of the **ribosome**, directly catalyzing the formation of peptide bonds between amino acids during translation — a chemical reaction, not merely an information-storage role, carried out by RNA rather than by a protein enzyme. (2) rRNA also base-pairs with the nucleotide sequences of mRNA and tRNA during translation (e.g., in ribosome assembly and reading frame positioning), showing that the same RNA molecule can combine an information-recognition role with catalytic activity. Together, these functions make the ribosome a compelling real, present-day example of a **ribozyme**, supporting the RNA world hypothesis that early self-replicating systems could have relied on RNA alone for both roles.

Bài tập luyện tập

Earth's atmosphere is thought to have become progressively richer in oxygen following the evolution of oxygen-releasing photosynthesis in cyanobacteria-like organisms. Explain, in terms of endosymbiotic theory, why a host cell engulfing (and retaining) an aerobic bacterium capable of efficient aerobic respiration would have been strongly favored as atmospheric oxygen became more abundant.

Lời giải chi tiết

Aerobic respiration extracts far more usable energy (ATP) from each glucose molecule than anaerobic metabolic pathways can. A host cell that engulfed and permanently retained a bacterium capable of aerobic respiration gained a built-in, highly efficient way to exploit the newly abundant atmospheric oxygen for energy production — a substantial competitive advantage over organisms restricted to anaerobic metabolism in an increasingly oxygenated (and, for many anaerobes, increasingly toxic) environment. In turn, the engulfed bacterium gained a stable, nutrient-rich, protected internal environment. This mutual benefit is proposed to explain why the relationship became permanent and universal among eukaryotes, with the engulfed aerobic bacterium evolving into the mitochondrion.

Bài tập luyện tập

The table below summarizes features observed by electron microscopy in three unidentified cell samples.

Feature	Cell 1	Cell 2	Cell 3
Nucleus	Absent	Present	Present
Cell wall	Peptidoglycan	Absent	Cellulose
Chloroplasts	Absent	Absent	Present
Ribosomes	$70S$ only	$80S$	$80S$ (+$70S$ in organelles)

Identify Cell 1, Cell 2, and Cell 3 as bacterial, animal, or plant, giving one piece of evidence for each.

Lời giải chi tiết

Cell 1 is bacterial: it has no nucleus, a peptidoglycan cell wall, and only $70S$ ribosomes — all hallmarks of a prokaryotic cell. **Cell 2 is animal**: it has a true nucleus and $80S$ ribosomes but no cell wall and no chloroplasts, matching a typical eukaryotic animal cell. **Cell 3 is plant**: it has a nucleus, a cellulose cell wall, and chloroplasts, with $80S$ cytoplasmic ribosomes alongside $70S$ ribosomes retained in its mitochondria and chloroplasts (consistent with endosymbiotic theory) — the presence of both cellulose and chloroplasts is decisive for identifying it as a plant cell rather than an animal cell.

Bài tập luyện tập

Modeling a cell as a cube, calculate the surface-area-to-volume ratio for a cell of side length $4\ \mu$m and for a cell of side length $12\ \mu$m. By what factor does the ratio change?

Lời giải chi tiết

For a cube of side s: $SA = 6s^2$, $V = s^3$, so $SA : V = 6/s$.

$s = 4\ \mu$**m:** $SA = 6(4)^2 = 96\ \mu\text{m}^2$; $V = (4)^3 = 64\ \mu\text{m}^3$; $SA : V = 96/64 =$ **1.5** μm^{-1} (matches $6/4 = 1.5$).

$s = 12\ \mu$**m:** $SA = 6(12)^2 = 864\ \mu\text{m}^2$; $V = (12)^3 = 1728\ \mu\text{m}^3$; $SA : V = 864/1728 =$ **0.5** μm^{-1} (matches $6/12 = 0.5$).

Tripling the linear size of the cell (from 4 to $12\ \mu$m) reduces its surface-area-to-volume ratio by a factor of 3 (from 1.5 to $0.5\ \mu\text{m}^{-1}$), directly reflecting the inverse relationship $SA : V = 6/s$: as s triples, $SA : V$ falls to one-third.

Bài tập luyện tập

A student takes a blurry light micrograph of a mitochondrion and simply enlarges the digital image many times over using photo-editing software, hoping to see its internal cristae membranes more clearly. Explain why this approach will not succeed.

Lời giải chi tiết

Digitally enlarging an image only increases **magnification** (how much bigger the image appears) — it cannot improve **resolution** (the ability to distinguish two very close points as separate), which is fundamentally limited by the wavelength of visible light used to form the original image (about 200 nm at best). Since the internal detail of cristae membranes lies below this resolution limit, no amount of enlarging can reveal detail that was never resolved in the original image — this produces only a bigger but no clearer picture, a phenomenon called **empty magnification**. Genuinely resolving the cristae would require an imaging method with a fundamentally shorter effective wavelength, such as electron microscopy.

Bài tập luyện tập

A bacteriophage infects *E. coli* and, instead of immediately producing new virus particles, its genome integrates into the host chromosome, where it is copied passively along with the host's DNA for many generations without harming the host. Name this state, and name the process by which the viral genome could later excise itself and resume active replication.

Lời giải chi tiết

The integrated, dormant viral genome is called a **prophage**, and the host cell is said to be **lysogenic** (undergoing the lysogenic cycle). The process by which the prophage later excises itself from the host chromosome and switches into the lytic cycle, typically triggered by host-cell stress such as UV damage, is called **induction**.

Bài tập luyện tập

A newly isolated bacteriophage has a burst size of 50 (each lysed host cell releases 50 new phage particles), and every released phage successfully infects a new cell in each subsequent, equally-timed cycle. (a) Starting from a single infected cell, calculate the number of phage particles released after 2 complete lytic cycles. (b) Determine the minimum number of complete cycles required for the phage population to first exceed one million particles.

Lời giải chi tiết

(a) After 1 cycle: 50 particles. After 2 cycles: $50 \times 50 = 50^2 =$ **2500** particles.

(b) Continue the pattern $N = 50^n$: $50^1 = 50$; $50^2 = 2500$; $50^3 = 125\,000$; $50^4 = 6\,250\,000$. The population first exceeds one million particles at $n =$ **4** complete cycles ($50^3 = 125\,000$ is still below one million, while $50^4 = 6.25$ million exceeds it).

Bài tập luyện tập

A newly discovered single-celled organism thrives in an acidic hot spring at $80°$C. It lacks a nuclear envelope, its cell wall lacks peptidoglycan, and its membrane lipids are joined by ether linkages with branched hydrocarbon chains. This organism most likely belongs to domain:

(A) Bacteria
(B) Archaea
(C) Eukarya
(D) Protista

Lời giải chi tiết

The absence of peptidoglycan combined with ether-linked, branched-chain membrane lipids are defining biochemical hallmarks of **Archaea**, distinguishing it from Bacteria (which have peptidoglycan walls and ester-linked, straight-chain lipids) despite both being prokaryotic; many archaea are also characteristically found in extreme environments such as hot, acidic springs. **(B)**.

Bài tập luyện tập

Members of kingdom Fungi obtain their nutrients by:

(A) Photosynthesis, using chlorophyll in chloroplasts
(B) Ingesting food particles and digesting them internally
(C) Secreting digestive enzymes onto external food material and absorbing the digested products
(D) Absorbing dissolved nutrients directly through root hairs

Lời giải chi tiết

Fungi are heterotrophic and feed by **absorptive nutrition**: they secrete digestive (hydrolytic) enzymes onto their food source, breaking it down externally, and then absorb the resulting small soluble molecules across their cell membranes — unlike animals (which ingest and digest internally) or plants (which are autotrophic). **(C)**.

Bài tập luyện tập

Four taxa (P, Q, R, S) are scored for three characters, given in the table below (S is the outgroup, lacking all derived states).

Taxon	Character 1	Character 2	Character 3
P	1	1	0
Q	1	1	1
R	1	0	0
S	0	0	0

Two candidate cladograms are proposed: **Tree 1**: $(((\mathrm{P},\mathrm{Q}),\mathrm{R}),\mathrm{S})$ — P and Q as sister taxa. **Tree 2**: $(((\mathrm{P},\mathrm{R}),\mathrm{Q}),\mathrm{S})$ — P and R as sister taxa. Using the principle of parsimony, determine which tree requires fewer independent character origins, and state which tree should be preferred.

Lời giải chi tiết

Character 1 (shared by P, Q, R, all absent in S) requires only 1 origin in either tree, since P, Q, and R form a single clade excluding S under both topologies.

Character 2 (present in P and Q, absent in R): under **Tree 1**, P and Q are sisters, so Character 2 can arise just **once**, on the branch leading to their common ancestor. Under **Tree 2**, P and R are sisters instead, which separates P from Q — Character 2 (present in both P and Q, but not in the intervening R) would then require **two** independent origins (once in the lineage leading to P, once again in the lineage leading to Q).

Character 3 (present in Q alone) requires exactly 1 origin (on the terminal branch to Q) under either tree.

Totals: Tree 1 requires $1+1+1=$ **3** independent character origins; Tree 2 requires $1+2+1=$ **4**. Since Tree 1 requires fewer independent evolutionary origins of the same character, **Tree 1 (grouping P and Q as sister taxa) is the more parsimonious tree and should be preferred** — consistent with P and Q being the only two taxa that share *both* Character 1 and Character 2.

Bài tập luyện tập

Consider a cladogram in which Node 1 is the common ancestor of taxa J, K, L, and M, and Node 2 (nested within Node 1) is the common ancestor of K, L, and M only. State whether each of the following groupings is a valid clade (monophyletic) or not, with reasoning: (a) $\{$J, K, L, M$\}$; (b) $\{$K, L, M$\}$; (c) $\{$J, K$\}$.

Lời giải chi tiết

(a) Valid clade. $\{$J, K, L, M$\}$ consists of the ancestor at Node 1 together with *every* one of its descendants — nothing is excluded, so it is monophyletic.

(b) Valid clade. $\{$K, L, M$\}$ consists of the ancestor at Node 2 together with all of its descendants (K, L, and M) — again, nothing is excluded, so it is monophyletic.

(c) Not a valid clade (paraphyletic). {J, K} does not correspond to any single ancestor plus *all* of its descendants: the most recent common ancestor of J and K is Node 1, but Node 1 is also the ancestor of L and M, which are excluded from this grouping. A grouping that leaves out some descendants of the relevant ancestor is paraphyletic, not a true clade.

Bài tập luyện tập

The table below shows representative data for a population of peppered moths (*Biston betularia*) sampled from an industrial area, both while heavy soot pollution had darkened tree bark and killed nearby lichen, and again some years after pollution-control measures allowed the bark to lighten and lichen to regrow.

Phenotype	% while bark was dark (sooty)	% after bark lightened
Light-colored (typica)	15%	78%
Dark-colored (carbonaria)	85%	22%

Explain this shift in phenotype frequencies in terms of natural selection.

Lời giải chi tiết

Peppered moths rest on tree trunks during the day and are preyed upon by birds that hunt visually, so camouflage against the bark is a major survival factor. While soot pollution had darkened the bark (and killed the lichen that would otherwise lighten it), light-colored moths stood out and were preferentially eaten, while dark-colored moths were camouflaged and survived and reproduced at higher rates — a selection pressure (visual predation) acting on a heritable trait (wing coloration) that favored the dark phenotype, driving its frequency up to 85%. After pollution controls reduced soot and the bark lightened again (with lichen regrowth), the camouflage advantage reversed: dark moths became conspicuous and light moths were camouflaged, so light-colored moths were now favored, and their frequency rose back to 78%. This is a clear example of natural selection: the direction of selection tracked a changing environmental factor (bark color, driven by pollution levels), acting on a heritable coloration trait to shift phenotype frequencies in the population within a relatively small number of generations.

Bài tập luyện tập

Two related plant species grow in the same meadow and flower at the same time of year, but one species' flowers have a long, narrow floral tube that only a long-tongued moth can pollinate, while the other has a short, open flower pollinated only by short-tongued bees; the physical mismatch prevents cross-pollination between the two species. This is an example of:

(A) Temporal isolation
(B) Mechanical isolation
(C) Gametic isolation
(D) Hybrid breakdown

Lời giải chi tiết

The two species are prevented from cross-pollinating specifically because of a physical (structural) mismatch between flower shape and pollinator anatomy, not because of timing, gamete incompatibility, or reduced hybrid fitness — this is **mechanical isolation**, a prezygotic reproductive isolating mechanism based on incompatible physical structures. **(B)**.

Bài tập luyện tập

A diploid plant species ($2n = 14$) undergoes an error during meiosis in one individual, producing tetraploid ($4n = 28$) offspring. The tetraploid plant can self-fertilize (or mate with other tetraploids) to produce fertile tetraploid offspring, but any cross with the original diploid population produces sterile triploid ($3n = 21$) hybrids. Explain how this scenario can lead to sympatric speciation, and identify the type of reproductive isolation involved.

Lời giải chi tiết

The new tetraploid plant is immediately reproductively isolated from the original diploid population: any cross between them produces triploid ($3n = 21$) hybrids whose odd, mismatched chromosome number prevents normal chromosome pairing during meiosis, causing **hybrid sterility** — a **postzygotic** reproductive isolating mechanism. Because the tetraploid can nonetheless reproduce successfully with other tetraploids (or by self-fertilization), a new, reproductively isolated lineage can become established within the very same geographic area as the parent population, with no geographic barrier involved at any point — this is **sympatric speciation via polyploidy**, notable for being able to produce a new species within a single generation, far faster than most other speciation mechanisms.

Bài tập luyện tập

Classify each of the following as primarily a provisioning, regulating, cultural, or supporting ecosystem service: (a) honeybees pollinating a commercial apple orchard; (b) a wetland removing excess nitrogen from agricultural runoff before it reaches a lake; (c) nutrient cycling carried out by decomposer fungi and bacteria in forest soil; (d) a coral reef used for recreational scuba-diving tourism.

Lời giải chi tiết

(a) Regulating service — pollination regulates the reproduction of the crop plants and is classified as a regulating rather than a direct provisioning service. **(b) Regulating service** — this is water purification, another regulating service. **(c) Supporting service** — nutrient cycling underlies and supports all other ecosystem functions and services, including primary production. **(d) Cultural service** — recreation and ecotourism value are classified as cultural services.

Bài tập luyện tập

The table below summarizes recent population trends for four species assessed by the IUCN.

Species	Population trend (last 3 generations)
Species W	Declined by about 35%; still widespread
Species X	Declined by about 60%; range now fragmented
Species Y	Declined by about 92%; only a few tiny, isolated wild subpopulations remain
Species Z	Stable; wide range; no significant identified threats

Match each species to the most appropriate IUCN Red List category: Least Concern, Vulnerable, Endangered, Critically Endangered.

Lời giải chi tiết

Species W — Vulnerable: a substantial decline (tens of percent) with an ongoing threat, but the species remains widespread, corresponds to the least severe of the three "threatened" categories.

Species X — Endangered: a more severe decline combined with range fragmentation indicates a higher extinction risk than Vulnerable, but the population is not yet reduced to the extremely low, fragmented state seen in Species Y.

Species Y — Critically Endangered: an extremely severe decline (over 90%) combined with only a few tiny, isolated wild subpopulations represents the highest extinction risk among species that still survive in the wild.

Species Z — Least Concern: a stable population with a wide range and no significant identified threats corresponds to the lowest level of extinction risk.

Bài tập luyện tập

A garden is surveyed for birds over one season, recording: Species 1 $= 14$, Species 2 $= 9$, Species 3 $= 7$, Species 4 $= 5$, Species 5 $= 5$. Calculate Simpson's Diversity Index for this bird community, and comment on what the value indicates about richness and evenness together.

Lời giải chi tiết

$N = 14 + 9 + 7 + 5 + 5 = 40$; $N(N-1) = 40 \times 39 = 1560$.

$$\sum n(n-1) = (14)(13) + (9)(8) + (7)(6) + (5)(4) + (5)(4) = 182 + 72 + 42 + 20 + 20 = 336.$$

$$D = 1 - \frac{336}{1560} = 1 - 0.215 = \textbf{0.78} \text{ (to 2 s.f.).}$$

A value of $D \approx 0.78$ indicates a fairly diverse bird community: five species are present (moderate richness) and no single species overwhelmingly dominates the sample — the most common species (Species 1, with 14 of 40 individuals) still makes up only 35% of the total, and the remaining individuals are reasonably evenly spread across the other four species, both richness and evenness contributing to the relatively high index value.

Theme B: Form and Function

Mục tiêu Unit: Sau khi hoàn thành Theme B, học sinh có thể: (1) mô tả cấu trúc phân tử của carbohydrate, lipid và protein, và liên hệ trực tiếp cấu trúc với chức năng (dự trữ năng lượng, vai trò cấu trúc, vận chuyển, xúc tác, miễn dịch, vận động); (2) giải thích mô hình khảm động của màng sinh chất và phân biệt các hình thức vận chuyển qua màng — khuếch tán đơn giản, khuếch tán tăng cường, thẩm thấu, vận chuyển chủ động, nhập bào và xuất bào — bao gồm kỹ năng tính phần trăm thay đổi khối lượng trong thí nghiệm thẩm thấu và xác định điểm đẳng trương; (3) mô tả cấu trúc và chức năng của các bào quan chính, giải thích lợi ích của sự phân chia ngăn (compartmentalization), phân loại tế bào gốc theo khả năng biệt hoá, và nêu các mức độ tổ chức từ tế bào đến cơ thể; (4) phân tích hệ thống trao đổi khí, hệ vận chuyển (tuần hoàn ở người, mạch gỗ và mạch rây ở thực vật) và cơ chế vận động ở mức phân tử (HL), bao gồm kỹ năng tính tỉ lệ diện tích bề mặt trên thể tích, lưu lượng tim, và đọc đường cong phân li oxy; (5) phân biệt các kiểu thích nghi với môi trường sống, tiến hoá hội tụ và phân li, và vận dụng khái niệm ổ sinh thái cơ bản/thực tế cùng nguyên lý loại trừ cạnh tranh để giải thích sự phân chia nguồn sống giữa các loài.

2.1 B1 Molecules: Carbohydrates, Lipids and Proteins

2.1.1 B1.1 Carbohydrates and Lipids

Carbohydrates are built from carbon, hydrogen, and oxygen, almost always in the ratio $\mathrm{C} : \mathrm{H} : \mathrm{O} = 1 : 2 : 1$. The simplest carbohydrates, **monosaccharides**, are single-ring or single-chain sugar units that serve as the building blocks for every larger carbohydrate.

Glucose, **fructose**, and **galactose** are the three biologically central monosaccharides. All three are hexoses with the same molecular formula, $\mathrm{C_6H_{12}O_6}$ — they are **structural isomers**: identical atoms, different arrangement. Glucose and galactose are **aldoses** (the carbonyl group is at the end of the chain) and typically form a six-membered ring; fructose is a **ketose** (the carbonyl group is internal) and typically forms a five-membered ring. In ring form, glucose exists as two interconvertible forms, α-glucose and β-glucose, differing only in the orientation of the $-\mathrm{OH}$ group on carbon 1 — a small difference with enormous structural consequences, since α-linked chains coil into storage polysaccharides while β-linked chains form straight, structural polysaccharides (see below). Glucose is the principal respiratory substrate of the cell; fructose is the sweetest of the three and abundant in fruit; galactose is a component of milk sugar.

VN **GIẢI THÍCH TIẾNG VIỆT**

Glucose, fructose và galactose đều là hexose (đường 6 carbon) với công thức phân tử giống nhau $\mathrm{C_6H_{12}O_6}$ — chúng là các **đồng phân cấu tạo** (structural isomers): cùng loại và số nguyên tử nhưng cách sắp xếp khác nhau. Glucose có hai dạng vòng α và β khác nhau ở vị trí nhóm $-\mathrm{OH}$ tại carbon số 1 — sự khác biệt nhỏ này quyết định việc một polysaccharide sẽ cuộn lại để dự trữ (liên kết α) hay xếp thẳng để làm khung cấu trúc (liên kết β).

Glycosidic bonds and disaccharides

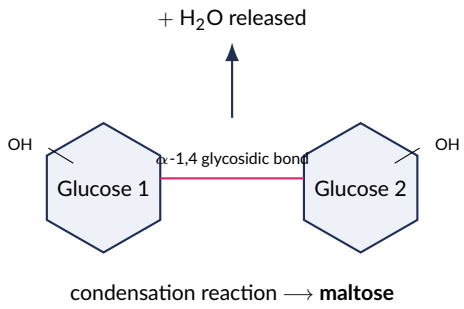
Two monosaccharides join by a **condensation reaction** (dehydration synthesis): an $-\mathrm{OH}$ group on one sugar reacts with an $-\mathrm{OH}$ group on the other, forming a covalent **glycosidic bond** and releasing

one molecule of H_2O. The reverse reaction, **hydrolysis**, adds a water molecule back across the bond to split the disaccharide into its two monosaccharides again — this is exactly how digestive enzymes (e.g., amylase, sucrase, lactase) break dietary carbohydrates apart.

Condensation vs. hydrolysis: condensation *joins* two monomers and *releases* one H_2O per bond formed; hydrolysis *splits* a bond by *adding* one H_2O back across it. Every glycosidic bond, ester bond, and peptide bond in this chapter is built by condensation and broken by hydrolysis — the same pattern, repeated across carbohydrates, lipids, and proteins.

The three key **disaccharides** for the syllabus are:

- **Maltose** = glucose + glucose, joined by an α-1,4 glycosidic bond (the product of starch digestion).
- **Sucrose** = glucose + fructose, joined by an α-1,2 glycosidic bond (table sugar; the sugar transported in phloem sap — Section B3.2).
- **Lactose** = galactose + glucose, joined by a β-1,4 glycosidic bond (milk sugar).



Formation of the disaccharide maltose from two glucose monomers by condensation: an $-$OH on each ring reacts to form an α-1,4 glycosidic bond, releasing one molecule of water. Hydrolysis (adding water back across the bond) reverses the reaction.

Ví dụ mẫu · Counting bonds and water molecules in a chain of monosaccharides

Three glucose molecules join end to end by condensation to form the linear trisaccharide maltotriose. (a) How many glycosidic bonds form? (b) How many water molecules are released? (c) If this trisaccharide is fully hydrolyzed back to monosaccharides, how many water molecules are consumed?

Joining n monomers into one unbranched chain always requires exactly $n-1$ bonds, because the first monomer needs one bond to attach the second, the growing chain needs one more bond to attach the third, and so on — one bond fewer than the number of monomers.

(a) $n = 3$ glucose units $\Rightarrow n - 1 = 2$ glycosidic bonds form.

(b) Each condensation reaction releases exactly one H_2O, so 2 molecules of water are released.

(c) Hydrolysis is the reverse of condensation, bond for bond, so exactly 2 molecules of water are consumed to break both bonds and regenerate the 3 separate glucose monomers.

VN **GIẢI THÍCH TIẾNG VIỆT**

Liên kết glycosidic hình thành giữa hai monosaccharide qua phản ứng **ngưng tụ** (condensation/dehydration synthesis), giải phóng một phân tử H_2O; phản ứng **thuỷ phân** (hydrolysis) làm ngược lại — thêm nước vào để cắt liên kết. Ba disaccharide cần nhớ: **maltose** (glucose + glucose, liên kết α-1,4), **sucrose** (glucose + fructose, liên kết α-1,2 — đường vận chuyển trong mạch rây), và **lactose** (galactose + glucose, liên kết β-1,4 — đường trong sữa). Quy tắc "n đơn phân → (n−1) liên kết → (n−1) phân tử nước" áp dụng cho mọi chuỗi polymer sinh học không phân nhánh (carbohydrate, protein, nucleic acid).

Polysaccharides: storage vs. structural roles

When many monosaccharides join by glycosidic bonds, the result is a **polysaccharide**. The syllabus distinguishes storage polysaccharides (starch, glycogen) from the structural polysaccharide cellulose, and the difference is a direct, testable case of structure determining function.

Starch is the glucose-storage polysaccharide of plants, made of two components: **amylose**, an unbranched chain of α-1,4-linked glucose that coils into a compact helix, and **amylopectin**, a branched chain of α-1,4-linked glucose with occasional α-1,6 branch points. **Glycogen**, the glucose-storage polysaccharide of animals (stored chiefly in liver and skeletal muscle), has the same basic α-1,4/α-1,6 chemistry as amylopectin but is *even more highly branched*.

Cellulose is the principal structural polysaccharide of plant cell walls: an unbranched chain of glucose monomers joined by β-1,4 glycosidic bonds. Because the β linkage forces each glucose unit to be rotated 180° relative to its neighbor, cellulose chains run straight rather than coiling, and adjacent parallel chains can pack side by side and cross-link through extensive **hydrogen bonding** between their $-$OH groups. Bundles of hydrogen-bonded chains form tough **microfibrils**, which in turn bundle into fibres with very high tensile strength.

Structure-function link in polysaccharides: *storage* polysaccharides (starch, glycogen) are built from α-glucose, are **compact** (helical amylose) or **highly branched** (amylopectin, glycogen) — branching creates many free ends so digestive/mobilizing enzymes can act simultaneously at multiple points, releasing glucose rapidly — and are large and insoluble, so they do not leak out of the cell or disturb its water potential. *Structural* polysaccharides (cellulose) are built from β-glucose, are **unbranched and straight**, and rely on extensive **hydrogen bonding** between parallel chains to build high-tensile-strength microfibrils.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tinh bột (starch, ở thực vật) gồm **amylose** (mạch thẳng không phân nhánh, cuộn xoắn, liên kết α-1,4) và **amylopectin** (mạch phân nhánh, có thêm liên kết α-1,6). **Glycogen** (ở động vật, dự trữ ở gan và cơ) có cấu trúc tương tự amylopectin nhưng phân nhánh **nhiều hơn** — giúp giải phóng glucose rất nhanh khi cơ thể cần năng lượng gấp (nhiều đầu mút → nhiều enzyme cùng hoạt động song song). **Cellulose** (thành tế bào thực vật) là mạch glucose không phân nhánh nối bằng liên kết β-1,4 — liên kết này làm mạch cellulose thẳng (không cuộn), các mạch song song liên kết với nhau bằng **liên kết hydro** tạo thành các **vi sợi** (microfibrils) rất bền, chịu lực kéo tốt — phù hợp với vai trò **cấu trúc/chịu lực** thay vì dự trữ.

Polysaccharide	Bond(s)	Structure	Role
Amylose (starch)	α-1,4	Unbranched, coils into a helix	Compact glucose storage (plants)
Amylopectin (starch)	α-1,4 + α-1,6	Branched	Glucose storage; branches allow faster enzymatic release
Glycogen	α-1,4 + α-1,6	Highly branched (more than amylopectin)	Rapidly mobilized glucose storage (liver, muscle)
Cellulose	β-1,4	Unbranched, straight; H-bonded into microfibrils	Structural — high tensile strength, plant cell wall

Ví dụ mẫu · Water released during synthesis of a storage polysaccharide

A single amylose molecule found in a potato starch granule is built from 600 glucose monomers joined end to end by α-1,4 glycosidic bonds. (a) How many glycosidic bonds does one amylose molecule contain, and how many water molecules are released during its synthesis? (b) A potato cell simultaneously synthesizes 1.00×10^{15} such amylose molecules. Calculate the total mass, in grams, of water released by this synthesis (molar mass of $H_2O = 18.0$ g/mol; Avogadro's constant $= 6.02 \times 10^{23}$ mol^{-1}).

(a) Using the same $n - 1$ rule established earlier for maltotriose: $n = 600$ glucose monomers $\Rightarrow n - 1 = 599$ glycosidic bonds, and therefore 599 molecules of H_2O released per amylose molecule.

(b) Total water molecules released $= 599 \times 1.00 \times 10^{15} = 5.99 \times 10^{17}$ molecules.

Converting to moles: $n(H_2O) = \dfrac{5.99 \times 10^{17}}{6.02 \times 10^{23}} \approx 9.95 \times 10^{-7}$ mol.

Converting to mass: $m = n \times M \approx 9.95 \times 10^{-7}$ mol $\times$ 18.0 g/mol $\approx 1.79 \times 10^{-5}$ g (about 17.9 μg).

Even though each individual amylose molecule is built from hundreds of monomers, the amount of water released by any realistic number of these condensation reactions remains a vanishingly small mass compared to the total water content of the cell — one reason a growing starch granule does not measurably dehydrate the surrounding cytoplasm.

VN **GIẢI THÍCH TIẾNG VIỆT**

Áp dụng quy tắc "n đơn phân $\rightarrow (n-1)$ liên kết $\rightarrow (n-1)$ phân tử nước" cho một phân tử amylose thực tế gồm 600 đơn vị glucose: 599 liên kết glycosidic hình thành, giải phóng 599 phân tử H_2O. Khi tính cho một số lượng lớn phân tử (ở đây $1{,}00 \times 10^{15}$ phân tử amylose), ta chuyển từ **số phân tử** sang **số mol** (chia cho hằng số Avogadro $6{,}02 \times 10^{23}$ mol^{-1}), rồi từ số mol sang **khối lượng** (nhân với khối lượng mol $18{,}0$ g/mol của nước) — đây là kỹ năng chuyển đổi đơn vị cơ bản, áp dụng được cho bất kỳ phản ứng hoá học nào tính theo số phân tử.

Lipids: structure and diversity

Lipids are a chemically diverse group united by one property: they are **nonpolar and hydrophobic**. This follows directly from their structure — lipids consist overwhelmingly of long hydrocarbon chains, dominated by nonpolar C − H and C − C covalent bonds that share electrons evenly and carry almost no partial charge, so a lipid molecule cannot hydrogen-bond with the surrounding water and is excluded from the hydrogen-bonded network of the aqueous phase.

A **triglyceride** (the main storage lipid, "fat" or "oil") is built from one molecule of **glycerol** (a three-carbon backbone with three −OH groups) and three **fatty acids** (a long hydrocarbon chain ending in a carboxyl group, −COOH). Each fatty acid condenses with one of glycerol's −OH groups, forming an **ester bond** and releasing one H_2O — three condensation reactions in total, releasing three water molecules to build one triglyceride.

Saturated fatty acids contain no carbon-carbon double bonds: every carbon in the tail is "saturated" with the maximum possible number of hydrogens, giving a straight, flexible hydrocarbon chain. Straight chains from neighboring triglyceride molecules can pack closely together, maximizing van der Waals attractions between them, which raises the **melting point** — saturated fats (e.g., animal fats such as butter and lard) are typically solid at room temperature. **Unsaturated** fatty acids contain one or more carbon-carbon double bonds; in the biologically common **cis** configuration, each double bond puts a rigid kink in the chain. These kinks prevent neighboring molecules from packing tightly, which lowers the melting point — unsaturated fats (e.g., most plant and fish oils) are typically

liquid at room temperature.

Ví dụ mẫu · Saturated vs. unsaturated fatty acids and melting point

Stearic acid (a saturated 18-carbon fatty acid, no C = C double bonds) has a melting point of approximately $69\,^{\circ}$C. Oleic acid (an 18-carbon fatty acid with one *cis* C = C double bond) melts at approximately $13\,^{\circ}$C. Linoleic acid (an 18-carbon fatty acid with two *cis* double bonds) melts at approximately $-5\,^{\circ}$C. (a) Predict which of the three would be solid and which would be liquid at room temperature ($\approx 20\,^{\circ}$C). (b) Explain the trend in molecular terms.

(a) Stearic acid ($69\,^{\circ}$C) is **solid** at $20\,^{\circ}$C since its melting point is far above room temperature; oleic acid ($13\,^{\circ}$C) and linoleic acid ($-5\,^{\circ}$C) are both **liquid** at $20\,^{\circ}$C, since room temperature exceeds both of their melting points.

(b) All three chains have the same length (18 carbons), so chain length is not the variable driving the trend — the number of *cis* double bonds is. Stearic acid's fully saturated, straight chain allows very close, regular packing with neighboring molecules, maximizing van der Waals attraction and requiring a high temperature to disrupt this packing (high melting point). Each additional *cis* double bond introduces one more rigid kink into the chain: oleic acid's single kink already disrupts packing enough to lower the melting point by more than $55\,^{\circ}$C relative to stearic acid, and linoleic acid's second kink disrupts packing further still, lowering the melting point below $0\,^{\circ}$C. More *cis* double bonds $\Rightarrow$ less efficient packing $\Rightarrow$ lower melting point.

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Triglyceride = glycerol + 3 acid béo (fatty acid), liên kết bằng **liên kết ester** (phản ứng ngưng tụ, giải phóng 3 H_2O). **Acid béo bão hoà** (saturated) không có liên kết đôi C = C $\rightarrow$ mạch thẳng $\rightarrow$ các phân tử xếp khít vào nhau $\rightarrow$ điểm nóng chảy **cao** $\rightarrow$ thường là chất rắn ở nhiệt độ phòng (mỡ động vật). **Acid béo không bão hoà** (unsaturated, dạng *cis*) có một hoặc nhiều liên kết đôi $\rightarrow$ mạch bị "gấp khúc" (kink) tại vị trí liên kết đôi $\rightarrow$ các phân tử không xếp khít được $\rightarrow$ điểm nóng chảy **thấp** $\rightarrow$ thường là chất lỏng ở nhiệt độ phòng (dầu thực vật). Số lượng liên kết đôi *cis* càng nhiều, điểm nóng chảy càng thấp.

A **phospholipid** replaces one of the three fatty acids of a triglyceride with a phosphate-containing group, producing a molecule with two very different ends: a small, charged, hydrophilic "head" (the phosphate group, often with an additional polar group attached) and two long, hydrophobic hydrocarbon "tails." A molecule with distinct hydrophilic and hydrophobic regions is called **amphipathic**. This single structural feature explains why phospholipids spontaneously assemble into the bilayers that form every biological membrane (Section B2.1) — the tails cluster together, away from water, while the heads face the surrounding aqueous solution on both sides.

Functions of lipids: (1) **energy storage** — lipids pack roughly twice as much chemical energy per gram as carbohydrates, because their carbon atoms are more reduced (more C — H bonds, fewer oxygen atoms already attached), releasing more energy on oxidation, and because they are insoluble and therefore do not raise the cell's internal solute concentration the way an equivalent mass of stored sugar would; (2) **thermal insulation** — subcutaneous fat and the thick blubber of marine mammals reduce heat loss to the environment; (3) **buoyancy** — fats and oils are less dense than water, helping some aquatic organisms (e.g., oily fish, whale blubber) maintain neutral or positive buoyancy; (4) **membrane structure** — phospholipids are the structural basis of every cell membrane.

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Phospholipid có cấu trúc **lưỡng tính** (amphipathic): đầu phosphate ưa nước (hydrophilic) và

hai đuôi acid béo kỵ nước (hydrophobic) — chính đặc điểm này khiến phospholipid tự sắp xếp thành lớp kép tạo nên mọi loại màng sinh học. **Lipid nói chung không phân cực/kỵ nước** vì cấu tạo chủ yếu từ liên kết C — H và C — C không phân cực, không thể tạo liên kết hydro với nước. Lipid có 4 vai trò chính: **dự trữ năng lượng** (đậm đặc năng lượng gấp đôi carbohydrate), **cách nhiệt**, **tạo lực nổi** ở sinh vật dưới nước, và **cấu trúc màng tế bào**.

Ví dụ mẫu · Comparing the energy content of lipids and carbohydrates

Complete oxidation of 1.00 g of carbohydrate releases approximately 17 kJ; complete oxidation of 1.00 g of lipid releases approximately 37 kJ. A food sample contains 12.0 g of carbohydrate and 8.0 g of lipid (and negligible protein). (a) Calculate the energy contributed by the carbohydrate, by the lipid, and the total energy content of the sample. (b) By what factor is the energy density of lipid greater than that of carbohydrate, per gram? (c) Explain this difference in terms of molecular structure.

(a) Carbohydrate: $12.0\ \text{g} \times 17\ \text{kJ/g} = 204\ \text{kJ}$. Lipid: $8.0\ \text{g} \times 37\ \text{kJ/g} = 296\ \text{kJ}$. Total $= 204 + 296 = 500\ \text{kJ}$.

(b) $\dfrac{37}{17} \approx 2.2$ — gram for gram, lipid releases roughly **twice** as much energy as carbohydrate on complete oxidation.

(c) A lipid molecule is built almost entirely from long hydrocarbon chains dominated by C — H and C — C bonds, so its carbon atoms are far more **reduced** (carrying many more hydrogens and far fewer oxygens already bonded to them) than the carbon atoms of a carbohydrate, which already carry roughly one oxygen atom (as —OH or C = O) per carbon. Because oxidation releases energy in proportion to how many electrons/hydrogens are transferred to oxygen during respiration, the more reduced carbon skeleton of a lipid has much further to be oxidized and therefore releases substantially more energy per gram than the already partly oxidized carbon skeleton of a carbohydrate.

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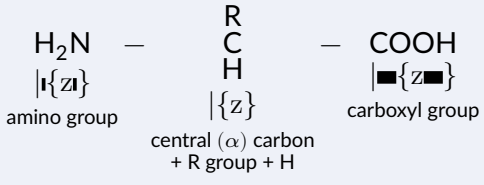
Xét trên cùng một khối lượng, **lipid** giải phóng năng lượng gấp khoảng **2** lần **carbohydrate** khi oxy hoá hoàn toàn (≈ 37 kJ/g so với ≈ 17 kJ/g), vì các nguyên tử carbon trong lipid ở dạng **khử nhiều hơn** (nhiều liên kết C — H, ít oxygen gắn sẵn hơn) so với carbohydrate — carbon "còn nhiều electron/hydrogen để nhường cho oxygen" hơn trong quá trình hô hấp, nên giải phóng nhiều năng lượng hơn trên mỗi gram.

2.1.2 B1.2 Proteins

Every protein is a polymer of **amino acids**. Each of the 20 standard amino acids shares the same core structure: a central (**alpha**) carbon bonded to four different groups — an **amino group** ($-NH_2$), a **carboxyl group** ($-COOH$), a single hydrogen atom ($-H$), and a variable **R group** (side chain) that is unique to each amino acid.

General amino acid structure



The amino group, carboxyl group, and hydrogen are identical in every amino acid; only the **R group** differs, and it is this variation alone that gives the 20 amino acids their distinct chemical personalities.

R groups fall into broad chemical classes that determine how a folded protein will behave: **non-polar/hydrophobic** R groups (e.g., glycine, alanine, valine, leucine, phenylalanine) avoid water and cluster in a protein's interior; **polar, uncharged** R groups (e.g., serine, threonine, asparagine, glutamine, cysteine) can hydrogen-bond with water and with each other; **acidic (negatively charged)** R groups (aspartate, glutamate) and **basic (positively charged)** R groups (lysine, arginine, histidine) can form ionic bonds with oppositely charged R groups elsewhere in the protein. This diversity of just 20 building blocks, combined in different sequences and numbers, is what allows proteins to build an almost unlimited range of three-dimensional shapes and functions.

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Mọi amino acid đều có cấu trúc chung: một carbon trung tâm (carbon α) liên kết với **nhóm amine** ($-NH_2$), **nhóm carboxyl** ($-COOH$), một nguyên tử **H**, và một **nhóm R** (gốc bên) — chỉ nhóm R khác nhau giữa 20 loại amino acid. Nhóm R được chia thành: **không phân cực/kỵ nước** (thường "chui vào trong" khi protein gấp lại), **phân cực không mang điện** (có thể tạo liên kết hydro), và **mang điện tích** (acid — âm; base — dương, có thể tạo liên kết ion với nhóm R mang điện ngược dấu). Chính sự đa dạng của 20 nhóm R này quyết định hình dạng và chức năng cuối cùng của mỗi protein.

Peptide bond formation

Two amino acids join when the carboxyl group of one condenses with the amino group of the next, forming a covalent **peptide bond** (C – N) and releasing one H_2O — the same condensation pattern seen for glycosidic and ester bonds. A chain of amino acids linked this way is a **polypeptide**.

Ví dụ mẫu · Counting peptide bonds and water released

A polypeptide chain contains 120 amino acid residues, synthesized one at a time by successive condensation reactions. (a) How many peptide bonds does the finished chain contain? (b) How many water molecules were released during its synthesis?

Using the same $n - 1$ rule as for polysaccharides (joining n monomers into one unbranched chain always requires $n - 1$ bonds):
(a) $n = 120$ amino acids $\Rightarrow n - 1 = 119$ peptide bonds.
(b) Each peptide bond releases exactly one H_2O, so 119 water molecules are released in total.

Levels of protein structure

A polypeptide's final, functional three-dimensional shape (its **conformation**) is built up through four levels of structure.

Level	What it is	Bonds/interactions involved
Primary	The linear sequence of amino acids in the chain	Peptide bonds (covalent)
Secondary	Regular local folding patterns: the α-helix (coiled) and the β-pleated sheet (extended, folded strands)	Hydrogen bonds between backbone C $=$ O and N $-$ H groups
Tertiary	The overall 3-D shape of one complete polypeptide, from folding of its secondary-structure elements	Hydrogen bonds, ionic bonds, hydrophobic interactions between R groups; disulfide bridges (S $-$ S) between cysteine R groups
Quaternary	The assembly of two or more separate polypeptide subunits into one functional complex	Same interactions as tertiary structure, but between separate chains

Primary structure is simply the order of amino acids, dictated by the gene sequence and held together only by covalent peptide bonds. **Secondary structure** arises when hydrogen bonds form in a regular, repeating pattern between the backbone atoms of the chain itself (not the R groups): in an **α-helix**, the chain coils and each turn is stabilized by hydrogen bonds to the turn below it; in a **β-pleated sheet**, extended strands of the chain lie side by side and are held together by hydrogen bonds between them. **Tertiary structure** is the overall folded shape of a single polypeptide, stabilized by a combination of weak **hydrogen bonds** and **ionic bonds** between charged/polar R groups, **hydrophobic interactions** that draw nonpolar R groups together and away from water, and — where two cysteine residues are brought close together — strong covalent **disulfide bridges** that cross-link and lock the shape in place. **Quaternary structure** exists only in proteins built from more than one polypeptide chain, held together by the same range of interactions that stabilize tertiary structure, now acting *between* subunits — hemoglobin, for example, is a quaternary protein made of four subunits ($2\,\alpha + 2\,\beta$), each carrying its own oxygen-binding heme group.

Ví dụ mẫu · Identifying a level of protein structure

Hemoglobin is composed of four separate polypeptide chains (two identical α-globin chains and two identical β-globin chains) held together as one functional oxygen-carrying complex. (a) Which level of protein structure does this four-chain assembly represent? (b) Name two types of interaction that could hold the four subunits together.

(a) Because hemoglobin's function depends on the association of *multiple separate polypeptide chains* into one complex, this is **quaternary structure** — by definition, quaternary structure only exists in proteins with more than one polypeptide subunit.

(b) The same interactions that stabilize tertiary structure hold quaternary assemblies together: e.g., **hydrogen bonds** between polar R groups on adjacent subunits, and **ionic bonds** between oppositely charged R groups at the subunit interfaces (hydrophobic interactions between nonpolar patches on adjoining subunit surfaces would also be acceptable).

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Bốn mức cấu trúc protein: **bậc 1** — trình tự amino acid (liên kết peptide, cộng hoá trị); **bậc 2** — các kiểu gấp cục bộ đều đặn: xoắn α và phiến gấp β (liên kết hydro giữa các nguyên tử *khung* của mạch, KHÔNG phải nhóm R); **bậc 3** — hình dạng 3D hoàn chỉnh của một chuỗi polypeptide (liên kết hydro, liên kết ion, tương tác kỵ nước, và cầu nối **disulfide** giữa hai cysteine); **bậc 4** — sự kết hợp của ≥ 2 chuỗi polypeptide riêng biệt thành một phức hợp chức năng (ví dụ: hemoglobin gồm 4 chuỗi).

Denaturation

Denaturation is the loss of a protein's specific secondary, tertiary, and (where present) quaternary structure, caused by extremes of **heat** or **pH** that disrupt the weak interactions — hydrogen bonds, ionic bonds, hydrophobic interactions, and sometimes disulfide bridges — holding the folded shape together. Excess heat provides enough kinetic energy to break these interactions and shake the chain out of its precise conformation; extreme pH changes the ionization state of acidic and basic R groups, destroying the pattern of ionic bonds and hydrogen bonds that stabilizes the fold. Once denatured, a protein loses its specific three-dimensional shape and, with it, its function — an enzyme's active site is distorted so it can no longer bind its substrate; a structural protein loses the shape that gave it strength.

(!) Lỗi thường gặp: Denaturation does *not* break peptide bonds. Denaturation disrupts only the *weak*, non-covalent interactions (and occasionally disulfide bridges) that maintain secondary/tertiary/quaternary structure — the primary sequence of amino acids, held by covalent peptide bonds, remains completely intact. Breaking peptide bonds themselves (reducing a protein to shorter fragments or free amino acids) is a completely different process, **hydrolysis**, and requires a specific hydrolytic enzyme (a protease) or strong acid/base plus much harsher conditions than typical denaturation.

Ví dụ mẫu · Predicting the effect of pH on enzyme activity

The graph below (data in the accompanying table) shows the relative activity of a digestive enzyme with a pH optimum close to neutral, measured across a range of pH values.

pH	2	4	6	7	8	10
Relative activity (%)	5	35	95	100	60	10

(a) Identify the enzyme's optimum pH. (b) Explain, in terms of protein structure, why activity is so low at pH 2. (c) Predict, with a reason, whether the enzyme would recover full activity if it were returned from pH 2 back to pH 7.

(a) Activity peaks at 100% at pH $= 7$, so the **optimum pH is 7**.

(b) At pH 2 (strongly acidic), the ionization state of the enzyme's acidic and basic R groups is altered from what it is at the optimum, disrupting the pattern of **ionic bonds** (and associated hydrogen bonds) that normally hold the enzyme's tertiary structure — and therefore its active site shape — in place. The enzyme becomes denatured: its active site no longer has the precise shape complementary to its substrate, so very little substrate can bind and catalysis falls to only 5% of maximum.

(c) Whether activity recovers depends on how severely the enzyme was denatured. A brief, moderate exposure to low pH may allow the disrupted ionic and hydrogen bonds to re-form correctly once neutral pH is restored, largely restoring activity. However, if the denaturation was prolonged or extreme (as pH 2 often is), the polypeptide may have unfolded so far that it re-folds incorrectly or aggregates with other unfolded molecules, in which case activity would *not* fully recover even after returning to pH 7 — denaturation is reversible only within limits.

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Biến tính protein (denaturation) là hiện tượng protein mất cấu trúc bậc 2/3/4 đặc trưng do nhiệt độ cao hoặc pH cực đoan phá vỡ các liên kết **yếu** (liên kết hydro, liên kết ion, tương tác kỵ nước, và đôi khi cả cầu nối disulfide) — liên kết peptide (bậc 1) **KHÔNG** bị phá vỡ. Hậu quả: hình dạng vị trí hoạt động (active site) của enzyme bị biến đổi, không còn khớp với cơ chất →

mất chức năng xúc tác. Đây khác hoàn toàn với **thuỷ phân** — quá trình phá vỡ chính liên kết peptide (bậc 1), cần enzyme protease hoặc acid/base mạnh.

Diversity of protein function

A protein's function is entirely determined by the precise three-dimensional shape produced by its amino acid sequence — the defining **structure-function relationship** of biological macromolecules. The same 20 amino acids, folded in different ways, build an extraordinary range of functional roles:

Functional class	Example	Structure-function link
Enzymes	Amylase, catalase	Precisely shaped active site binds and catalyzes a specific reaction
Structural	Collagen, keratin	Fibrous, often repetitive shape gives mechanical strength
Transport	Hemoglobin; membrane channel/carrier proteins	Binding site reversibly holds and releases a specific transported molecule
Hormones	Insulin	Shape allows specific binding to a receptor to trigger a response
Antibodies	Immunoglobulins	Variable binding region recognizes a specific antigen shape
Receptors	Membrane receptor proteins	Extracellular binding site recognizes a specific signal molecule
Motor proteins	Myosin, kinesin	Conformational changes convert chemical energy into mechanical movement

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Protein đảm nhiệm rất nhiều vai trò khác nhau — **enzyme** (xúc tác), **protein cấu trúc** (collagen, keratin), **protein vận chuyển** (hemoglobin, protein màng), **hormone** (insulin), **kháng thể** (nhận diện kháng nguyên), **thụ thể** (receptor), và **protein vận động** (myosin, kinesin) — nhưng tất cả đều tuân theo cùng một nguyên lý: **hình dạng 3D quyết định chức năng**, và hình dạng đó lại được quyết định hoàn toàn bởi trình tự amino acid (cấu trúc bậc 1).

2.2 B2 Cells: Membranes, Organelles and Specialization

2.2.1 B2.1 Membranes and Membrane Transport

Every cell is bounded by a **plasma membrane**, described by the **fluid mosaic model**: a **phospholipid bilayer** in which a varied assortment of proteins is embedded and free to drift.

Fluid mosaic model

Amphipathic phospholipids arrange themselves into a bilayer with hydrophilic heads facing the aqueous cytosol and extracellular fluid on either side, and hydrophobic tails packed together in the water-free interior. **Integral (transmembrane) proteins** span the full bilayer; **peripheral proteins** attach loosely to just one face. **Cholesterol** molecules are wedged between the phospholipid tails (chiefly in animal cell membranes): at high temperature they restrain

excess movement of the phospholipids (reducing fluidity), while at low temperature they prevent the tails from packing tightly and solidifying (maintaining fluidity) — cholesterol therefore stabilizes membrane fluidity across a range of temperatures. **Glycoproteins** and **glycolipids** (proteins/lipids with a short carbohydrate chain attached on the extracellular face only) act as cell-surface identity markers for cell-cell recognition. The membrane is **fluid** because phospholipids and many proteins move laterally within their own layer, and a **mosaic** because of the diverse mix of proteins scattered through it.

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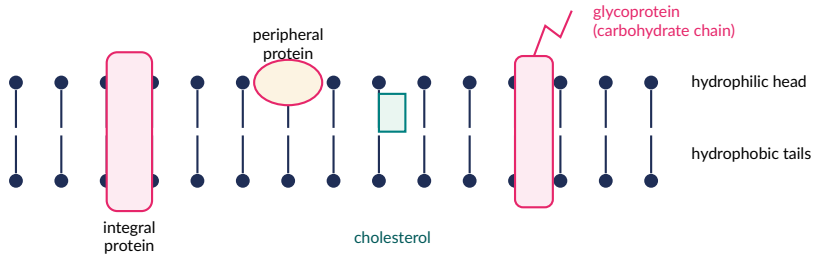
"**Khảm động**" (fluid mosaic): **khảm** vì màng là một "bức tranh ghép" của nhiều loại protein khác nhau nằm rải rác trong lớp phospholipid kép; **động** vì các phospholipid và nhiều protein có thể trượt ngang tự do. **Cholesterol** hoạt động như "bộ đệm" ổn định độ linh động của màng ở cả nhiệt độ cao và thấp. **Glycoprotein/glycolipid** ở mặt ngoài màng đóng vai trò như "thẻ căn cước" giúp tế bào nhận diện nhau.



Cross-section of the fluid mosaic membrane: phospholipid bilayer (hydrophilic heads outward, hydrophobic tails inward); an integral (transmembrane) protein; a peripheral protein attached to only the outer face; a cholesterol molecule wedged between phospholipid tails; and a glycoprotein bearing a short carbohydrate chain on its extracellular face, used for cell-cell recognition.

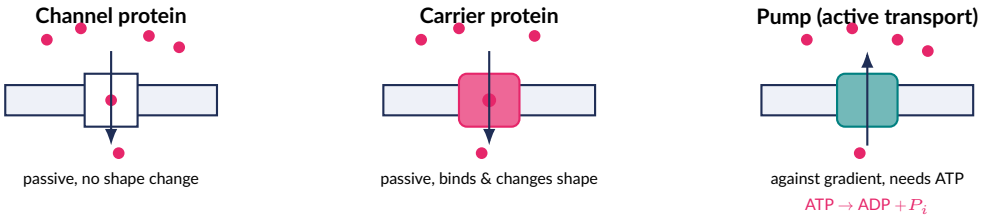
Membrane permeability depends on the hydrophobic interior of the bilayer: small, nonpolar molecules (O_2, CO_2, lipid-soluble hormones) and very small uncharged polar molecules (H_2O, slowly) can cross directly, while larger or charged/polar solutes (glucose, amino acids, Na^+, K^+, Cl^-) cannot cross unaided and require a specific transport protein. Permeability also depends on **temperature** — raised temperature increases the kinetic energy and fluidity of the bilayer, and past a critical point begins to denature membrane proteins, both of which increase leakiness — and on **organic solvents**, which dissolve the lipid bilayer itself and destroy the membrane's integrity (the classic reason ethanol and other solvents damage living tissue).

Simple diffusion and facilitated diffusion

Passive transport moves a substance down its concentration gradient (from high to low concentration) and needs no metabolic energy, because the gradient itself supplies the driving force. **Simple diffusion** is the unassisted movement of small nonpolar molecules directly through the lipid bilayer. **Facilitated diffusion** is passive movement of polar or charged solutes *with the help of* a transport protein — either a **channel protein**, which forms a permanent or gated hydrophilic pore (e.g., aquaporins for water; ion channels), or a **carrier protein**, which binds its solute and changes shape to shuttle it across (e.g., GLUT transporters for glucose).

(!) Lỗi thường gặp: Facilitated diffusion is still **passive** transport, even though it needs a protein. What makes a transport process "passive" versus "active" is not whether a protein is involved, but whether the solute moves *down* its gradient without any ATP hydrolysis. A channel or

carrier protein is needed here only because the solute is too polar, charged, or large to cross the lipid bilayer directly — the protein does not push the solute uphill, it simply provides a path down the existing gradient.



Left/centre: facilitated diffusion via a channel protein (a fixed hydrophilic pore) and a carrier protein (binds solute, changes conformation) — both passive, moving solute down its gradient with no ATP. Right: active transport via a pump protein, moving solute against its gradient using ATP hydrolysis.

VN **GIẢI THÍCH TIẾNG VIỆT**

Khuếch tán đơn giản: phân tử nhỏ, không phân cực đi trực tiếp qua lớp lipid kép, không cần protein. **Khuếch tán tăng cường** (facilitated diffusion): chất tan phân cực/mang điện vẫn đi THEO chiều gradient (không cần ATP) nhưng cần một **protein kênh** (channel — tạo lỗ xuyên màng cố định) hoặc **protein mang** (carrier — gắn với chất tan rồi đổi hình dạng để "chuyển" qua màng). Lỗi thường gặp: nhầm khuếch tán tăng cường với vận chuyển chủ động chỉ vì nó cần protein — điểm mấu chốt để phân biệt là chiều di chuyển so với gradient nồng độ và việc có cần ATP hay không, không phải việc có protein tham gia hay không.

Osmosis

Osmosis is the diffusion of *water* across a selectively permeable membrane, from a region of higher water concentration (lower solute concentration) to a region of lower water concentration (higher solute concentration) — that is, water moves down its own concentration gradient, exactly as any other diffusing substance does. This can also be described using **water potential**: water always moves from a region of higher water potential to a region of lower water potential, and dissolving any solute in water always *lowers* its water potential relative to pure water.

(!) Lỗi thường gặp: Osmosis is not a separate phenomenon from diffusion — it *is* diffusion, specifically the diffusion of water molecules down their own concentration gradient across a selectively permeable membrane. A very common error is to memorize "water moves toward the solution with less water" and then apply it backwards under pressure — the safer anchor is: water always moves toward the side with the *higher* solute concentration (equivalently, the *lower* water potential).

To determine and quantify the direction and extent of osmotic water movement experimentally, biologists commonly measure the change in **mass** of plant tissue (e.g., potato or carrot cylinders) placed into a range of solute concentrations.

$$\%\text{ change in mass} = \frac{\text{final mass} - \text{initial mass}}{\text{initial mass}} \times 100$$

A **positive** % change means the tissue gained water (surrounding solution was hypotonic to the tissue); a **negative** % change means the tissue lost water (surrounding solution was hypertonic to the tissue). The **isotonic point** is the solute concentration at which % change $= 0$ — at this concentration, the solution's water potential exactly matches the tissue's own internal water potential, so there is no net water movement in either direction.

Ví dụ mẫu · Osmosis in potato tissue — a full worked experiment

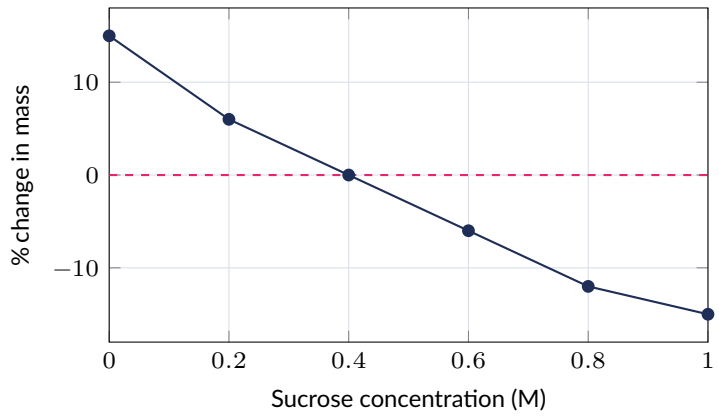
Six potato cylinders of equal starting mass (5.00 g each) were placed into open beakers of sucrose solution at six different concentrations for 30 minutes, then reweighed. The results are shown below.

Sucrose conc. (M)	Initial mass (g)	Final mass (g)	% change in mass
0.0	5.00	5.75	
0.2	5.00	5.30	
0.4	5.00	5.00	
0.6	5.00	4.70	
0.8	5.00	4.40	
1.0	5.00	4.25	

(a) Complete the % change column. (b) Identify the isotonic point of the potato tissue. (c) State the tonicity of the 1.0 M solution relative to the potato tissue, with a reason.

(a) Applying $\%\text{ change} = \dfrac{\text{final} - \text{initial}}{\text{initial}} \times 100$ to each row (initial mass $= 5.00$ g throughout):

Sucrose conc. (M)	Final mass (g)	Change (g)	% change
0.0	5.75	$+0.75$	$+15.0\%$
0.2	5.30	$+0.30$	$+6.0\%$
0.4	5.00	0.00	0.0%
0.6	4.70	-0.30	-6.0%
0.8	4.40	-0.60	-12.0%
1.0	4.25	-0.75	-15.0%



% change in potato cylinder mass vs. external sucrose concentration. The curve crosses the zero line (dashed) at the isotonic point.

(b) The % change is exactly 0.0% at 0.4 M, so the **isotonic point of this potato tissue is** 0.4 **M sucrose** — at this external concentration, the potato tissue's own internal solute concentration is matched, and there is no net water movement.

(c) At 1.0 M, the tissue *lost* mass (-15.0%), meaning water left the potato cells; this happens only when the surrounding solution has a higher solute concentration (lower water potential) than the cells — so the 1.0 M solution is **hypertonic** to the potato tissue.

VN **GIẢI THÍCH TIẾNG VIỆT**

Thí nghiệm thẩm thấu kinh điển: ngâm các khối mô thực vật (khoai tây, cà rốt...) vào dung dịch đường ở nhiều nồng độ khác nhau, đo khối lượng trước/sau, tính **% thay đổi khối lượng** $= \dfrac{\text{khối lượng cuối} - \text{khối lượng đầu}}{\text{khối lượng đầu}} \times 100$. % thay đổi **dương** → mô hút nước (dung dịch nhược trương so với mô); % thay đổi **âm** → mô mất nước (dung dịch ưu trương so với mô). **Điểm đẳng trương** (isotonic point) là nồng độ mà tại đó % thay đổi $= 0$ — đây chính là nồng độ chất tan bên trong mô. Đây là kỹ năng tính toán và đọc đồ thị quan trọng cần luyện thành thạo.

Tonicity	Animal cell (no wall)	Plant cell (has wall)
Isotonic	No net water movement	No net water movement (flaccid)
Hypertonic (more solute outside)	Water exits; cell shrinks	Water exits; membrane pulls away from wall (plasmolysis)
Hypotonic (less solute outside)	Water enters; may lyse (burst)	Water enters; wall resists — cell becomes turgid, does not burst

Active transport

Active transport moves a solute *against* its concentration (or electrochemical) gradient, from low to high concentration — an energetically unfavorable direction that requires an input of **ATP**. Active transport is always carried out by a specific **protein pump**. The defining example is the Na^+/K^+ **pump**, found in the plasma membrane of essentially all animal cells: for every ATP hydrolyzed, it exports 3 Na^+ ions and imports 2 K^+ ions, both against their own gradients, maintaining the steep ionic gradients that neurons and muscle cells depend on for electrical signaling.

Ví dụ mẫu · Classifying a transport process from a description

Classify each scenario below as simple diffusion, facilitated diffusion, or active transport, and justify each answer.
(a) O_2 moves from the alveolar air space (high concentration) into the blood (lower concentration) with no protein involved.
(b) A neuron's Na^+/K^+ pump moves Na^+ out of the cell, from a region of lower Na^+ concentration (inside) to a region of higher Na^+ concentration (outside), using ATP.
(c) Glucose moves into a cell through a GLUT carrier protein, from a region of higher extracellular glucose concentration to a region of lower intracellular glucose concentration, with no ATP used.

(a) **Simple diffusion**: O_2 is small and nonpolar, moves down its own concentration gradient, and needs no transport protein.

(b) **Active transport**: Na^+ is moved *against* its concentration gradient (low → high), which requires both a specific pump protein and ATP hydrolysis — the hallmark of active transport.
(c) **Facilitated diffusion**: although a carrier protein is required (glucose is too polar to cross the bilayer unaided), glucose is still moving *down* its own concentration gradient (high → low) and no ATP is consumed — this is passive transport assisted by a protein, not active transport.

VN GIẢI THÍCH TIẾNG VIỆT

Vận chuyển chủ động luôn đi NGƯỢC chiều gradient nồng độ và luôn cần **ATP** cùng một **protein bơm** chuyên biệt — ví dụ kinh điển là **bơm Na^+/K^+**: mỗi ATP thuỷ phân bơm 3 Na^+ ra ngoài và 2 K^+ vào trong tế bào, ngược chiều gradient của cả hai ion. Ba yếu tố cần kiểm tra để phân loại đúng một quá trình vận chuyển: (1) chiều di chuyển so với gradient, (2) có cần ATP không, (3) có cần protein không — chỉ riêng "có protein" không đủ để kết luận là vận chuyển chủ động.

Bulk transport: endocytosis and exocytosis

Material too large for any transport protein — macromolecules, particles, even whole cells — crosses the membrane packaged inside vesicles. **Endocytosis** brings material *into* the cell as the plasma membrane invaginates and pinches off a vesicle (e.g., a macrophage engulfing a bacterium by **phagocytosis**). **Exocytosis** is the reverse: an intracellular vesicle fuses with the plasma membrane, releasing its contents outside the cell (e.g., secretion of digestive enzymes or hormones). Both processes require ATP, since they involve active remodeling of the membrane and cytoskeleton.

VN GIẢI THÍCH TIẾNG VIỆT

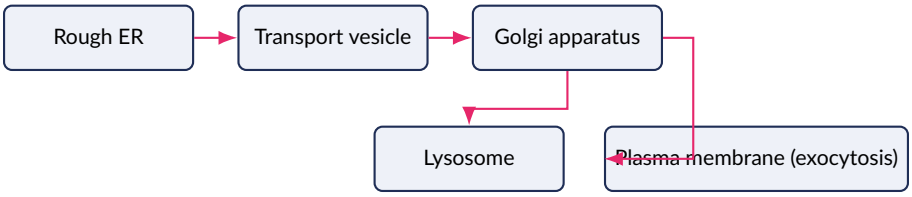
Nhập bào (endocytosis): màng tế bào lõm vào, "nuốt" vật chất vào trong dưới dạng túi (ví dụ: thực bào — phagocytosis). **Xuất bào** (exocytosis): túi nội bào hợp nhất với màng sinh chất để giải phóng chất ra ngoài. Cả hai đều cần ATP vì liên quan đến sự biến dạng chủ động của màng.

2.2.2 B2.2 Organelles and Compartmentalization

Eukaryotic cells subdivide their cytoplasm into a series of membrane-bound compartments that work together as a coordinated system for making, processing, and delivering proteins and lipids — the **endomembrane system**.

The protein secretory pathway

A secreted or membrane-bound protein typically travels: **nuclear envelope** (continuous with) → **rough endoplasmic reticulum** (ribosomes on its cytosolic face synthesize the protein directly into the ER lumen, where it begins folding and initial modification) → **transport vesicle** → **Golgi apparatus** (a stack of flattened membranous sacs; the protein is further modified, sorted, and tagged with an "address" as it passes from the receiving *cis* face to the shipping *trans* face) → **vesicle** → final destination: either the **plasma membrane** (released by exocytosis, or inserted as a membrane protein) or a **lysosome** (delivered as a digestive enzyme). The **smooth ER** (no ribosomes) branches off this system to synthesize lipids and detoxify drugs, rather than handling proteins.



The secretory pathway: proteins made on the rough ER are packaged into vesicles, processed and sorted through the Golgi apparatus, and delivered either to lysosomes or to the plasma membrane.

Mitochondria generate ATP by aerobic respiration. Their inner membrane is folded into **cristae**, dramatically increasing the surface area available to hold the electron transport chain proteins and ATP synthase enzymes that carry out the final, energy-yielding stages of respiration, without increasing the organelle's overall volume. **Chloroplasts** carry out photosynthesis; their internal membranes are folded into flattened, chlorophyll-containing sacs called **thylakoids** (often stacked into grana) bathed in a fluid **stroma** — the thylakoid membrane maximizes the surface area available for the light-dependent reactions, while the stroma holds the enzymes of the light-independent reactions.

Both mitochondria and chloroplasts are additionally bounded by a **double membrane** — an outer and an inner membrane, separated by a narrow intermembrane space — rather than the single membrane that encloses most other organelles. This double envelope adds a further, outer layer of compartmentalization on top of each organelle's own internal folded membranes (cristae; thylakoids), tightly controlling which molecules are allowed to cross into or out of the organelle, separately from the folding that amplifies internal surface area.

VN **GIẢI THÍCH TIẾNG VIỆT**

Cả **ty thể** và **lục lạp** đều được bao bọc bởi **màng kép** (màng ngoài và màng trong, ngăn cách bởi khoang gian màng hẹp) thay vì chỉ một lớp màng đơn như hầu hết bào quan khác. Lớp màng kép này tạo thêm một tầng phân chia ngăn (compartmentalization) nữa, kiểm soát chặt chẽ những phân tử nào được phép ra vào bào quan — tách biệt với việc gấp nếp màng bên trong (mào ty thể; thylakoid) vốn có vai trò tăng diện tích bề mặt.

Ví dụ mẫu · Cristae and surface area amplification

A hypothetical mitochondrion with a completely smooth (unfolded) inner membrane has an inner-membrane surface area of $6\ \mu\text{m}^2$ and a matrix volume of $2\ \mu\text{m}^3$. Folding the same amount of membrane into cristae increases the inner-membrane surface area to $24\ \mu\text{m}^2$ while the matrix volume stays at $2\ \mu\text{m}^3$ (folding adds surface area, not volume). Calculate the SA:V ratio of the inner membrane before and after folding, and state the factor by which cristae increase it.

Before folding: SA:V $= 6/2 = 3.0\ \mu\text{m}^{-1}$. After folding (cristae): SA:V $= 24/2 = 12.0\ \mu\text{m}^{-1}$. $\frac{12.0}{3.0} = 4$ — cristae increase the inner membrane's SA:V ratio (and hence the number of electron transport chain complexes and ATP synthase enzymes that can be packed into the same volume) by a factor of **4**, without requiring the mitochondrion to occupy any more space in the cell.

Ví dụ mẫu · Granal stacking and thylakoid surface area

An unstacked arrangement of a chloroplast's thylakoid membranes would occupy a stromal volume of $9\ \mu\text{m}^3$ while providing $54\ \mu\text{m}^2$ of thylakoid membrane surface area. By stacking the same total membrane area into compact grana (piles of disc-shaped thylakoids), the chloroplast fits this identical $54\ \mu\text{m}^2$ of membrane into a much smaller stromal volume of only $3\ \mu\text{m}^3$. (a) Calculate the SA:V ratio of the thylakoid system before and after granal stacking. (b) State the factor by which grana stacking increases this ratio. (c) Explain the functional benefit of this

increase for photosynthesis.

(a) Unstacked: SA:V $= 54/9 = 6.0\ \mu\text{m}^{-1}$. Stacked into grana: SA:V $= 54/3 = 18.0\ \mu\text{m}^{-1}$.

(b) $18.0/6.0 = 3$ — grana stacking triples the thylakoid system's SA:V ratio.

(c) The light-dependent reactions of photosynthesis occur on the thylakoid membrane, where photosystems, the electron transport chain, and ATP synthase are embedded. A higher SA:V ratio means more of this membrane — and therefore more photosynthetic machinery — can be packed into the same chloroplast volume, increasing the chloroplast's overall capacity to capture light energy and generate ATP/NADPH without the chloroplast itself needing to become larger.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tương tự việc gấp nếp màng trong ở ty thể (mào — cristae), lục lạp **xếp chồng** các túi thylakoid thành các **grana** để nén một diện tích màng lớn (chứa hệ quang hợp — photosystem, chuỗi truyền electron, ATP synthase) vào một thể tích stroma nhỏ hơn nhiều, làm tăng tỉ lệ SA:V của hệ thống màng thylakoid mà không cần lục lạp phải to hơn.

Compartmentalization — dividing the cell into distinct membrane-bound spaces — increases efficiency in two related ways. First, it creates **localized chemical environments** suited to specific reactions: lysosomes maintain an acidic interior (pH $\approx$ 4.5–5) that activates their hydrolytic enzymes, sharply different from the near-neutral cytosol; mitochondria maintain a proton gradient across the inner membrane that would be impossible in an open compartment. Second, it allows **incompatible reactions to proceed simultaneously**: powerful digestive enzymes are safely confined within lysosomes rather than roaming free in the cytosol, where they would degrade the cell's own proteins and organelles; and it concentrates specific enzymes and substrates together in one small volume, increasing local reaction rates well above what would occur if the same molecules were diluted throughout the entire cell.

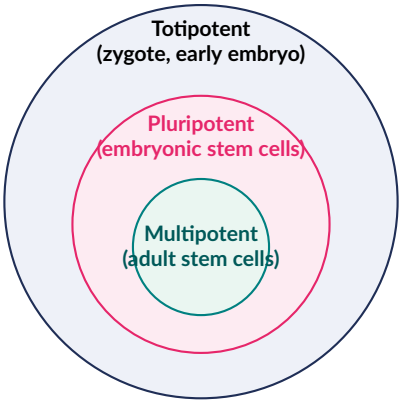
VN **GIẢI THÍCH TIẾNG VIỆT**

Hệ thống màng nội bào: nhân → lưới nội chất hạt (tổng hợp/gấp protein) → túi vận chuyển → Golgi (chỉnh sửa, phân loại, gắn "địa chỉ") → túi vận chuyển → đích cuối (màng sinh chất để xuất bào, hoặc lysosome). **Ty thể** gấp màng trong thành **mào** (cristae) để tăng diện tích chứa chuỗi truyền electron/ATP synthase mà không cần tăng thể tích. **Lục lạp** có hệ thống **thylakoid**/**grana** trong **stroma** để tăng diện tích cho phản ứng sáng. **Phân chia ngăn** (compartmentalization) giúp: (1) tạo môi trường hoá học cục bộ phù hợp cho từng phản ứng, và (2) cho phép các phản ứng không tương thích xảy ra đồng thời một cách an toàn, đồng thời tăng hiệu quả nhờ tập trung enzyme/cơ chất vào một không gian nhỏ.

2.2.3 B2.3 Cell Specialization

Multicellular organisms develop from a single fertilized cell through repeated division and **differentiation** — the process by which cells become structurally and functionally specialized by switching on some genes and permanently switching off others, even though every cell in the body carries an identical genome. The capacity of a cell to differentiate into other cell types is called its **potency**, and **stem cells** are classified by how much potency they retain:

Stem cell type	Can differentiate into	Example
Totipotent	Any cell type in the body *and* extra-embryonic tissues (e.g., placenta)	The zygote and cells of the very early embryo
Pluripotent	Any cell type in the body, but not extra-embryonic tissues	Embryonic stem cells
Multipotent	A limited range of related cell types	Adult bone-marrow (hematopoietic) stem cells → red cells, white cells, platelets



Potency is nested: pluripotent cells (pink) are a more restricted subset of totipotent capability (navy), and multipotent cells (teal) are more restricted still. Differentiation moves progressively inward on this diagram, permanently narrowing the range of cell types a lineage can still become.

Differentiation gives rise to cells whose structure is precisely matched to a single specialized function:

Specialized cell	Key structural features	Function served
Red blood cell	Biconcave disc (high SA:V); no nucleus or mitochondria; packed with hemoglobin	Maximizes O_2 transport capacity and diffusion
Neuron	Long axon, often myelinated; many dendrites	Rapid transmission of electrical signals over distance
Sperm cell	Flagellum; acrosome; many mitochondria; streamlined head, minimal cytoplasm	Motility and fertilization
Root hair cell	Long, thin extension of the cell surface	Increases SA:V for water/mineral absorption
Palisade mesophyll cell	Columnar shape, packed just under the upper leaf surface, many chloroplasts	Maximizes light capture for photosynthesis
Striated (skeletal) muscle fibre	Multinucleate; densely packed myofibrils/sarcomeres; many mitochondria	Force generation for movement (Section B3.3)

VN **GIẢI THÍCH TIẾNG VIỆT**

Tế bào gốc được phân loại theo khả năng biệt hoá: **toàn năng** (totipotent — thành mọi loại tế

bào, cả mô ngoài phôi), **đa năng** (pluripotent — thành mọi loại tế bào của cơ thể, không gồm mô ngoài phôi), và **vạn năng/đa tiềm năng hạn chế** (multipotent — chỉ thành một số loại tế bào liên quan, ví dụ tế bào gốc tuỷ xương chỉ tạo các dòng tế bào máu). **Biệt hoá** (differentiation) là quá trình tế bào trở nên chuyên hoá về cấu trúc và chức năng bằng cách bật/tắt các gene khác nhau, dù tất cả tế bào đều mang bộ gene giống nhau. Mỗi loại tế bào chuyên hoá (hồng cầu, neuron, tinh trùng, tế bào lông hút, tế bào mô giậu, sợi cơ vân) đều có cấu trúc được "thiết kế" khớp với đúng một chức năng riêng.

Ví dụ mẫu · Surface area amplification through cell specialization

An unspecialized root epidermal cell is modeled as a simple box with a surface area of $900\ \mu\text{m}^2$ and a volume of $1500\ \mu\text{m}^3$. Once this cell differentiates into a root hair cell, it grows a single long, thin tubular extension that increases its total surface area to $2700\ \mu\text{m}^2$ while its volume increases only slightly, to $1600\ \mu\text{m}^3$. (a) Calculate the SA:V ratio of the cell before and after differentiation. (b) By what factor has differentiation increased the cell's SA:V ratio? (c) Explain why this increase is advantageous for the cell's specialized function.

(a) Before: $\text{SA:V} = 900/1500 = 0.60\ \mu\text{m}^{-1}$. After: $\text{SA:V} = 2700/1600 \approx 1.69\ \mu\text{m}^{-1}$.

(b) $\dfrac{1.69}{0.60} \approx 2.8$ — differentiation into a root hair cell increases SA:V by roughly a factor of **2.8**, chiefly by adding surface area (the thin extension) while adding comparatively little volume.

(c) A root hair cell's specialized function is absorbing water and mineral ions from the soil solution, a process that occurs by diffusion and active transport across its plasma membrane. A higher SA:V ratio means more membrane surface (and therefore more transport proteins) is available per unit of cytoplasm the cell must maintain, directly increasing the rate at which water and minerals can be absorbed relative to the cell's size — the same surface-area-amplification principle already seen in cristae (Section B2.2) and alveoli (Section B3.1), here achieved through cell shape rather than internal membrane folding.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tương tự nguyên lý khuếch đại diện tích bề mặt bằng cách gấp nếp màng (mào ty thể — Section B2.2) hay bề mặt phế nang (Section B3.1), tế bào lông hút (root hair cell) khuếch đại SA:V bằng cách thay đổi **hình dạng** — mọc dài ra thành một phần lồi mỏng — làm tăng đáng kể diện tích màng sinh chất (nơi chứa protein vận chuyển) mà không làm tăng tương ứng thể tích tế bào, giúp tăng tốc độ hấp thu nước và khoáng chất.

Differentiated cells do not act alone: cells of a similar type organize into a **tissue** performing a shared function (e.g., muscle tissue); tissues combine into an **organ** performing a more complex function (e.g., the heart); organs combine into an **organ system** (e.g., the circulatory system); and organ systems together constitute the whole **organism**.

Levels of biological organization:

$$\text{Cells} \longrightarrow \text{Tissues} \longrightarrow \text{Organs} \longrightarrow \text{Organ systems} \longrightarrow \text{Organism}$$

Each level is built from, and depends on, the coordinated function of the level below it — a theme that returns throughout Section B3 (gas exchange, transport, and movement systems).

VN **GIẢI THÍCH TIẾNG VIỆT**

Các mức độ tổ chức của cơ thể sống: **tế bào** → **mô** (nhiều tế bào cùng loại, cùng chức năng)

→ **cơ quan** (nhiều loại mô phối hợp) → **hệ cơ quan** (nhiều cơ quan phối hợp) → **cơ thể**. Đây là khung tổ chức sẽ được áp dụng xuyên suốt phần B3 khi phân tích các hệ trao đổi khí, tuần hoàn và vận động.

2.3 B3 Organisms: Gas Exchange, Transport and Movement

2.3.1 B3.1 Gas Exchange

As an organism gets larger and more metabolically active, its **surface-area-to-volume ratio (SA:V)** falls — volume (and therefore metabolic demand for O_2 and nutrients) scales with the cube of linear size, while surface area (and therefore raw exchange capacity) scales only with the square. A small, inactive organism can exchange all the gases it needs directly across its outer body surface; a large or highly active organism cannot, because its enormous volume of respiring tissue would need far more gas exchange than its comparatively small outer surface can supply. This single geometric constraint is why large and/or active organisms evolve specialized, internal gas exchange surfaces rather than relying on their outer body surface.

For a sphere of radius r: SA $= 4\pi r^2$, $V = \frac{4}{3}\pi r^3$, so $\dfrac{\text{SA}}{V} = \dfrac{3}{r}$ — SA:V is inversely proportional to size. Doubling an organism's linear dimension halves its SA:V ratio.

Ví dụ mẫu · SA:V and the need for a specialized gas exchange surface

Two small aquatic organisms are modeled as spheres: Organism A has radius $r_A = 0.5$ mm; Organism B has radius $r_B = 5$ mm (ten times larger). (a) Calculate the SA:V ratio of each. (b) Explain what this implies about each organism's gas exchange strategy.

(a) Using SA:V $= 3/r$:
Organism A: SA:V $= 3/0.5 = 6.0$ mm^{-1}. Organism B: SA:V $= 3/5 = 0.6$ mm^{-1}.

(b) Organism B's SA:V ratio is exactly $10\times$ smaller than Organism A's — a direct consequence of B's radius being $10\times$ larger. Organism A, with its very high SA:V, can supply all its respiring tissue with O_2 by simple diffusion straight across its outer body surface. Organism B cannot: its outer surface area, relative to the volume of tissue it must supply, is ten times less adequate, so simple diffusion across the outer body surface alone would be far too slow to meet its metabolic demand. Organism B therefore needs a **specialized gas exchange surface** — internally folded or extended to add far more exchange area without adding proportionally more volume (exactly the amplification strategy seen in alveoli, gill lamellae, and leaf mesophyll).

VN **GIẢI THÍCH TIẾNG VIỆT**

Khi kích thước cơ thể tăng, thể tích (nhu cầu trao đổi khí) tăng theo luỹ thừa 3 trong khi diện tích bề mặt (khả năng trao đổi khí) chỉ tăng theo luỹ thừa 2 → tỉ lệ SA:V giảm dần. Sinh vật nhỏ, ít hoạt động có thể trao đổi khí trực tiếp qua toàn bộ bề mặt cơ thể; sinh vật lớn hoặc hoạt động mạnh (trao đổi chất cao) bắt buộc phải có **bề mặt trao đổi khí chuyên hoá** với diện tích được khuếch đại (gấp nếp, phế nang, phiến mang, mô giậu lá...) để bù lại tỉ lệ SA:V thấp.

An effective gas exchange surface shares four structural features, all of which maximize the rate of diffusion described qualitatively by **Fick's law**.

Fick's law (qualitative): the rate of diffusion across a surface is directly proportional to the **surface area** available and the **concentration (partial pressure) difference** across the surface, and inversely proportional to the **thickness** of the surface (the diffusion distance). A good gas exchange surface therefore has: (1) a **large surface area** (raises the numerator); (2) a very **thin** exchange surface — often just one cell thick (lowers the denominator, shortening the diffusion pathway); (3) a **moist** surface, since respiratory gases must dissolve before they can diffuse; and (4) a good **blood or ventilation supply**, which continuously replenishes the gradient by carrying gas away/toward the surface, keeping the concentration difference across the surface as large as possible.

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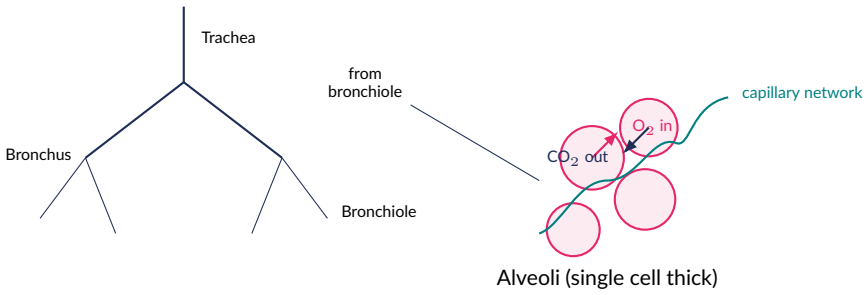
Định luật Fick (định tính): tốc độ khuếch tán tỉ lệ THUẬN với diện tích bề mặt và chênh lệch nồng độ (áp suất riêng phần), và tỉ lệ NGHỊCH với độ dày bề mặt trao đổi. Từ đó suy ra 4 đặc điểm của một bề mặt trao đổi khí tốt: **diện tích lớn**, **mỏng** (quãng đường khuếch tán ngắn), **ẩm ướt** (khí phải hoà tan trước khi khuếch tán), và **được cung cấp máu/thông khí tốt** (duy trì chênh lệch nồng độ luôn ở mức cao).

The human gas exchange system

Air travels from the **trachea** into two **bronchi** (one per lung), which branch repeatedly into progressively narrower **bronchioles**, ending in clusters of tiny air sacs called **alveoli** — the actual gas exchange surface, each wrapped in a dense network of capillaries. Alveoli satisfy every requirement of a good exchange surface: hundreds of millions of them give the lungs an enormous total surface area; their walls (and the adjacent capillary walls) are each only one cell thick, minimizing diffusion distance; their internal surface is coated in a thin film of moisture; and the capillary network continuously supplies deoxygenated blood and removes oxygenated blood, maintaining a steep diffusion gradient for both O_2 (into the blood) and CO_2 (out of the blood).

Ventilation — the physical movement of air into and out of the lungs — is driven by the **diaphragm** and the **intercostal muscles**, which change the volume (and therefore the pressure) of the thoracic cavity. On **inhalation**, the diaphragm contracts and flattens while the external intercostal muscles contract to lift the ribcage up and outward, increasing thoracic volume; this drop in internal pressure (below atmospheric pressure) draws air in. On **exhalation**, the diaphragm relaxes and domes upward while the ribcage falls, decreasing thoracic volume and raising internal pressure above atmospheric, pushing air out. This inverse pressure-volume relationship is the same principle as Boyle's law: for a fixed quantity of gas at constant temperature, pressure and volume vary inversely.



The human gas exchange system: trachea → bronchi → bronchioles → alveoli. Each alveolus is a thin-walled, moist air sac wrapped in capillaries, giving a short diffusion pathway, a huge total surface area, and a continuous blood supply.

Comparative gas exchange: leaves and fish gills

In a **leaf**, gases enter and leave through pores called **stomata** in the epidermis, each flanked by a pair of guard cells that open or close it. Beneath the stomata lies a moist **sub-stomatal air space**, and beyond that, the loosely packed **spongy mesophyll** cells, whose irregular shape creates a large, moist internal surface area for CO_2 to dissolve into and diffuse to the photosynthesizing cells.

Fish gills use **counter-current flow** to maximize O_2 extraction from water: blood in the gill lamellae flows in the *opposite* direction to the water flowing over them. Because the two flows run counter to each other, blood that is already fairly oxygenated is still exposed to water that is even more oxygenated, and blood that is poorly oxygenated meets water that has not yet given up any oxygen — a favorable diffusion gradient for O_2 is maintained along the *entire* length of the gill lamella, allowing fish to extract a much higher percentage of the dissolved O_2 in water than a parallel (concurrent) flow arrangement ever could, since concurrent flow would let the two fluids equilibrate partway along the exchange surface and lose the gradient over the rest of its length.

VN **GIẢI THÍCH TIẾNG VIỆT**

Ở **lá cây**: khí đi qua **khí khổng** (stomata) → **khoang dưới khí khổng** (ẩm) → **mô giậu/mô xốp** (diện tích bề mặt ẩm lớn nhờ hình dạng không đều của tế bào mô xốp). Ở **mang cá**: dòng máu chảy **ngược chiều** với dòng nước qua các phiến mang (**dòng chảy ngược chiều** — counter-current flow) giúp duy trì chênh lệch nồng độ O_2 suốt chiều dài phiến mang, cho phép cá lấy được lượng oxy tối đa từ nước — hiệu quả hơn hẳn nếu hai dòng chảy **cùng chiều** (nồng độ sẽ cân bằng giữa chừng và mất gradient ở phần còn lại của bề mặt trao đổi).

Ví dụ mẫu · Interpreting a ventilation (breathing) record

A subject's breathing was monitored at rest and during moderate exercise:

	Tidal volume (mL/breath)	Breathing rate (breaths/min)
Rest	500	15
Exercise	800	24

(a) Calculate the minute ventilation (total volume of air moved per minute = tidal volume × breathing rate) at rest and during exercise. (b) Calculate the percentage increase in minute ventilation from rest to exercise. (c) Explain the physiological reason for this change.

(a) Rest: $500 \times 15 = 7\,500$ mL/min $= 7.5$ L/min.
Exercise: $800 \times 24 = 19\,200$ mL/min $= 19.2$ L/min.

(b) $\%$ increase $= \dfrac{19\,200 - 7\,500}{7\,500} \times 100 = \dfrac{11\,700}{7\,500} \times 100 = 156\%$.

(c) Exercising muscle respires aerobically at a much higher rate, consuming O_2 and producing CO_2 far faster than at rest. To meet this demand, both the depth of each breath (tidal volume, driven by stronger contraction of the diaphragm and intercostal muscles, producing a larger change in thoracic volume) and the rate of breathing increase together, more than doubling minute ventilation and maintaining steep diffusion gradients for O_2 and CO_2 across the alveolar surface despite the much higher gas exchange demand.

2.3.2 B3.2 Transport

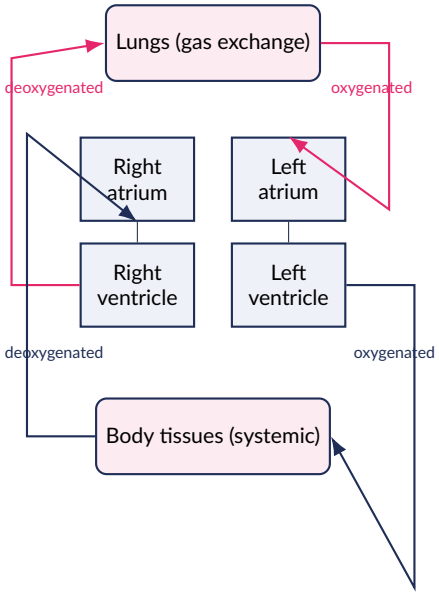
The same SA:V logic that demands a specialized gas exchange surface also demands a **mass transport system** in large or active organisms: diffusion alone is far too slow to move substances over distances greater than about a millimetre, so once an organism is larger than a few cell layers, it needs a bulk transport system to carry O_2, nutrients, hormones, and wastes rapidly between a specialized exchange surface and every respiring cell in the body.

The human heart and double circulation

The human heart is a four-chambered, muscular pump: two upper **atria** receive blood, two lower **ventricles** pump it out. Humans have a **double circulation** — two separate circuits, both driven by the same heart:

- **Pulmonary circulation**: the right ventricle pumps deoxygenated blood to the lungs, where it is oxygenated and returns to the left atrium.
- **Systemic circulation**: the left ventricle pumps oxygenated blood at high pressure to the rest of the body, where it delivers O_2 and collects CO_2, returning deoxygenated to the right atrium.

Keeping these two circuits separate (rather than a single mixed circuit) allows blood to be re-pressurized *after* the low-pressure lung capillaries and before it is sent around the whole body at high pressure — delivering oxygenated blood to tissues faster and more effectively than a single circuit could.



Double circulation: the pulmonary circuit (pink) carries blood between the right ventricle and the lungs; the systemic circuit (navy) carries blood between the left ventricle and the rest of the body. Both circuits pass back through the heart, which re-pressurizes blood before it enters the systemic circuit.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tuần hoàn kép ở người gồm hai vòng riêng biệt: **vòng tuần hoàn phổi** (tâm thất phải → phổi → tâm nhĩ trái) và **vòng tuần hoàn hệ thống** (tâm thất trái → toàn thân → tâm nhĩ phải). Việc tách riêng hai vòng cho phép máu được **tăng áp lại** sau khi đi qua mao mạch phổi (áp suất thấp), trước khi được bơm đi khắp cơ thể với áp suất cao — giúp vận chuyển máu giàu oxy đến các mô hiệu quả hơn nhiều so với một vòng tuần hoàn duy nhất.

$$\text{Cardiac output (CO)} = \text{Heart rate (HR)} \times \text{Stroke volume (SV)}$$

where HR is beats per minute and SV is the volume of blood pumped by one ventricle per beat (mL/beat); CO is typically expressed in mL/min or L/min.

Ví dụ mẫu · Calculating cardiac output

At rest, a person's heart rate is 72 beats/min and stroke volume is 70 mL/beat. During moderate exercise, heart rate rises to 150 beats/min and stroke volume rises to 110 mL/beat. (a)

Calculate resting cardiac output. (b) Calculate cardiac output during exercise. (c) By what factor has cardiac output increased?

(a) $CO_{rest} = 72 \times 70 = 5\,040$ mL/min $= 5.04$ L/min.
(b) $CO_{exercise} = 150 \times 110 = 16\,500$ mL/min $= 16.5$ L/min.
(c) $\frac{16.5}{5.04} \approx 3.3$ — cardiac output has increased by a factor of about 3.3, achieved through a combined rise in *both* heart rate (via increased sympathetic nervous stimulation of the pacemaker) and stroke volume (via stronger ventricular contraction), matching the sharply increased O_2 demand of exercising muscle.

Blood vessels and blood composition

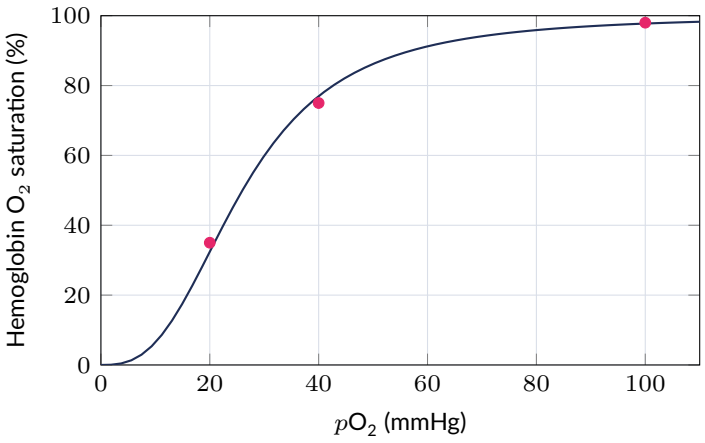
The three vessel types are each structurally matched to the pressure and function of the blood they carry:

Vessel	Structure	Function
Artery	Thick, muscular, elastic wall; narrow lumen	Carries blood *away* from the heart at high pressure; elastic wall stretches and recoils to smooth pulsatile flow
Vein	Thin wall; wide lumen; contains valves	Carries blood *toward* the heart at low pressure; valves prevent backflow
Capillary	Wall only one cell thick; large total cross-sectional/surface area	Site of exchange between blood and tissue fluid; short diffusion distance

Blood itself is a tissue composed of a liquid **plasma** (carrying dissolved nutrients, hormones, wastes, and heat) suspending three cellular/cell-fragment components: **red blood cells** (erythrocytes, carrying O_2 bound to hemoglobin), **white blood cells** (leukocytes, providing immune defense), and **platelets** (cell fragments involved in blood clotting).

Hemoglobin is the oxygen-transport protein packed into red blood cells; each molecule (a quaternary protein of four subunits, Section B1.2) can bind up to four O_2 molecules. The relationship between the partial pressure of oxygen (pO_2) and the percentage of hemoglobin's binding sites occupied (% saturation) is described by the sigmoid **oxygen dissociation curve**: at the high pO_2 found in the lungs, hemoglobin becomes almost fully saturated (loads O_2 efficiently); at the much lower pO_2 found in actively respiring tissue, hemoglobin's affinity for O_2 falls sharply and it releases (unloads) a large fraction of its bound O_2 — precisely where it is needed most.

Ví dụ mẫu · Interpreting an oxygen dissociation curve



A typical adult oxygen dissociation curve, with saturation marked at lung ($pO_2 \approx 100$ mmHg), resting tissue (≈ 40 mmHg), and actively respiring tissue (≈ 20 mmHg).

Using the marked points (100 mmHg → 98% saturated; 40 mmHg → 75%; 20 mmHg → 35%): (a) Describe the shape of the curve. (b) Calculate the percentage of hemoglobin's oxygen-carrying capacity unloaded as blood travels from the lungs to resting tissue, and separately to actively respiring tissue. (c) Explain why the curve is an advantage for supplying oxygen preferentially to more active tissue.

(a) The curve is **sigmoid (S-shaped)**: it rises gently at very low pO_2, steeply through the middle range, and flattens toward a plateau near 100% saturation at high pO_2 — a signature of **cooperative binding**, where each O_2 that binds makes it easier for the next to bind.

(b) To resting tissue: $98\% - 75\% = 23$ percentage points of saturation are unloaded. To actively respiring tissue: $98\% - 35\% = 63$ percentage points are unloaded.

(c) Because the curve is steepest across the range of pO_2 found in respiring tissue, a relatively small further drop in pO_2 (from resting tissue's ≈ 40 mmHg to active tissue's ≈ 20 mmHg) triggers a disproportionately large additional release of O_2 (63 vs. 23 percentage points) — hemoglobin automatically delivers far more oxygen to the tissue that is consuming it fastest (and therefore has driven its local pO_2 down the most), without requiring any separate regulatory signal.

(HL only) The oxygen dissociation curve is not fixed — it **shifts** depending on local conditions, a phenomenon called the **Bohr shift**. Actively respiring tissue produces CO_2 faster than resting tissue, and dissolved CO_2 lowers local pH (mostly by forming carbonic acid, which dissociates into H^+ and HCO_3^-). Both the raised CO_2 concentration and the raised H^+ concentration (lower pH) bind hemoglobin at sites away from the oxygen-binding heme groups, stabilizing its low-affinity (deoxygenated) conformation. The practical effect is that hemoglobin's dissociation curve **shifts to the right** under high-CO_2, low-pH conditions: for the *same* pO_2, hemoglobin now holds a *lower* percentage saturation than it would at resting pH/CO_2 — it releases more of its bound oxygen. Because the most active tissue produces the most CO_2 and lowers its own local pH the most, the Bohr shift automatically directs extra oxygen to exactly the tissue that is respiring fastest, on top of the effect of low pO_2 alone.

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(HL) Hiệu ứng Bohr (Bohr shift): mô hoạt động mạnh sinh ra nhiều CO_2 hơn → pH cục bộ giảm (do CO_2 tạo acid carbonic, phân ly ra H^+) → cả CO_2 và H^+ đều gắn vào hemoglobin ở vị trí khác với vị trí gắn oxy, làm ổn định dạng hemoglobin **ái lực thấp** với oxy → đường cong phân li

dịch chuyển sang **phải**: cùng một $p\text{O}_2$, hemoglobin giữ ít oxy hơn (giải phóng nhiều oxy hơn). Hiệu ứng này tự động ưu tiên cung cấp oxy cho mô đang hoạt động/hô hấp mạnh nhất — nơi có CO_2 cao nhất và pH thấp nhất.

Ví dụ mẫu · The Bohr shift — comparing two dissociation curves

The table below shows hemoglobin's % oxygen saturation at three values of $p\text{O}_2$, measured under two conditions: normal resting $p\text{CO}_2$, and the raised $p\text{CO}_2$ (lower pH) found in actively exercising muscle.

$p\text{O}_2$ (mmHg)	20	40	100
% saturation, resting $p\text{CO}_2$	35	75	98
% saturation, raised $p\text{CO}_2$ (exercising muscle)	20	55	95

(a) At $p\text{O}_2 = 40$ mmHg (typical of tissue capillaries), calculate the additional percentage of hemoglobin's oxygen that is unloaded under the raised-CO_2 condition compared with the resting condition. (b) Explain, in molecular terms, why raised CO_2 produces this shift. (c) Explain the physiological advantage of this effect specifically for exercising muscle.

(a) At 40 mmHg: resting $p\text{CO}_2$ gives 75% saturation; raised $p\text{CO}_2$ gives 55% saturation — a further $75 - 55 =$ **20** percentage points of saturation are lost, i.e., an extra 20% of hemoglobin's total oxygen-carrying capacity is unloaded at this $p\text{O}_2$ simply because of the raised CO_2/lower pH.

(b) Raised CO_2 increases local H^+ concentration (lower pH); both CO_2 and H^+ bind hemoglobin at allosteric sites away from the heme groups and stabilize its low-affinity, deoxygenated conformation, shifting the whole dissociation curve to the right — at any given $p\text{O}_2$, less oxygen remains bound.

(c) Exercising muscle both consumes O_2 faster (lowering local $p\text{O}_2$) and produces CO_2 faster (raising local CO_2, lowering local pH) than resting tissue. The Bohr shift means this same muscle also unloads a larger fraction of hemoglobin's oxygen than resting tissue would at the identical $p\text{O}_2$ — the tissue that needs oxygen most urgently automatically receives extra oxygen delivery, precisely because it is the tissue generating the most CO_2.

Xylem and phloem transport in plants

Plants also require mass transport, carried out by two separate vascular tissues.

Xylem transports water and dissolved minerals upward from roots to leaves, explained by the **transpiration-cohesion-tension theory**: water evaporates from the moist walls of leaf mesophyll cells into the sub-stomatal air space and out through open stomata (**transpiration**); this loss of water lowers the water potential of the mesophyll cells, pulling water out of the adjacent xylem vessels to replace it, which creates **tension** (negative pressure) that is transmitted all the way down the continuous water column inside the xylem, right down to the roots. Because water molecules hydrogen-bond strongly to one another (**cohesion**) and to the walls of the xylem vessel (**adhesion**), the water column does not break under this tension, and the whole column is drawn upward as one continuous thread — evaporation at the top does the "pulling," with no metabolic energy expenditure required from the plant itself.

Phloem transports the products of photosynthesis (mainly sucrose) from a **source** (a region making or releasing sugar, e.g., a photosynthesizing leaf) to a **sink** (a region consuming or storing sugar, e.g., a growing root or fruit) — a process called **translocation**. The **mass flow (pressure flow) hypothesis** explains the mechanism: companion cells actively load sucrose into the phloem sieve tubes at

the source (active transport, using ATP), which lowers the water potential inside the sieve tube there; water follows by osmosis from the adjacent xylem, raising hydrostatic pressure at the source end of the tube. At the sink, sucrose is actively unloaded and consumed/converted to storage products, raising the local water potential inside the sieve tube and causing water to leave by osmosis, which lowers hydrostatic pressure at the sink end. The resulting pressure gradient — high at the source, low at the sink — drives a passive, bulk **mass flow** of phloem sap from source to sink, carrying the dissolved sucrose along with it.

VN **GIẢI THÍCH TIẾNG VIỆT**

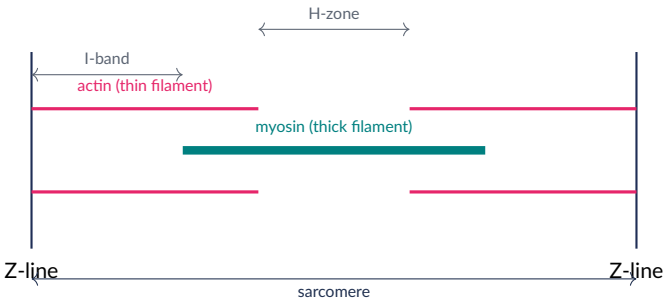
Mạch gỗ (xylem): thuyết **thoát hơi nước – lực liên kết – lực căng** (transpiration-cohesion-tension). Nước bốc hơi ở lá (thoát hơi nước qua khí khổng) → kéo nước ra khỏi mạch gỗ để bù lại → tạo **lực căng** (áp suất âm) truyền dọc xuống toàn bộ cột nước liên tục trong mạch gỗ. Nhờ **lực liên kết** (cohesion — liên kết hydro giữa các phân tử nước) và **lực bám dính** (adhesion — với thành mạch), cột nước không bị đứt gãy và được kéo lên cao mà cây không cần tiêu tốn năng lượng trực tiếp.

Mạch rây (phloem): **giả thuyết dòng khối** (mass flow/pressure flow hypothesis). Tại **nguồn** (source, ví dụ lá đang quang hợp), sucrose được nạp chủ động vào ống rây → nước theo vào bằng thẩm thấu → tăng áp suất thuỷ tĩnh. Tại **đích** (sink, ví dụ củ/quả đang phát triển), sucrose được lấy ra → nước rời khỏi ống rây bằng thẩm thấu → giảm áp suất. Chênh lệch áp suất (cao ở nguồn, thấp ở đích) đẩy dòng dịch mạch rây di chuyển hàng loạt (mass flow) từ nguồn đến đích.

2.3.3 B3.3 Muscle and Motility (HL only)

The content of this subsection (B3.3) is assessed at Higher Level only.

Skeletal muscle is built from long, multinucleate muscle fibres packed with **myofibrils**, each divided along its length into repeating contractile units called **sarcomeres** — the fundamental unit of muscle contraction. A sarcomere is bounded at each end by a **Z-line**; thin **actin** filaments are anchored to the Z-lines and project inward, while thick **myosin** filaments occupy the centre of the sarcomere, overlapping with the actin filaments on either side.



A relaxed sarcomere: thin actin filaments anchored at each Z-line, thick myosin filaments centred between them. During contraction the filaments slide past each other — the sarcomere, H-zone, and I-band all shorten, while the filaments themselves stay the same length.

Sliding filament theory

Muscle contraction does *not* shorten the actin or myosin filaments themselves — instead, the thin and thick filaments **slide past one another**, increasing their overlap and pulling the Z-lines at each end of the sarcomere closer together. The sarcomere shortens; the H-zone (myosin-only zone) and I-band (actin-only zone) both shrink; the length of each individual filament does not change.

The sliding is powered by the repeating **cross-bridge cycle**, regulated by two additional proteins wound around the actin filament: **tropomyosin**, a long strand that normally blocks the myosin-binding sites on actin, and **troponin**, a small protein complex attached to tropomyosin that is sensitive to Ca^{2+}.

The cross-bridge cycle (sliding filament mechanism):

1. A nerve impulse triggers release of Ca^{2+} from the sarcoplasmic reticulum into the muscle fibre's cytosol.
2. Ca^{2+} binds **troponin**, causing a conformational change that shifts **tropomyosin** away from the myosin-binding sites on actin, exposing them.
3. A myosin head, already energized by prior ATP hydrolysis (bound ADP $+P_i$), binds the exposed site on actin, forming a **cross-bridge**.
4. The myosin head pivots (the **power stroke**), releasing ADP $+P_i$ and pulling the actin filament toward the centre of the sarcomere.
5. A new **ATP** molecule binds the myosin head, causing it to detach from actin.
6. ATP is hydrolyzed, re-energizing (re-cocking) the myosin head; the cycle repeats for as long as Ca^{2+} and ATP remain available.

(!) Lỗi thường gặp: A very common error is describing myosin as "shortening" during contraction. Neither actin nor myosin filaments change length at any point in the cycle — only the amount of **overlap** between them changes, as the myosin heads repeatedly bind, pull, release, and re-bind further along the actin filament (like hands pulling in a rope). It is this progressive increase in filament overlap that shortens the sarcomere as a whole.

Ví dụ mẫu · Calculating sarcomere shortening (HL)

A relaxed sarcomere is measured (Z-line to Z-line) at $2.4\ \mu$m. During a single contraction, the thick (myosin) and thin (actin) filaments — each of fixed length throughout, $1.60\ \mu$m and $1.00\ \mu$m respectively — slide across one another so that the sarcomere shortens to $1.9\ \mu$m. (a) Calculate the percentage decrease in sarcomere length. (b) State what happens to the length of the actin and myosin filaments themselves during this shortening, and explain why. (c) A muscle fibre contains many sarcomeres arranged end to end along each myofibril. Explain why the whole-muscle shortening produced by many sarcomeres in series is far greater than the shortening of any single sarcomere.

(a) $\%$ decrease $= \dfrac{2.4 - 1.9}{2.4} \times 100 \approx 20.8\%$.

(b) Neither filament changes length: the myosin filament remains $1.60\ \mu$m and the actin filament remains $1.00\ \mu$m throughout. Sliding filament theory states that contraction results entirely from the filaments sliding past one another, increasing their region of overlap — no filament is compressed or shortened.

(c) Every sarcomere along a myofibril shortens by approximately the same percentage simultaneously, and a myofibril (and the whole muscle fibre) is built from thousands of sarcomeres joined end to end in series. Shortening is therefore additive along the whole chain: even though any one sarcomere only shortens by a fraction of a micrometre, the combined shortening of every sarcomere in series along the full length of the myofibril produces a macroscopic contraction of the whole muscle, visible as movement of the attached bone.

VN **GIẢI THÍCH TIẾNG VIỆT**

(HL) Trong một lần co cơ, sarcomere rút ngắn (ví dụ từ $2{,}4$ μm xuống $1{,}9$ μm, giảm $\approx 20{,}8\%$) nhưng **độ dài của sợi actin và myosin không đổi** — chỉ có mức độ chồng lấp (overlap) giữa chúng tăng lên. Vì mỗi sợi cơ (myofibril) được nối từ hàng ngàn sarcomere xếp nối tiếp nhau, tổng độ rút ngắn của toàn bộ sợi cơ là **tổng cộng dồn** từ độ rút ngắn nhỏ của từng sarcomere riêng lẻ — đây là lý do vì sao toàn cơ có thể co ngắn đáng kể dù mỗi sarcomere chỉ co lại vài phần trăm micromet.

Three types of muscle occur in the body: **skeletal muscle** (striated, multinucleate, under voluntary control, attaches to bone); **cardiac muscle** (striated, single nucleus per cell, connected by intercalated discs, contracts involuntarily and rhythmically without fatiguing); and **smooth muscle** (not striated, single nucleus, involuntary, found in the walls of internal organs such as the gut and blood vessels, capable of slow, sustained contraction).

Cells also achieve motility by mechanisms unrelated to sarcomeres. **Cilia** and **flagella** are both built around a **"9+2" arrangement** of microtubules — nine outer doublets surrounding a central pair — that bend when adjacent doublets slide past each other, powered by the motor protein dynein using ATP; cilia beat in short, coordinated strokes (e.g., sweeping mucus along the respiratory tract), while flagella undulate in longer whip-like waves (e.g., propelling a sperm cell). **Amoeboid movement**, used by cells such as *Amoeba* and white blood cells, instead relies on localized, ATP-driven remodeling of the actin cytoskeleton to extend temporary cytoplasmic projections (pseudopodia) in the direction of movement, with the rest of the cell body flowing after them.

VN **GIẢI THÍCH TIẾNG VIỆT**

(HL) Sarcomere: đơn vị co cơ cơ bản, giới hạn bởi hai **đường Z**, chứa sợi actin (mảnh) và sợi myosin (dày). **Thuyết trượt sợi cơ** (sliding filament theory): các sợi actin và myosin **không ngắn lại**, mà **trượt lên nhau**, kéo hai đường Z lại gần nhau hơn. Chu trình cầu nối ngang (cross-bridge cycle) cần Ca^{2+} (gắn troponin, đẩy tropomyosin lộ vị trí gắn myosin trên actin) và **ATP** (tách đầu myosin khỏi actin và "nạp lại năng lượng" cho đầu myosin). Ba loại cơ: **cơ vân** (theo ý muốn), **cơ tim** (không theo ý muốn, không mỏi), **cơ trơn** (không theo ý muốn, co chậm và bền). **Lông/roi** (cilia/flagella) dùng cấu trúc vi ống "9+2"; **chuyển động dạng amip** dùng sự tái cấu trúc bộ khung actin.

2.4 B4 Ecosystems: Adaptation and Niches

2.4.1 B4.1 Adaptation to Environment

An **adaptation** is any heritable trait that increases an organism's fitness (survival and reproductive success) in its particular environment, arising through natural selection over many generations. Adaptations fall into three overlapping categories: **structural** (anatomical features — e.g., a thick coat of fur), **physiological** (internal biochemical or metabolic processes — e.g., the ability to concentrate urine to conserve water), and **behavioural** (patterns of action — e.g., migrating seasonally, or being active only at night).

Biome	Structural / physiological adaptation	Behavioural adaptation
Desert (e.g., camel)	Fat stored in the hump (not spread under the skin, so it does not act as insulation and trap heat); highly efficient kidneys that produce very concentrated urine to conserve water	Nocturnal or crepuscular activity to avoid the hottest part of the day
Polar (e.g., Arctic fox)	Thick fur and a dense layer of insulating fat; small, rounded ears and short limbs, reducing SA:V to minimize heat loss; counter-current heat exchange in limb blood vessels	Huddling in groups; seasonal fur colour change (white in winter) for camouflage

Superficially similar adaptive structures can arise in two very different evolutionary ways, and distinguishing them is a core syllabus skill.

Convergent vs. divergent evolution

Convergent evolution occurs when unrelated species independently evolve similar structures because they face similar environmental/selective pressures, *not* because they share a recent common ancestor. The resulting structures are **analogous**: similar in function and often in outward appearance, but with different underlying anatomy and developmental origin (e.g., the wings of birds, bats, and insects — flight evolved independently in each lineage).

Divergent evolution occurs when closely related species, descended from a common ancestor, evolve differences over time — often as they adapt to different environments or ways of life. Structures inherited from that shared ancestor, even when they now look and function very differently, are **homologous** (e.g., the pentadactyl limb, sharing the same underlying bone arrangement in a human arm, a bird wing, a whale flipper, and a bat wing, despite their very different current functions).

(!) Lỗi thường gặp: Do not judge homology vs. analogy from outward appearance or even shared function alone. **Homologous** structures share an underlying anatomical/developmental origin from a common ancestor, even if their current function is completely different (e.g., a human arm for manipulation and a whale flipper for swimming share the same pentadactyl bone plan). **Analogous** structures can look and function almost identically (e.g., a bird wing and an insect wing both enable flight) yet have completely different underlying structure and *no* shared ancestral origin for that structure — the similarity arose independently, by convergent evolution, purely because both lineages faced the same selective pressure (the need to fly).

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Tiến hoá hội tụ (convergent evolution): các loài KHÔNG có quan hệ họ hàng gần tiến hoá **độc lập** ra cấu trúc tương tự do cùng chịu áp lực chọn lọc giống nhau → tạo ra **cấu trúc tương đồng chức năng** (analogous structures — giống nhau về chức năng/hình dạng bên ngoài nhưng nguồn gốc giải phẫu khác nhau; ví dụ: cánh chim, cánh dơi, cánh côn trùng). **Tiến hoá phân li** (divergent evolution): các loài có họ hàng gần (chung tổ tiên) dần trở nên khác nhau khi thích nghi với môi trường khác nhau → tạo ra **cấu trúc tương đồng nguồn gốc** (homologous structures — cùng nguồn gốc giải phẫu nhưng chức năng hiện tại có thể rất khác nhau; ví dụ: chi năm ngón ở người, cá voi, dơi). Lỗi thường gặp: chỉ nhìn vẻ ngoài hoặc chức năng giống

nhau rồi vội kết luận là "tương đồng nguồn gốc" — phải xét đến **nguồn gốc giải phẫu/phát triển**.

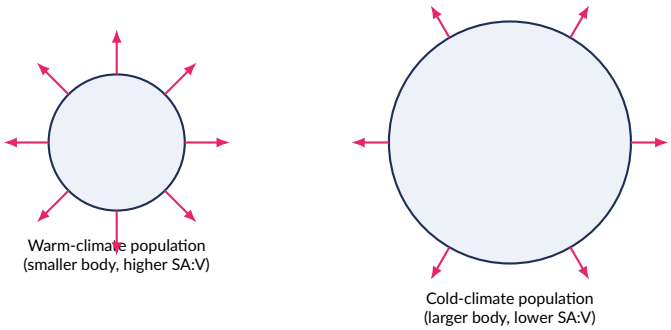
Adaptations are rarely free: most involve a **trade-off**, an inescapable cost that accompanies the adaptive benefit. A cactus's reduced, spine-like leaves dramatically cut water loss through transpiration in an arid environment (benefit), but the same reduction sacrifices most of the leaf's photosynthetic surface area, so the stem must take over photosynthesis instead (cost); the spines also deter herbivores (added benefit), at the metabolic cost of producing rigid, lignified structures (added cost). Similarly, the Arctic fox's thick winter coat conserves heat superbly in extreme cold (benefit), but the same insulation becomes a liability — restricting movement and risking overheating — if the animal is active during unusually warm conditions or vigorous exertion (cost). Evolution optimizes traits for the *typical* conditions a population experiences, not for every possible condition, which is exactly why such trade-offs persist rather than being eliminated by selection.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hầu hết các đặc điểm thích nghi đều đi kèm một **sự đánh đổi** (trade-off): lợi ích ở khía cạnh này thường phải trả giá ở khía cạnh khác. Ví dụ: gai xương rồng giảm mất nước (lợi) nhưng cũng giảm diện tích quang hợp, buộc thân cây phải đảm nhận vai trò quang hợp thay lá (hại). Chọn lọc tự nhiên tối ưu hoá đặc điểm cho **điều kiện phổ biến/thường gặp** của quần thể, không phải cho mọi tình huống có thể xảy ra — đó là lý do các sự đánh đổi này vẫn tồn tại thay vì bị loại bỏ hoàn toàn.

Body size, shape, and heat conservation: Bergmann's and Allen's rules

Two well-established ecogeographical patterns link an animal's size and shape directly to the SA:V principle introduced in Section B3.1. **Bergmann's rule**: within a widely distributed group of closely related endothermic (warm-blooded) species or populations, individuals living in colder climates tend to be larger-bodied than close relatives in warmer climates. A larger body has a lower SA:V ratio, so it loses relatively less heat to the environment per unit of body mass — an advantage in the cold, where retaining metabolic heat is critical, but a disadvantage in the heat, where a smaller, higher-SA:V body sheds excess heat more easily. **Allen's rule** applies the same logic to body extremities: cold-climate populations tend to have shorter, more compact limbs, ears, and tails than warm-climate relatives, since protruding extremities disproportionately increase SA:V and heat loss (see the Arctic fox's short limbs and rounded ears, above).



Bergmann's rule: a larger body (right) has proportionally less surface area per unit volume than a smaller body of the same shape (left), so it loses relatively less heat (pink arrows represent heat loss per unit surface) — an advantage for conserving body heat in cold climates.

VN **GIẢI THÍCH TIẾNG VIỆT**

Quy tắc Bergmann: trong cùng một nhóm loài/quần thể động vật máu nóng có quan hệ họ hàng gần, các cá thể sống ở vùng khí hậu lạnh thường có kích thước cơ thể **lớn hơn** — cơ thể lớn có tỉ lệ SA:V **thấp hơn**, giảm mất nhiệt tương đối, có lợi trong môi trường lạnh. **Quy tắc Allen**: động vật vùng lạnh thường có tai, chi, đuôi **ngắn/nhỏ hơn** (giảm SA:V ở các phần phụ, hạn chế mất nhiệt) so với họ hàng ở vùng nóng. Cả hai quy tắc đều là ứng dụng trực tiếp của nguyên lý SA:V đã học ở Section B3.1.

Ví dụ mẫu · Applying Bergmann's rule with SA:V calculations

Two populations of the same fox species are modeled as spheres for simplicity. The warm-climate population has an average body radius of 10 cm; the cold-climate population (same species, different region) has an average body radius of 16 cm. (a) Calculate the SA:V ratio of each population, using SA:V $= 3/r$. (b) State which population is predicted to lose relatively less heat per unit of body mass, and explain why. (c) Explain how this observation is consistent with Bergmann's rule.

(a) Warm-climate population: SA:V $= 3/10 = 0.30$ cm^{-1}. Cold-climate population: SA:V $= 3/16 \approx 0.19$ cm^{-1}.

(b) The **cold-climate population** has the lower SA:V ratio (0.19 vs. 0.30 cm^{-1}), meaning it has less surface area available for heat loss relative to its heat-generating body mass/volume — it therefore loses relatively less heat to its surroundings per unit of body mass than the warm-climate population does.

(c) Bergmann's rule predicts that populations of the same species living in colder climates will tend to be larger-bodied than those in warmer climates, because the resulting lower SA:V conserves metabolic heat more effectively — exactly the pattern shown here: the larger-bodied ($r = 16$ cm) population is the one found in the colder climate, consistent with selection favouring reduced relative heat loss where retaining body heat is most critical for survival.

2.4.2 B4.2 Ecological Niches

An organism's **ecological niche** is the full set of biotic and abiotic conditions and resources it requires to survive and reproduce — not just *where* it lives (its **habitat**), but its functional **role** in the community (what it eats, what eats it, how and where it reproduces, its interactions with every other species around it, and the range of physical conditions — temperature, pH, moisture — it can tolerate).

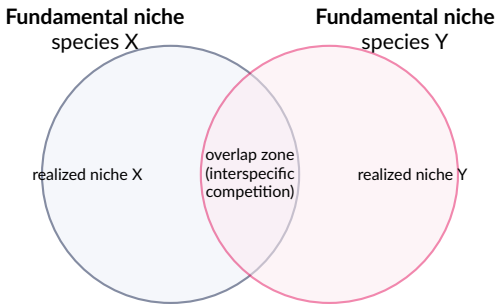
Fundamental vs. realized niche

The **fundamental niche** is the full range of conditions and resources a species *could* theoretically occupy in the total absence of competitors and other biotic constraints. The **realized niche** is the narrower range a species *actually* occupies in practice, once interactions with competitors, predators, and other species restrict it. A species' realized niche is always a subset of (never larger than) its fundamental niche.

When two species' niches overlap enough that they compete for the same limited resource, **interspecific competition** results — one species uses a resource, reducing its availability to the other. The **competitive exclusion principle** states that two species with *identical* niches (requiring exactly the same limited resource in exactly the same way) cannot coexist indefinitely in the same habitat: the species that is even slightly more efficient at exploiting the shared resource will eventually outcompete and locally eliminate the other.

In practice, complete niche overlap is rare, because competition itself drives **resource partitioning**: natural selection favours individuals of each competing species that use the contested resource

slightly differently (e.g., feeding at a different time, in a different location, or on a slightly different food size), progressively reducing the overlap between their realized niches — **niche differentiation**. This is exactly why competing species so often persist side by side in nature despite superficially similar requirements: ongoing selection has already narrowed each species' realized niche away from direct, head-on competition with the other.



Overlapping fundamental niches of two competing species. In the shaded overlap zone, interspecific competition for shared resources occurs; each species' realized niche is pushed toward the non-overlapping region as resource partitioning reduces competition.

Two classic field examples illustrate these principles. On Galápagos islands, different species of Darwin's finches have evolved distinctly shaped and sized beaks suited to different food items (e.g., large, deep beaks for cracking hard seeds; slender beaks for probing flowers or catching insects) — a clear case of resource partitioning that reduces competition between co-occurring finch species. On rocky European shores, Joseph Connell's classic experiment with two barnacle species showed that *Chthamalus* can survive across a broad vertical range of the shore (its fundamental niche) but is restricted in practice to the upper shore (its realized niche), because the faster-growing *Balanus* out-competes and physically smothers it lower down — direct evidence of competitive exclusion shaping a realized niche.

Ví dụ mẫu · Niche overlap and the competitive exclusion principle

Two insectivorous bird species share the same woodland habitat. Their diet, recorded as the percentage of foraging time spent on three prey-size categories, is shown below.

Species	Small insects (%)	Medium insects (%)	Large insects (%)
Species X	60	30	10
Species Y	10	30	60

(a) Calculate the total dietary niche overlap between the two species (the overlap in each category is the *smaller* of the two percentages; total overlap is the sum across all categories). (b) Based on this overlap, predict whether the competitive exclusion principle predicts that one species will exclude the other, and explain your reasoning.

(a) Small insects: $\min(60, 10) = 10$. Medium insects: $\min(30, 30) = 30$. Large insects: $\min(10, 60) = 10$.
Total overlap $= 10 + 30 + 10 =$ **50**%.

(b) A 50% overlap means the two species share roughly half of their foraging effort, concentrated almost entirely in the medium-insect category, while each species obtains the majority of its diet (60%) from a prey-size class the other barely uses (10%). This pattern is evidence of substantial **resource partitioning**: rather than competing head-on for the same resource across their entire diet, each species has differentiated into a largely separate feeding niche (small insects for X, large insects for Y), with competition confined mainly to the shared medium-insect category. Because the overlap is only partial rather than near-total, the competitive exclusion

principle does *not* predict that one species will eliminate the other — partial resource partitioning of this kind is exactly the mechanism that typically allows ecologically similar competing species to coexist.

VN **GIẢI THÍCH TIẾNG VIỆT**

Ổ sinh thái (niche) không chỉ là nơi sống (habitat) mà là toàn bộ vai trò chức năng và các mối tương tác của loài trong quần xã. **Ổ sinh thái cơ bản** (fundamental niche): phạm vi loài CÓ THỂ chiếm giữ nếu không có đối thủ cạnh tranh. **Ổ sinh thái thực tế** (realized niche): phạm vi loài THỰC SỰ chiếm giữ sau khi bị giới hạn bởi cạnh tranh/thiên địch — luôn là tập con của ổ sinh thái cơ bản. **Nguyên lý loại trừ cạnh tranh**: hai loài có ổ sinh thái GIỐNG HỆT nhau không thể cùng tồn tại lâu dài — loài hiệu quả hơn sẽ loại trừ loài kia. Trong tự nhiên, cạnh tranh thường thúc đẩy **phân chia nguồn sống** (resource partitioning) và **phân hoá ổ sinh thái** (niche differentiation), giúp các loài cùng tồn tại — ví dụ kinh điển: mỏ các loài chim sẻ Darwin ở Galápagos, và sự phân vùng theo độ cao của hai loài hà biển (barnacle) trong thí nghiệm của Connell.

2.5 Theme B Practice Bank

Bài tập luyện tập

A glycosidic bond forms between two monosaccharides by which type of reaction, and what small molecule is released?

(A) Hydrolysis; a water molecule is consumed

(B) Condensation; a water molecule is released

(C) Phosphorylation; a phosphate group is released

(D) Oxidation; a carbon dioxide molecule is released

Lời giải chi tiết

A glycosidic bond forms when an –OH group on each monosaccharide reacts, joining the two sugars and releasing one H_2O — this is a condensation (dehydration synthesis) reaction. Hydrolysis is the reverse process (adds water to break the bond). **(B)**.

Bài tập luyện tập

Glycogen is far more highly branched than amylose. Explain how this structural difference makes glycogen better suited than amylose to its role as a rapidly mobilized energy reserve in animal muscle and liver cells.

Lời giải chi tiết

Amylose is an unbranched, coiled chain with only two free ends (one at each end of the chain) where a hydrolytic enzyme can begin removing glucose units. Glycogen's extensive branching creates a very large number of free ends distributed throughout the molecule, so many enzyme molecules (e.g., glycogen phosphorylase) can act simultaneously at different branch points, releasing glucose monomers far more rapidly than a chain with only two accessible ends could. This matches glycogen's biological role: animal cells often need a fast burst of glucose (e.g., at the start of exercise), whereas amylose's more compact, less accessible structure suits the

comparatively slower, longer-term storage needs of a plant.

Bài tập luyện tập

Cellulose and starch are both polymers of glucose, yet cellulose is used as a structural material in plant cell walls while starch is used for storage. Which of the following best explains this difference?

(A) Cellulose is made of fructose, not glucose, giving it more tensile strength.

(B) Cellulose's β-1,4 glycosidic bonds produce straight, unbranched chains that hydrogen-bond into strong microfibrils, while starch's α-1,4 bonds produce a coiled or branched, compact structure suited to storage.

(C) Starch molecules are covalently cross-linked to each other, while cellulose molecules are not.

(D) Cellulose is soluble in water, allowing it to be transported easily to the cell wall.

Lời giải chi tiết

The β-1,4 linkage in cellulose rotates each successive glucose unit 180° relative to its neighbour, producing long, straight chains that pack side by side and hydrogen-bond extensively into tough microfibrils — ideal for a load-bearing structural role. The α-1,4 (and α-1,6) linkages in starch instead produce a coiled (amylose) or branched (amylopectin) compact structure suited to dense, space-efficient storage. Cellulose is made of glucose, not fructose; it is not cross-linked by covalent bonds to other cellulose chains (only hydrogen bonds); and it is insoluble, not soluble, in water. **(B)**.

Bài tập luyện tập

The table below shows the number of C = C double bonds and the melting point of four 18-carbon fatty acids.

Fatty acid	Number of C = C double bonds	Melting point (°C)
Stearic acid	0	69
Oleic acid	1	14
Linoleic acid	2	−5
α-Linolenic acid	3	−11

(a) Describe the relationship shown in the table. (b) Explain this relationship in terms of molecular packing. (c) Which of these four fatty acids would be liquid at normal human body temperature (37 °C)?

Lời giải chi tiết

(a) As the number of C = C double bonds increases, melting point decreases — the relationship is a negative (inverse) one, and it is not linear (each additional double bond has a smaller effect than the first).

(b) All four chains have the same length, so chain length cannot explain the trend. Stearic acid, being fully saturated, has a straight, flexible chain that packs closely against neighbouring molecules, maximizing van der Waals attraction and requiring high temperature to melt. Each *cis* C = C double bond introduces a rigid kink into the chain, progressively disrupting this close

packing; more double bonds mean less efficient packing and weaker intermolecular attraction, so less thermal energy (a lower temperature) is needed to melt the fatty acid.
(c) At $37\,^{\circ}$C, any fatty acid with a melting point below $37\,^{\circ}$C is liquid: oleic acid ($14\,^{\circ}$C), linoleic acid ($-5\,^{\circ}$C), and α-linolenic acid ($-11\,^{\circ}$C) are all liquid. Stearic acid ($69\,^{\circ}$C) remains solid at $37\,^{\circ}$C.

Bài tập luyện tập

An α-helix and a β-pleated sheet are both examples of which level of protein structure, and what type of bond stabilizes them?

(A) Tertiary structure; ionic bonds between R groups

(B) Secondary structure; hydrogen bonds between backbone C$=$O and N$-$H groups

(C) Primary structure; peptide bonds

(D) Quaternary structure; disulfide bridges

Lời giải chi tiết

Both the α-helix and β-pleated sheet are regular, local folding patterns stabilized by hydrogen bonds between the backbone carbonyl (C$=$O) and amine (N$-$H) groups of the polypeptide chain itself — not the R groups — which is the defining feature of secondary structure. **(B)**.

Bài tập luyện tập

A functional protein is built from two identical polypeptide chains, each independently folded into a compact 3-D shape, joined together to form the working molecule. (a) Name the level of structure formed by the joining of the two chains. (b) Name two types of interaction that could hold the two chains together.

Lời giải chi tiết

(a) The association of two or more separate polypeptide chains into one functional complex is **quaternary structure**.
(b) Any two of: hydrogen bonds between polar R groups on the two chains; ionic bonds between oppositely charged R groups; hydrophobic interactions between nonpolar patches where the two subunit surfaces meet; disulfide bridges, if cysteine residues on each chain are positioned close enough together.

Bài tập luyện tập

The table shows the relative activity of an enzyme at six temperatures.

Temperature (°C)	10	20	30	40	50	60
Relative activity (%)	20	55	85	100	60	10

(a) Identify the optimum temperature. (b) Explain why activity is lower at $20\,^{\circ}$C than at the optimum. (c) Explain why activity is lower at $60\,^{\circ}$C than at the optimum, and state whether this cause is the same as in part (b).

Lời giải chi tiết

(a) Activity peaks at 100% at $40\,^{\circ}$C, so the **optimum temperature is** $40\,^{\circ}$C.

(b) At $20\,^{\circ}$C, molecules (enzyme and substrate) have lower kinetic energy and move more slowly, so they collide with the correct orientation and sufficient energy less often — the reaction proceeds more slowly simply because of reduced collision frequency, *not* because the enzyme's structure has been damaged.

(c) At $60\,^{\circ}$C, the high temperature provides enough energy to break the hydrogen bonds, ionic bonds, and hydrophobic interactions holding the enzyme's tertiary structure together — the enzyme has become **denatured**, its active site distorted so that substrate can no longer bind effectively. This is a *different* cause from part (b): the drop in activity at $20\,^{\circ}$C is due to insufficient kinetic energy for effective collisions (a reversible, temporary effect), while the drop in activity at $60\,^{\circ}$C is due to permanent structural damage (denaturation, generally not reversible).

Bài tập luyện tập

Explain the difference between denaturation and hydrolysis of a protein, stating clearly which level(s) of protein structure each process affects.

Lời giải chi tiết

Denaturation disrupts only the weak, non-covalent interactions (hydrogen bonds, ionic bonds, hydrophobic interactions) — and sometimes covalent disulfide bridges — that hold secondary, tertiary, and quaternary structure in place; it unfolds the protein's specific 3-D shape but leaves the primary sequence of amino acids completely intact, since peptide bonds are not broken. Hydrolysis, by contrast, breaks the covalent peptide bonds themselves (by adding water back across each bond, the reverse of the condensation reaction that formed them), destroying primary structure and reducing the polypeptide to smaller fragments or individual amino acids. Denaturation is a change in shape only; hydrolysis is a change in the chain itself.

Bài tập luyện tập

Facilitated diffusion is correctly classified as a form of passive transport because:

(A) it requires ATP, just like active transport, but uses a different type of protein.

(B) the solute moves down its concentration gradient and no ATP is consumed, even though a channel or carrier protein is required because the solute cannot cross the lipid bilayer unaided.

(C) it only occurs in plant cells, not animal cells.

(D) the transport protein pumps the solute against its concentration gradient without using energy.

Lời giải chi tiết

Whether a transport process is passive or active depends on the direction of movement relative to the gradient and whether ATP is consumed — not on whether a protein is involved. In facilitated diffusion, the solute still moves down its gradient and no ATP is used; a channel or carrier protein is needed only because the solute (polar, charged, or large) cannot cross the hydrophobic bilayer core unassisted. **(B)**.

Bài tập luyện tập

Five plant tissue cylinders of equal starting mass (4.00 g each) were placed into sucrose solutions of increasing concentration for 40 minutes.

Sucrose conc. (M)	0.00	0.25	0.50	0.75	1.00
Initial mass (g)	4.00	4.00	4.00	4.00	4.00
Final mass (g)	4.56	4.20	3.92	3.64	3.40

(a) Calculate the % change in mass at each concentration. (b) The isotonic point does not fall exactly on one of the tested concentrations. Using your answers to (a), estimate the isotonic point by linear interpolation between the two concentrations where % change changes sign. (c) State the tonicity of the 1.00 M solution relative to the tissue.

Lời giải chi tiết

(a) Using $\%$ change $= \dfrac{\text{final} - \text{initial}}{\text{initial}} \times 100$ with initial mass $= 4.00$ g throughout:

Conc. (M)	0.00	0.25	0.50	0.75	1.00
% change	$+14.0\%$	$+5.0\%$	-2.0%	-9.0%	-15.0%

(b) The sign changes between 0.25 M ($+5.0\%$) and 0.50 M (-2.0%). By linear interpolation:

$$\text{isotonic point} = 0.25 + \left(\frac{5.0}{5.0 - (-2.0)}\right) \times (0.50 - 0.25) = 0.25 + \left(\frac{5.0}{7.0}\right)(0.25) \approx 0.25 + 0.18 = 0.43 \text{ M}.$$

(c) At 1.00 M, the tissue lost 15.0% of its mass, meaning it lost water — this occurs only when the external solution has a higher solute concentration than the tissue, so the 1.00 M solution is **hypertonic** to the tissue.

Bài tập luyện tập

A red blood cell (no cell wall) and a walled plant cell are both placed in the same strongly hypertonic solution. Which pair correctly describes what each cell will do?

(A) Red blood cell swells and lyses; plant cell becomes turgid

(B) Red blood cell shrinks (crenates); plant cell undergoes plasmolysis

(C) Red blood cell shrinks; plant cell swells and bursts

(D) Neither cell is affected because both have a plasma membrane

Lời giải chi tiết

In a hypertonic solution, water leaves both cells by osmosis. The red blood cell, with no wall to resist shrinkage, shrivels up (crenates). The plant cell's protoplast also shrinks as it loses water, but its rigid cell wall does not shrink with it, so the plasma membrane visibly pulls away from the wall — plasmolysis. **(B)**.

Bài tập luyện tập

Describe the role of the Na^+/K^+ pump, including the direction and stoichiometry of ion movement, and explain why this process requires ATP.

Lời giải chi tiết

The Na^+/K^+ pump is an integral membrane protein that, for every one ATP molecule hydrolyzed, exports 3 Na^+ ions from the cell and imports 2 K^+ ions into the cell. Both ions are moved *against* their own concentration gradients (Na^+ is pumped from an area of lower concentration inside the cell to higher concentration outside; K^+ is pumped from lower concentration outside to higher concentration inside). Because moving a solute against its gradient is thermodynamically unfavourable (it does not happen spontaneously), the pump must couple this movement to an energy-releasing reaction — the hydrolysis of ATP to ADP $+P_i$ — which is why this process is active transport and requires a continuous supply of ATP, unlike passive transport.

Bài tập luyện tập

Trace the pathway of a protein destined for secretion from the cell, from the moment it is synthesized to the moment it leaves the cell, naming every structure involved in the correct order.

Lời giải chi tiết

The protein is synthesized by a ribosome bound to the **rough endoplasmic reticulum**, with the growing polypeptide threaded directly into the ER lumen, where it begins folding and initial modification. It is then packaged into a **transport vesicle** that buds off the rough ER and travels to the **Golgi apparatus**, entering at the *cis* face. Passing through the Golgi's stacked cisternae, the protein is further modified, sorted, and tagged with an address marking it for secretion. It leaves the *trans* face of the Golgi inside a new **secretory vesicle**, which travels to and fuses with the **plasma membrane**, releasing the finished protein outside the cell by **exocytosis**.

Bài tập luyện tập

Which structural feature most directly explains why mitochondria can support a high rate of ATP production without needing a correspondingly large increase in overall cell volume?

(A) The mitochondrial matrix is filled with hydrolytic enzymes.

(B) The inner membrane is folded into cristae, increasing the surface area available for electron transport chain proteins and ATP synthase without increasing volume.

(C) Mitochondria contain a large central vacuole for water storage.

(D) Mitochondria have a cell wall that resists osmotic pressure.

Lời giải chi tiết

Folding the inner mitochondrial membrane into cristae increases the surface area on which electron transport chain complexes and ATP synthase enzymes can be packed, without requiring a proportional increase in the mitochondrion's volume — precisely the same surface-area-amplification strategy seen in intestinal microvilli and root hairs. The matrix contains citric-acid-cycle enzymes, not hydrolytic (digestive) enzymes; mitochondria have no central

vacuole and no cell wall. **(B)**.

Bài tập luyện tập

A stem cell isolated from adult bone marrow can differentiate into red blood cells and several types of white blood cells and platelets, but cannot differentiate into nerve, muscle, or skin cells. This stem cell is best classified as:

(A) Totipotent

(B) Pluripotent

(C) Multipotent

(D) Fully differentiated (no remaining potency)

Lời giải chi tiết

A stem cell that can give rise to a limited range of related cell types (here, several blood cell lineages), but not to any cell type in the body, is multipotent — this is a narrower potency than pluripotent (any body cell type) or totipotent (any body cell type plus extra-embryonic tissue), and it is clearly not "fully differentiated," since it can still give rise to multiple distinct cell types. **(C)**.

Bài tập luyện tập

Explain, with reference to at least three structural features, how a red blood cell's structure is suited to its function of transporting oxygen.

Lời giải chi tiết

(1) Its **biconcave disc shape** increases its surface-area-to-volume ratio compared to a simple sphere of the same volume, shortening the diffusion pathway for O_2 entering and leaving the cell and allowing faster gas exchange. (2) It has **no nucleus**, freeing up internal space that is instead packed almost entirely with **hemoglobin**, maximizing the cell's oxygen-carrying capacity. (3) It has **no mitochondria**, so it respires anaerobically and does not consume any of the oxygen it is carrying for its own use, ensuring more oxygen reaches the tissues that need it. (A fourth acceptable point: its flexible biconcave shape also allows it to deform and squeeze through capillaries narrower than its own resting diameter.)

Bài tập luyện tập

Two spherical single-celled organisms rely on diffusion across their entire outer surface for gas exchange: Organism P has radius 2 mm; Organism Q has radius 8 mm. (a) Calculate the SA:V ratio of each, using SA:V $= 3/r$. (b) Explain which organism is more likely to require a specialized internal gas exchange surface instead of relying on diffusion across its outer body surface.

Lời giải chi tiết

(a) Organism P: SA:V $= 3/2 = 1.5$ mm^{-1}. Organism Q: SA:V $= 3/8 = 0.375$ mm^{-1}.
(b) Organism Q's SA:V ratio (0.375 mm^{-1}) is exactly one-quarter of Organism P's (1.5 mm^{-1}), matching the fourfold difference in radius. Because Q's outer surface area is so much smaller relative to its metabolically demanding volume, simple diffusion across its outer body surface alone cannot supply oxygen and remove carbon dioxide fast enough to meet its needs

— **Organism Q** is far more likely to require a specialized, surface-area-amplified gas exchange structure (e.g., gills or an internal respiratory surface) than the much smaller Organism P, which can plausibly exchange gases directly across its body surface.

Bài tập luyện tập

Which of the following changes would make a gas exchange surface LESS effective at moving gas by diffusion, rather than more effective?

(A) Increasing the total surface area of the exchange surface

(B) Increasing the thickness of the exchange surface

(C) Keeping the exchange surface moist

(D) Maintaining a strong blood or ventilation supply on one side of the surface

Lời giải chi tiết

By Fick's law, diffusion rate is inversely proportional to the thickness (diffusion distance) of the exchange surface — increasing thickness lengthens the diffusion pathway and *slows* gas exchange, making the surface less effective. Increasing surface area, keeping the surface moist, and maintaining a strong blood/ventilation supply are all features of an effective exchange surface that speed up diffusion, not slow it. **(B)**.

Bài tập luyện tập

Explain why counter-current flow of blood and water in a fish gill allows more efficient oxygen extraction than a concurrent (parallel) flow arrangement would.

Lời giải chi tiết

In counter-current flow, blood moves through the gill lamella in the opposite direction to the water flowing over it. This means that at every point along the lamella, the blood — however oxygenated it has already become — is still exposed to water that is even more oxygenated than it is, since fresh, fully oxygenated water is always meeting blood that has already picked up some oxygen further along its path. A favourable diffusion gradient for O_2 (from water into blood) is therefore maintained along the *entire* length of the exchange surface. In a concurrent (parallel) arrangement, by contrast, blood and water moving in the same direction would rapidly approach the same oxygen concentration partway along the lamella, after which the gradient — and therefore net diffusion — would fall to almost zero for the rest of the exchange surface, extracting far less oxygen overall.

Bài tập luyện tập

Which blood vessel is correctly matched with a key structural feature and the functional reason for it?

(A) Artery — thin wall and wide lumen, to carry blood slowly away from the heart

(B) Vein — valves, to prevent backflow of blood under the low pressure of the venous system

(C) Capillary — thick muscular wall, to withstand high blood pressure

(D) Vein — walls only one cell thick, to allow diffusion of substances into tissues

Lời giải chi tiết

Veins carry blood back to the heart under low pressure; without the driving force of ventricular contraction behind them, blood could otherwise flow backward, so veins are equipped with one-way valves to prevent this. Arteries have thick, muscular, elastic walls (not thin) to withstand high pressure; capillary walls (not vein walls) are only one cell thick, to allow diffusion at the actual exchange site. **(B)**.

Bài tập luyện tập

The table shows heart rate and stroke volume for a subject at rest, during moderate exercise, and during intense exercise.

	Heart rate (beats/min)	Stroke volume (mL/beat)
Rest	70	70
Moderate exercise	110	100
Intense exercise	170	110

(a) Calculate cardiac output at rest, during moderate exercise, and during intense exercise. (b) Describe the trend in stroke volume shown in the table as exercise intensity increases from moderate to intense, and explain how the body continues to increase cardiac output despite this trend.

Lời giải chi tiết

(a) CO $=$ HR $\times$ SV.
Rest: $70 \times 70 = 4\,900$ mL/min $= 4.9$ L/min.
Moderate exercise: $110 \times 100 = 11\,000$ mL/min $= 11.0$ L/min.
Intense exercise: $170 \times 110 = 18\,700$ mL/min $= 18.7$ L/min.

(b) Stroke volume rises substantially from rest to moderate exercise ($70 \rightarrow 100$ mL/beat) but increases only slightly further from moderate to intense exercise ($100 \rightarrow 110$ mL/beat) — it is levelling off (plateauing) rather than continuing to rise proportionally, because there is a physical limit to how much extra blood the ventricle can fill with and eject each beat, especially as the time available for filling shortens at very high heart rates. Because stroke volume can only rise so far, the body relies increasingly on **heart rate**, which keeps climbing substantially ($110 \rightarrow 170$ beats/min), to continue increasing cardiac output at high exercise intensities.

Bài tập luyện tập

Explain the transpiration-cohesion-tension theory of water transport in the xylem, and explain why this mechanism does not require the plant to expend metabolic energy directly moving the water itself.

Lời giải chi tiết

Water evaporates from the moist walls of leaf mesophyll cells into the sub-stomatal air space and diffuses out through open stomata (transpiration). This water loss lowers the water potential of the mesophyll cells, so water is drawn out of the adjacent xylem vessels by osmosis to replace it. Because the xylem forms a continuous, unbroken column of water from root to leaf, removing water at the top pulls the entire column upward, creating tension (negative pressure) that is transmitted all the way down to the roots. This works only because water molecules

hydrogen-bond strongly to each other (**cohesion**), preventing the column from breaking apart under tension, and hydrogen-bond to the walls of the xylem vessels (**adhesion**), helping support the column and counteract the pull of gravity. The energy driving the whole process comes from the sun (evaporation at the leaf surface, powered by solar heating), not from ATP hydrolysis inside the plant — the plant itself expends no direct metabolic energy moving the water column.

Bài tập luyện tập

Explain the mass flow (pressure flow) hypothesis of phloem translocation, including the roles of active loading, osmosis, and the resulting pressure gradient.

Lời giải chi tiết

At the source (e.g., a photosynthesizing leaf), companion cells actively load sucrose into the phloem sieve tubes using ATP-dependent active transport, raising the solute concentration (and lowering the water potential) inside the sieve tube at that point. Water then follows the sucrose into the sieve tube by osmosis from the adjacent xylem, raising the hydrostatic pressure at the source end of the tube. At the sink (e.g., a growing root or developing fruit), sucrose is actively unloaded and consumed or converted into storage products, raising the local water potential inside the sieve tube; water then leaves the sieve tube by osmosis, lowering hydrostatic pressure at the sink end. This creates a pressure gradient along the sieve tube — high at the source, low at the sink — and this pressure difference passively drives a bulk, mass flow of the entire phloem sap solution from source to sink, carrying dissolved sucrose along with it.

Bài tập luyện tập (HL)

During a single muscle contraction cycle, sliding filament theory predicts that the sarcomere shortens. Which of the following structures does NOT change length during this process?

(A) The sarcomere (Z-line to Z-line distance)
(B) The H-zone
(C) The myosin (thick) filament itself
(D) The I-band

Lời giải chi tiết

Sliding filament theory states that actin and myosin filaments slide past each other, increasing their region of overlap — the filaments themselves do not change length. The sarcomere, the H-zone (myosin-only region), and the I-band (actin-only region) all shorten as overlap increases, but the length of the myosin filament itself stays constant throughout the cycle. **(C)**.

Bài tập luyện tập (HL)

Describe, in the correct sequence, the roles of Ca^{2+}, troponin, tropomyosin, and ATP in one cross-bridge cycle of skeletal muscle contraction.

Lời giải chi tiết

A nerve impulse triggers release of Ca^{2+} from the sarcoplasmic reticulum into the muscle fibre's cytosol. Ca^{2+} binds to **troponin**, causing a conformational change that shifts **tropomyosin** away from the myosin-binding sites on the actin filament, exposing them. A myosin head,

already energized from a previous round of ATP hydrolysis, binds the newly exposed site on actin, forming a cross-bridge, and then pivots in the power stroke, pulling the actin filament toward the centre of the sarcomere while releasing ADP and inorganic phosphate. A fresh molecule of **ATP** then binds the myosin head, causing it to detach from actin; hydrolysis of this ATP re-energizes ("re-cocks") the myosin head, ready to bind a new site further along the actin filament and repeat the cycle for as long as Ca^{2+} and ATP remain available.

Bài tập luyện tập (HL)

The "9+2" arrangement of microtubules (nine outer doublets surrounding a central pair) is the structural basis of which cellular structure(s)?

(A) Cilia and flagella
(B) The mitotic spindle only
(C) Microvilli
(D) Amoeboid pseudopodia

Lời giải chi tiết

Both cilia and flagella are built around a core (the axoneme) of nine outer microtubule doublets surrounding a central pair, which bends as dynein motor proteins use ATP to slide adjacent doublets past one another. The mitotic spindle is built from microtubules but does not have this specific 9+2 arrangement; microvilli are supported by actin microfilaments, not microtubules; amoeboid pseudopodia are driven by actin cytoskeleton remodeling. **(A)**.

Bài tập luyện tập

The wing of a bird and the wing of a bumblebee both enable flight but have completely different underlying anatomical structure and no shared winged ancestor. These two structures are best described as:

(A) Homologous structures, resulting from divergent evolution
(B) Analogous structures, resulting from convergent evolution
(C) Vestigial structures, with no current function
(D) Identical structures, resulting from a shared common ancestor

Lời giải chi tiết

Structures that perform a similar function and often look superficially similar, but evolved independently in unrelated lineages facing similar selective pressures (here, the need to fly), with no shared anatomical origin, are analogous structures produced by convergent evolution. Homologous structures (produced by divergent evolution) instead share an underlying anatomical origin from a common ancestor. **(B)**.

Bài tập luyện tập

Identify and explain one trade-off associated with a cactus's adaptation of having greatly reduced, spine-shaped leaves in an arid desert environment.

Lời giải chi tiết

Reducing leaf surface area to thin spines dramatically cuts water loss by transpiration, which is highly advantageous in an arid environment where water conservation is critical for survival

(benefit). However, leaves are normally the primary site of photosynthesis, so reducing them to spines also removes most of the plant's photosynthetic surface area (cost) — the cactus compensates by shifting photosynthesis into its thick, fleshy, chlorophyll-containing stem instead, but this is a less area-efficient photosynthetic surface than a full leaf would provide. (An additional acceptable trade-off: spines deter herbivores, at the ongoing metabolic cost of producing rigid, lignified structures.)

Bài tập luyện tập

A species of insect could theoretically survive and reproduce across a wide range of forest elevations if no other species competed with it for food. In practice, however, it is only ever found at high elevations, because a competing species excludes it from lower elevations where their food requirements overlap. Which pair of terms correctly labels the insect's full theoretical range and its actual observed range?

(A) Full theoretical range = realized niche; actual observed range = fundamental niche

(B) Full theoretical range = fundamental niche; actual observed range = realized niche

(C) Full theoretical range = habitat; actual observed range = niche

(D) Both ranges are examples of the realized niche

Lời giải chi tiết

The fundamental niche is the full range of conditions a species could occupy in the absence of competitors — here, the wide range of elevations the insect could theoretically survive at. The realized niche is the narrower range it actually occupies once competition restricts it — here, only the high elevations, after being excluded from lower elevations by a competitor. **(B)**.

Bài tập luyện tập

Two barnacle species occupy a rocky shore. The table shows the percentage of each species found in three shore zones under natural conditions (with both species present and competing).

Species	High shore (%)	Mid shore (%)	Low shore (%)
Chthamalus	70	25	5
Balanus	5	30	65

When *Balanus* is experimentally removed from the shore, *Chthamalus* is subsequently found at high abundance across all three zones, including the low shore. (a) Calculate the total zonal overlap between the two species under natural (competing) conditions. (b) Using the removal-experiment result, explain which zone represents *Chthamalus*'s realized niche and which represents (part of) its fundamental niche, and identify the ecological process responsible for the difference.

Lời giải chi tiết

(a) Overlap in each zone is the smaller of the two percentages: High shore $\min(70, 5) = 5$; Mid shore $\min(25, 30) = 25$; Low shore $\min(5, 65) = 5$. Total overlap $= 5 + 25 + 5 =$ **30**%.

(b) Under natural, competing conditions, *Chthamalus* is found mainly on the high shore (70%)

— this restricted distribution is its **realized niche**. When the competitor *Balanus* is removed, *Chthamalus* successfully occupies the mid and low shore as well, showing that its **fundamental niche** (the range it is physiologically capable of tolerating) extends across the whole shore, including zones from which it is normally excluded. The process responsible for this restriction is **interspecific competition** leading to **competitive exclusion**: *Balanus* grows faster and physically out-competes (smothers) *Chthamalus* in the mid and low shore, confining *Chthamalus*'s realized niche to the high shore, where *Balanus* is presumably less tolerant of the harsher conditions (e.g., desiccation at low tide).

Bài tập luyện tập

Glucose and fructose share the identical molecular formula $C_6H_{12}O_6$ but differ in the position of their carbonyl group. Which statement correctly distinguishes them?

(A) Glucose is a ketose with an internal carbonyl group; fructose is an aldose with a terminal carbonyl group.

(B) Glucose is an aldose with a terminal carbonyl group; fructose is a ketose with an internal carbonyl group.

(C) Both are aldoses, differing only in ring size.

(D) Glucose contains one more oxygen atom than fructose.

Lời giải chi tiết

Glucose's carbonyl group sits at the end of its carbon chain, making it an aldose; fructose's carbonyl group is internal (on an interior carbon), making it a ketose. Both are structural isomers with the identical molecular formula $C_6H_{12}O_6$ — they differ in atomic arrangement, not in the number or type of atoms present. **(B)**.

Bài tập luyện tập

Complete oxidation of carbohydrate releases approximately 17 kJ/g; complete oxidation of lipid releases approximately 37 kJ/g. A snack bar contains 18.0 g of carbohydrate, 6.0 g of lipid, and negligible protein. (a) Calculate the total energy content of the snack bar. (b) A second snack bar of the same total mass contains no lipid, replacing it entirely with additional carbohydrate. Calculate its total energy content and compare it with the first bar.

Lời giải chi tiết

(a) Carbohydrate: $18.0 \times 17 = 306$ kJ. Lipid: $6.0 \times 37 = 222$ kJ. Total $= 306 + 222 =$ **528** kJ.

(b) The second bar has the same total mass ($18.0 + 6.0 = 24.0$ g), now entirely carbohydrate: $24.0 \times 17 =$ **408** kJ. This is $528 - 408 = 120$ kJ *less* energy than the original bar, even though both bars have identical total mass — because gram for gram, lipid stores roughly twice as much chemical energy as carbohydrate (its carbon atoms are more reduced), replacing lipid with an equal mass of carbohydrate always lowers the total energy content of a food of fixed mass.

Bài tập luyện tập

A phospholipid is described as "amphipathic." What does this mean, and what is its structural consequence in water?

(A) It has two hydrophilic tails and one hydrophobic head, causing it to dissolve completely in water.

(B) It has a hydrophilic head and hydrophobic tails, causing it to spontaneously form a bilayer with tails hidden from water.

(C) It contains no charged or polar groups at all, so it does not interact with water in any way.

(D) It is composed entirely of glycerol, with no fatty acid component.

Lời giải chi tiết

"Amphipathic" describes a molecule with distinct hydrophilic and hydrophobic regions. A phospholipid has one hydrophilic (polar/charged) phosphate-containing head and two hydrophobic fatty acid tails. In water, phospholipids spontaneously arrange so that hydrophilic heads face the surrounding water on both sides while hydrophobic tails cluster together in a water-free interior — forming the bilayer structure of every biological membrane. **(B)**.

Bài tập luyện tập

Explain why storing energy as lipid (rather than as an equivalent mass of free glucose dissolved in the cytosol) helps a cell avoid disturbing its internal water potential.

Lời giải chi tiết

Lipids are nonpolar and hydrophobic, so triglyceride molecules aggregate into compact, insoluble droplets rather than dissolving in the aqueous cytosol; because they are not in solution, they contribute essentially nothing to the cell's total solute concentration. An equivalent mass of energy stored as free glucose, by contrast, would dissolve in the cytosol and substantially raise the solute concentration there, lowering the cytosol's water potential and drawing water in by osmosis (risking excessive swelling). This is exactly the same reasoning that explains why glucose is stored as large, insoluble polysaccharides (starch, glycogen) rather than as free glucose (Section B1.1) — in both cases, converting a potentially large number of soluble molecules into one large, insoluble storage form avoids disturbing the cell's osmotic balance.

Bài tập luyện tập

When a polypeptide chain folds into its tertiary structure in an aqueous (watery) environment, where would you expect most of its nonpolar (hydrophobic) R groups to be located, and why?

(A) On the outer surface of the folded protein, because they repel water most strongly there.

(B) Buried in the interior of the folded protein, away from the surrounding water.

(C) Randomly distributed with no consistent pattern, since R groups do not influence folding.

(D) Only at the very ends of the polypeptide chain (the N- and C-termini).

Lời giải chi tiết

Nonpolar R groups cannot hydrogen-bond with water and are energetically unfavourable when exposed to an aqueous environment. As a polypeptide folds, hydrophobic interactions drive nonpolar R groups to cluster together away from water, typically ending up buried in the protein's interior, while polar and charged R groups — which can hydrogen-bond or ionically interact with water — tend to remain on the exposed outer surface. **(B)**.

Bài tập luyện tập

The table shows the relative activity of pepsin, a protein-digesting enzyme secreted in the stomach, across a range of pH values.

pH	1	2	3	5	7	9
Relative activity (%)	80	100	70	15	2	0

(a) Identify pepsin's optimum pH. (b) Explain why pepsin's optimum pH is so different from the near-neutral optimum pH of many other enzymes (such as the digestive enzyme discussed earlier in this chapter, with optimum pH 7). (c) Predict what would happen to pepsin's activity if it were moved from the stomach into the near-neutral environment of the small intestine, and explain why.

Lời giải chi tiết

(a) Activity peaks at 100% at pH $= 2$, so **pepsin's optimum pH is 2**.

(b) An enzyme's optimum pH reflects the pH of the environment in which it normally functions, because its tertiary structure (and therefore its active site shape) is stabilized by a particular pattern of ionic and hydrogen bonds between R groups that are only correctly ionized within a specific pH range. Pepsin evolved to function in the stomach, which is strongly acidic (roughly pH 1–2, due to secreted hydrochloric acid), so its R groups are arranged to form their most stable, correctly folded, catalytically active conformation at low pH — very different from an enzyme that normally functions in a near-neutral compartment such as the mouth or small intestine.

(c) Moved into the near-neutral small intestine, pepsin's activity would fall sharply (matching the low relative activity already shown at pH 7 in the table) because the change in pH alters the ionization of pepsin's acidic and basic R groups, disrupting the ionic and hydrogen bonds that hold its active-site shape in place — the enzyme becomes denatured and can no longer bind its protein substrate effectively. (In the body, pepsin is in fact inactivated as it passes into the small intestine, where the near-neutral environment favours other proteases, such as trypsin, instead.)

Bài tập luyện tập

Which statement correctly distinguishes a channel protein from a carrier protein in facilitated diffusion?

(A) A channel protein changes shape to bind and release its solute; a carrier protein forms a fixed hydrophilic pore.

(B) A channel protein forms a fixed (or gated) hydrophilic pore through which solute passes; a carrier protein binds its solute and changes conformation to shuttle it across.

(C) Channel proteins require ATP; carrier proteins do not.

(D) Only carrier proteins are involved in passive transport; channel proteins are only involved in active transport.

Lời giải chi tiết

A channel protein forms a permanent or gated pore lined with hydrophilic amino acid residues, allowing a specific solute (e.g., ions through an ion channel, water through an aquaporin) to diffuse straight through without the protein itself changing shape. A carrier protein instead

binds its specific solute and undergoes a conformational change that shuttles the solute from one side of the membrane to the other. Both are passive (no ATP required) when carrying out facilitated diffusion; neither statement about ATP nor exclusive association with active/passive transport is correct. **(B)**.

Bài tập luyện tập

Explain how a single molecule, cholesterol, can act to maintain membrane fluidity both at high temperature and at low temperature.

Lời giải chi tiết

Cholesterol molecules are wedged between the fatty acid tails of membrane phospholipids. At **high temperature**, phospholipids gain kinetic energy and tend to move too freely, making the membrane excessively fluid; cholesterol's rigid ring structure restrains this excess movement of neighbouring phospholipid tails, reducing fluidity back toward a normal range. At **low temperature**, phospholipid tails would otherwise pack closely together and solidify into a rigid gel; cholesterol, wedged between the tails, prevents them from packing this tightly, keeping the membrane fluid enough to function. In both cases cholesterol acts as a buffer, moderating fluidity toward an intermediate, functional level regardless of temperature.

Bài tập luyện tập

Red blood cells were placed into five sodium chloride solutions of different concentration for 10 minutes, then observed under a microscope. The results are shown below.

NaCl conc. (% w/v)	0.30	0.60	0.90	1.20	1.50
Observation	lysed	shrunken/lysed	normal biconcave	crenated	strongly crenated

(a) Identify the approximate NaCl concentration that is isotonic to red blood cells. (b) Explain, in terms of water movement, what happened to the cells at 0.30% NaCl. (c) Explain what happened to the cells at 1.50% NaCl.

Lời giải chi tiết

(a) Cells retain their normal shape (no net water movement) at $\mathbf{0.90}\%$ NaCl — this is the isotonic concentration for red blood cells (this is also why 0.9% saline, "normal" or "physiological" saline, is used for intravenous fluids and rinsing biological tissue).

(b) At 0.30% NaCl, the external solution has a much lower solute concentration than the inside of the red blood cell — the solution is strongly **hypotonic** to the cell. Water therefore moves into the cell by osmosis (down its own concentration gradient, from the dilute external solution toward the more concentrated cytoplasm), and because a red blood cell has no cell wall to resist expansion, it swells until its plasma membrane ruptures — lysis.

(c) At 1.50% NaCl, the external solution has a much higher solute concentration than the cell interior — it is strongly **hypertonic**. Water moves out of the cell by osmosis toward the more concentrated external solution, and with no wall to maintain its shape, the cell shrivels and shrinks — crenation.

Bài tập luyện tập

A macrophage engulfs an entire bacterium by folding its plasma membrane around it and pinching off a large vesicle containing the bacterium. This process is an example of:

(A) Facilitated diffusion
(B) Active transport via a pump protein
(C) Endocytosis (specifically, phagocytosis)
(D) Simple diffusion

Lời giải chi tiết

Engulfing large particles (or whole cells) by invaginating the plasma membrane and pinching off a vesicle is endocytosis; when the material engulfed is solid (such as a bacterium), this specific form of endocytosis is called phagocytosis. This process is far too large-scale to involve simple diffusion, facilitated diffusion, or a single pump protein, all of which move individual dissolved solutes rather than whole particles or cells. **(C)**.

Bài tập luyện tập

Lysosomes maintain an internal pH of approximately 4.5–5, much more acidic than the near-neutral pH (≈ 7.2) of the surrounding cytosol. Explain the advantage of this arrangement for the cell.

Lời giải chi tiết

The hydrolytic (digestive) enzymes packaged inside lysosomes have evolved to work optimally at acidic pH, so keeping the lysosome interior acidic ensures these enzymes are active and able to break down worn-out organelles, ingested food particles, or foreign material efficiently. This compartmentalized acidic environment also protects the rest of the cell: if these same enzymes leaked into the near-neutral cytosol, they would be far less active (denatured/inactivated by the higher pH) and could not efficiently digest the cell's own proteins and organelles, providing a built-in safety margin. This is a direct example of compartmentalization creating a localized chemical environment suited to a specific reaction while also protecting the rest of the cell from an incompatible (potentially destructive) process.

Bài tập luyện tập

Which of the following best describes the role of the Golgi apparatus in the endomembrane system?

(A) It synthesizes ATP for the whole cell.
(B) It receives proteins from the rough ER at its *cis* face, modifies and sorts them, and ships them from its *trans* face in vesicles addressed to their final destination.
(C) It is the primary site of DNA replication.
(D) It breaks down worn-out organelles by autophagy.

Lời giải chi tiết

The Golgi apparatus is a stack of flattened membranous sacs that receives transport vesicles (containing newly synthesized proteins) from the rough ER at its receiving (*cis*) face, further modifies and sorts these proteins as they move through the stack, and packages them into new vesicles addressed to their correct destination as they leave the shipping (*trans*) face. ATP synthesis occurs in mitochondria, not the Golgi; DNA replication occurs in the nucleus;

breakdown of worn-out organelles (autophagy) is primarily a lysosomal function. **(B)**.

Bài tập luyện tập

A single fertilized egg cell (zygote) and the cells of the very early embryo can differentiate into any cell type in the body as well as extra-embryonic tissues such as the placenta. This level of potency is called:

(A) Multipotent
(B) Pluripotent
(C) Totipotent
(D) Unipotent

Lời giải chi tiết

Only totipotent cells can differentiate into every cell type of the body *and* extra-embryonic tissues (e.g., the placenta) — a capability restricted to the zygote and the cells of the very earliest embryonic divisions. Pluripotent cells (e.g., embryonic stem cells) can form any body cell type but not extra-embryonic tissue; multipotent cells are restricted to a limited range of related cell types. **(C)**.

Bài tập luyện tập

An unspecialized intestinal epithelial cell has a surface area of $850\ \mu\text{m}^2$ and a volume of $1400\ \mu\text{m}^3$. After differentiating into a mature absorptive cell bearing thousands of microvilli on its exposed surface, its surface area increases to $2550\ \mu\text{m}^2$ while its volume increases only to $1500\ \mu\text{m}^3$. (a) Calculate the SA:V ratio before and after differentiation. (b) Calculate the factor by which SA:V has increased. (c) Explain why this change in SA:V is functionally important for this cell's role in the small intestine.

Lời giải chi tiết

(a) Before: SA:V $= 850/1400 \approx 0.61\ \mu\text{m}^{-1}$. After: SA:V $= 2550/1500 = 1.70\ \mu\text{m}^{-1}$.

(b) $\dfrac{1.70}{0.61} \approx 2.8$ — differentiation increases SA:V by roughly a factor of 2.8 (an increase of about 180%).

(c) This cell's role is absorbing digested nutrients from the small intestine by diffusion, facilitated diffusion, and active transport across its plasma membrane. A much higher SA:V ratio means far more membrane area (and therefore more transport proteins) is available per unit of cytoplasm the cell must maintain, directly increasing the rate at which nutrients can be absorbed relative to the cell's size — the same amplification principle already seen in cristae, alveoli, and root hair cells.

Bài tập luyện tập

The heart is composed of cardiac muscle tissue, connective tissue, and epithelial tissue, all working together to pump blood. At which level of biological organization does the heart itself sit?

(A) Cell
(B) Tissue
(C) Organ
(D) Organ system

Lời giải chi tiết

A structure built from two or more different tissue types working together to carry out a more complex function is an organ (here, the heart, combining muscle, connective, and epithelial tissue to pump blood). A single tissue is made of one cell type performing a shared function; an organ system is a group of organs (e.g., the heart together with blood vessels forms the circulatory organ system). **(C)**.

Bài tập luyện tập

According to Fick's law, why does a rich capillary blood supply increase the effectiveness of a gas exchange surface such as the alveolus?

(A) It increases the thickness of the exchange surface, slowing diffusion in a useful way.

(B) It continuously removes gas that has diffused across and replenishes the supply on the other side, maintaining a steep concentration gradient across the surface.

(C) It replaces the need for a moist surface.

(D) It decreases the total surface area needed for adequate gas exchange.

Lời giải chi tiết

Diffusion rate depends on the concentration (partial pressure) difference across the exchange surface being maintained as large as possible. A rich, continuous blood supply constantly carries newly diffused gas away from the exchange surface (and delivers a fresh supply of the gas moving in the other direction), preventing the two sides from ever reaching equilibrium and keeping the concentration gradient steep. This is separate from — not a substitute for — the need for a thin, moist, large-area surface. **(B)**.

Bài tập luyện tập

The table shows hemoglobin's % oxygen saturation at two values of $p\mathrm{O}_2$, under resting conditions and under conditions of raised CO_2 (as in exercising muscle).

$p\mathrm{O}_2$ (mmHg)	% saturation, resting CO_2	% saturation, raised CO_2
20	35	18
40	75	52

(a) At $p\mathrm{O}_2 = 20$ mmHg, calculate how many additional percentage points of saturation are lost due to the raised CO_2. (b) Name and describe this phenomenon. (c) Explain briefly, in terms of hemoglobin's conformation, why raised CO_2 produces this effect.

Lời giải chi tiết

(a) At 20 mmHg: 35% (resting) -18% (raised CO_2) $=$ **17** additional percentage points of saturation are lost.

(b) This is the **Bohr shift**: raised CO_2 (and the resulting drop in local pH) shifts the entire oxygen dissociation curve to the right, so that hemoglobin holds less oxygen at any given $p\mathrm{O}_2$ than it would under resting conditions.

(c) Raised CO_2 increases local H^+ concentration (lower pH); both CO_2 and H^+ bind hemoglobin at sites away from the oxygen-binding heme groups and stabilize its low-affinity, deoxygenated

conformation, making it release oxygen more readily at any given pO_2 — delivering extra oxygen exactly to the tissue producing the most CO_2, i.e., the tissue respiring (and working) hardest.

Bài tập luyện tập (HL)

Shortly after death, skeletal muscles become temporarily rigid and difficult to bend (rigor mortis), because cellular ATP production stops. Which explanation best accounts for this stiffening, in terms of the cross-bridge cycle?

(A) Without ATP, Ca^{2+} floods permanently into the cytosol, causing sustained but weak contraction.

(B) Without ATP to bind the myosin head, myosin cannot detach from actin, so cross-bridges remain locked and the filaments cannot slide apart.

(C) Without ATP, tropomyosin permanently exposes the myosin-binding sites, causing uncontrolled contraction.

(D) Without ATP, sarcomeres lengthen indefinitely, producing stiffness.

Lời giải chi tiết

In the normal cross-bridge cycle, a fresh ATP molecule must bind the myosin head *after* the power stroke in order for myosin to detach from actin; ATP is then hydrolyzed to re-energize the head for the next cycle. After death, ATP production stops (no aerobic or anaerobic respiration), so any myosin heads still bound to actin at that moment cannot detach — cross-bridges become permanently locked, holding actin and myosin filaments together and preventing the muscle from relaxing or being stretched, producing the characteristic stiffness of rigor mortis (which persists until the muscle proteins themselves begin to break down). **(B)**.

Bài tập luyện tập

The table shows the average stomatal density (number of stomata per mm^2) on the upper and lower leaf surfaces of a typical mesophyte (a plant of moist habitats) and a xerophyte (a plant adapted to arid conditions).

	Upper surface (stomata/mm^2)	Lower surface (stomata/mm^2)
Mesophyte	40	280
Xerophyte	0	60

(a) Describe the difference in total stomatal density between the two plant types. (b) Explain how a lower stomatal density is an adaptation to an arid environment. (c) Suggest one additional structural adaptation (besides reduced stomatal density) that a xerophyte's stomata might show to further reduce water loss.

Lời giải chi tiết

(a) The mesophyte has a much higher stomatal density on both surfaces ($40 + 280 = 320$ stomata/mm^2 total) than the xerophyte ($0 + 60 = 60$ stomata/mm^2 total) — roughly five times fewer stomata overall, and the xerophyte has none at all on its upper surface.

(b) Each stoma is an open pore through which water vapour escapes by transpiration in addition to allowing gas exchange. Fewer stomata (and none on the more sun-exposed, typically hotter, upper surface) directly reduces the total area available for water vapour to diffuse out of the

leaf, conserving water — a critical adaptation where water is scarce.

(c) Xerophytes often also have stomata sunken into small pits (sunken stomata), sometimes further sheltered by hairs, which traps a layer of still, humid air immediately outside the pore and reduces the water vapour concentration gradient driving transpiration, further slowing water loss without completely closing the stomata.

Bài tập luyện tập

Sharks (fish), dolphins (mammals), and the extinct ichthyosaurs (reptiles) all independently evolved a similar streamlined, fusiform (torpedo-shaped) body with a dorsal fin and a tail fin, despite belonging to three very different vertebrate lineages that do not share a recent common ancestor with this body shape. Explain what type of evolution produced this pattern, and name the resulting structures.

Lời giải chi tiết

This is an example of **convergent evolution**: sharks, dolphins, and ichthyosaurs each independently evolved a similar external body shape because all three lineages faced the same strong selective pressure — minimizing drag while swimming efficiently through water — despite not sharing a recent common ancestor with that streamlined, aquatic body plan (their most recent common ancestor was not itself a streamlined aquatic swimmer). Because the resulting similarity in outward shape arose independently in each lineage rather than by common descent, the body shapes (and fins) of these three groups are described as **analogous** structures, not homologous ones — similar in outward form and function, but without a shared anatomical/developmental origin for that specific streamlined body plan.

Bài tập luyện tập

Two closely related bird species initially compete strongly for the same insect prey in the same part of a forest canopy. Over many generations, one species shifts to foraging mainly in the upper canopy while the other shifts to foraging mainly in the lower canopy, reducing their dietary overlap. This outcome is best described as:

(A) Competitive exclusion, in which one species has been eliminated

(B) Resource partitioning (niche differentiation), reducing competition and allowing coexistence

(C) Convergent evolution toward an identical niche

(D) A fundamental niche expanding to fill the entire realized niche

Lời giải chi tiết

When natural selection favours individuals of each competing species that use a contested resource slightly differently — here, foraging in different parts of the canopy — the overlap between their realized niches is progressively reduced. This is resource partitioning (niche differentiation): rather than one species eliminating the other (competitive exclusion), both species persist by dividing up the shared resource differently, reducing direct competition. **(B)**.

Bài tập luyện tập

In a classic laboratory experiment, *Paramecium aurelia* and *Paramecium caudatum* were each grown separately in nutrient broth, and also grown together in the same culture vessel. Population density (individuals/mL) was recorded over 16 days.

	Day 0	Day 8	Day 16
P. aurelia alone	2	110	180
P. caudatum alone	2	95	150
P. aurelia in mixed culture	2	90	170
P. caudatum in mixed culture	2	35	0

(a) Compare the growth of each species when cultured alone versus in the mixed culture. (b) Identify the ecological principle this experiment demonstrates, and explain the result in terms of niche overlap. (c) Suggest what result would be expected if *P. caudatum* were instead grown together with a third species, *P. bursaria*, which feeds on bacteria settled at the bottom of the culture vessel rather than in the open broth.

Lời giải chi tiết

(a) Grown alone, both species reach a substantial population by day 16 (180/mL for *P. aurelia*; 150/mL for *P. caudatum*). In mixed culture, *P. aurelia*'s growth is only slightly reduced (reaching 170/mL), while *P. caudatum*'s population collapses to **extinction** (0/mL) by day 16.

(b) This demonstrates the **competitive exclusion principle**: the two species have such similar, heavily overlapping niches (both feed on the same bacteria suspended in the open broth) that they cannot coexist indefinitely in the same culture vessel — *P. aurelia*, being the more efficient competitor for this shared, limited resource, drives *P. caudatum* to local extinction, exactly as the principle predicts for species with (near-)identical niches.

(c) *P. bursaria* occupies a different part of the culture vessel (feeding on bacteria at the bottom) than *P. caudatum* (feeding in the open broth), so their niches barely overlap. Because there is little direct competition for the same resource in the same location, both species would be expected to coexist rather than one excluding the other — consistent with the general finding that species with sufficiently differentiated (non-overlapping) niches can persist together.

Theme C: Interaction and Interdependence

Mục tiêu Unit: Giải thích cơ chế xúc tác của enzyme (mô hình khớp cảm ứng, các yếu tố ảnh hưởng đến hoạt tính enzyme, ức chế cạnh tranh/không cạnh tranh, khái niệm Km và Vmax); trình bày đầy đủ hô hấp tế bào hiếu khí (đường phân, phản ứng liên kết, chu trình Krebs, chuỗi chuyền điện tử và hoá thẩm thấu) và lên men kỵ khí (lactic acid ở động vật, alcoholic ở nấm men), tính và biện luận hệ số hô hấp RQ; trình bày quang hợp (phản ứng phụ thuộc ánh sáng tại màng thylakoid, chu trình Calvin tại chất nền stroma) và phân tích đồ thị các yếu tố giới hạn tốc độ quang hợp; phân biệt tín hiệu hoá học nội tiết (HL) với tín hiệu thần kinh (điện thế nghỉ, điện thế hoạt động, dẫn truyền qua synap, tốc độ dẫn truyền có bao myelin); phân tích sự tích hợp giữa các hệ cơ quan qua cơ chế phản hồi âm/dương và hệ miễn dịch không đặc hiệu/đặc hiệu (kháng thể, tế bào lympho B/T, miễn dịch chủ động/bị động, vắc-xin, HIV/AIDS); và vận dụng các mô hình sinh thái học quần thể (tăng trưởng mũ/logistic, chỉ số Lincoln) cùng dòng năng lượng qua các bậc dinh dưỡng (GPP/NPP, quy tắc 10%, tháp năng lượng) để giải các bài toán định lượng.

3.1 C1 Molecules: Enzymes, Respiration and Photosynthesis

3.1.1 C1.1 Enzymes and Metabolism

Every chemical reaction in a living cell – building macromolecules, breaking down nutrients, replicating DNA – depends on **enzymes**, globular proteins (or, in a minority of cases, RNA molecules called ribozymes) that act as **biological catalysts**. A catalyst is a substance that increases the rate of a chemical reaction without being consumed or permanently altered in the process, and without changing the overall energy released or absorbed by the reaction. Enzymes achieve this by lowering the **activation energy** (E_a) – the minimum energy that reacting molecules (substrates) must possess for a reaction to proceed. By providing an alternative reaction pathway with a lower energy barrier, an enzyme allows a much larger proportion of substrate molecules to react at a given temperature, dramatically increasing reaction rate (often by factors of 10^6 or more) without requiring extreme heat, which would damage the cell.

Khái niệm cốt lõi

Enzymes lower the activation energy of the specific chemical reaction they catalyse. They do not alter the free-energy difference between reactants and products (so they do not change whether a reaction is thermodynamically favourable, only how fast it reaches equilibrium), and each enzyme molecule can be used repeatedly, catalysing many reaction events without being used up.

VN **GIẢI THÍCH TIẾNG VIỆT**

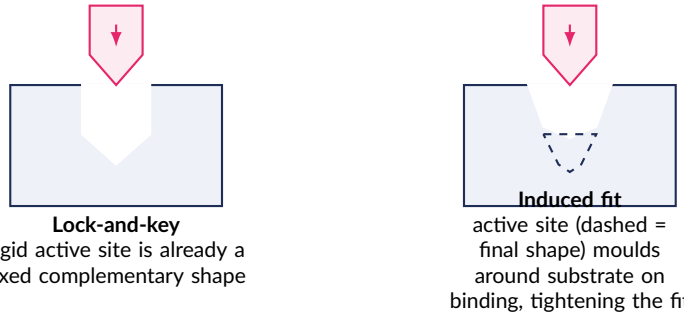
Enzyme là chất xúc tác sinh học (hầu hết là protein hình cầu), có chức năng làm **giảm năng lượng hoạt hoá (E_a)** – mức năng lượng tối thiểu cần thiết để phản ứng xảy ra – nhờ đó làm tăng tốc độ phản ứng mà không bị tiêu hao và không làm thay đổi năng lượng tự do giải phóng/hấp thu của phản ứng. Một phân tử enzyme có thể được tái sử dụng liên tục để xúc

tác nhiều lượt phản ứng.

Active site and substrate specificity. The region of an enzyme that binds its substrate(s) and carries out catalysis is the **active site** – typically a pocket or cleft formed by the folding of the polypeptide chain into its tertiary (or quaternary) structure, bringing together a small number of amino acid side chains (R-groups) from positions that may be far apart in the primary sequence. The active site's three-dimensional shape and chemical properties (charge distribution, polarity, hydrogen-bonding groups) are complementary to one particular substrate or a small family of closely related substrates – this is **substrate specificity**, and it explains why a given enzyme catalyses only one reaction (or a narrow range of reactions) rather than acting indiscriminately on any molecule it encounters.

Two models describe how an enzyme's active site interacts with its substrate:

- **Lock-and-key model**: the active site is treated as a rigid shape that is already, before binding, precisely complementary to the substrate – like a key fitting a specific lock. This model correctly captures the idea of geometric and chemical specificity but does not explain why some enzymes bind substrates that are not a perfect rigid match, or why binding itself can strain and destabilise substrate bonds.
- **Induced-fit model**: the active site is flexible rather than rigid. As the substrate approaches and begins to bind, the enzyme's active site changes shape slightly, moulding itself more closely around the substrate. This closer fit (1) positions catalytic side chains more precisely for the reaction, (2) can strain particular bonds within the substrate, helping to lower the activation energy further, and (3) explains why binding of the substrate causes a measurable conformational change in the enzyme. The induced-fit model is now regarded as the more accurate general description of enzyme-substrate binding.



Left: the lock-and-key model treats the active site as a rigid, pre-formed complementary shape. Right: the induced-fit model shows the flexible active site closing around the substrate as it binds, improving the fit and straining substrate bonds.

VN **GIẢI THÍCH TIẾNG VIỆT**

Có hai mô hình mô tả sự tương tác giữa enzyme và cơ chất (substrate): **mô hình ổ khoá – chìa khoá (lock-and-key)** coi trung tâm hoạt động là một hình dạng cố định, khớp sẵn với cơ chất; **mô hình khớp cảm ứng (induced fit)** coi trung tâm hoạt động có tính linh hoạt, thay đổi hình dạng để ôm khít lấy cơ chất khi cơ chất gắn vào, đồng thời tạo áp lực làm căng các liên kết trong cơ chất, hỗ trợ phản ứng xảy ra dễ dàng hơn. Mô hình khớp cảm ứng được xem là mô tả chính xác hơn về mặt cơ chế phân tử.

Factors affecting enzyme activity. The rate of an enzyme-catalysed reaction depends on several measurable variables, each producing a characteristic graph shape.

Temperature. As temperature rises from a low starting point, reaction rate increases: molecules (both enzyme and substrate) possess more kinetic energy, moving and colliding more frequently and

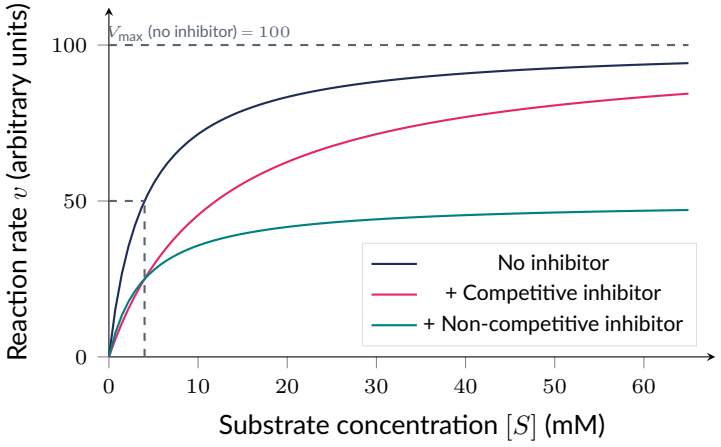
with greater energy, so a larger proportion of collisions between substrate and active site are successful. Rate increases up to an **optimum temperature**, at which the enzyme works fastest. Beyond the optimum, rate falls away sharply: excess thermal energy disrupts the weak bonds (hydrogen bonds, ionic interactions) that hold the enzyme's tertiary structure in shape, progressively distorting the active site until the substrate can no longer bind effectively – the enzyme becomes **denatured**. Because denaturation is usually irreversible (the original folded conformation is not spontaneously regained once the stabilising interactions are lost), activity does not recover if temperature is lowered again after severe denaturation.

pH. Each enzyme has an **optimum pH** at which its rate is maximal, producing a characteristic bell-shaped rate-versus-pH curve. Away from the optimum in either direction, changes in hydrogen ion concentration alter the ionisation of acidic and basic side chains in and around the active site, disrupting the ionic bonds and hydrogen bonds that maintain the active site's precise shape and chemical environment, reducing substrate binding and catalytic efficiency. At sufficiently extreme pH, the enzyme denatures altogether. Optimum pH varies enormously between enzymes according to their working environment: pepsin (stomach) has an optimum around pH 1.5–2; salivary amylase (mouth) around pH 6.5–7.5; pancreatic trypsin (small intestine) around pH 8.

Enzyme	Optimum pH	Site of action
Pepsin	≈ 1.5–2	Stomach (highly acidic gastric juice)
Salivary amylase	≈ 6.5–7.5	Mouth (near-neutral saliva)
Trypsin (pancreatic)	≈ 8	Small intestine (alkaline pancreatic secretions)

Substrate concentration. At low substrate concentration, reaction rate rises steeply and roughly linearly as $[S]$ increases: enzyme active sites are mostly free, so adding more substrate simply increases the frequency of successful enzyme-substrate collisions. As $[S]$ continues to rise, the rate of increase slows and the curve levels off at a maximum rate, V_{max}: at this point essentially every enzyme active site is occupied at all times (the enzyme is **saturated**), so adding still more substrate cannot increase the rate further – the fixed quantity of enzyme, not substrate availability, is now the limiting factor.

Enzyme concentration. Provided substrate is present in excess (non-limiting) and all other conditions are held constant, reaction rate is directly proportional to enzyme concentration – a straight line through the origin – because each additional enzyme molecule adds one more active site available to bind substrate at any instant.



Rate versus substrate concentration for an uninhibited enzyme (navy), the same enzyme with a competitive inhibitor (pink – same eventual V_{max}, larger apparent K_m), and with a non-competitive inhibitor (teal – reduced V_{max}, unchanged K_m).

V_{max} is the maximum rate of reaction, reached when the enzyme is fully saturated with substrate. K_m **(Michaelis constant)** is the substrate concentration at which reaction rate equals half of V_{max}. K_m is an inverse measure of the enzyme's **affinity** for its substrate: a **low** K_m means the enzyme reaches half-maximal rate at a low substrate concentration (high affinity – binds substrate readily), while a **high** K_m means a much greater substrate concentration is needed to reach half-maximal rate (low affinity).

Ví dụ mẫu · Reading K_m and V_{max} from data

An enzyme's initial reaction rate v was measured at a series of substrate concentrations $[S]$, with enzyme concentration and temperature held constant:

$[S]$ (mM)	1	2	4	8	16	32	64
v (μmol min^{-1})	20	33	50	67	80	89	94

Estimate V_{max} and K_m for this enzyme, and explain your reasoning.

As $[S]$ increases, v rises steeply at first, then increases by smaller and smaller amounts and is clearly levelling off towards a plateau – the data are approaching but have not yet reached a maximum. Extrapolating the trend, the curve is heading towards a plateau at approximately $V_{max} \approx 100$ μmol min^{-1} (the rate is still climbing slowly toward this ceiling even at the highest substrate concentration tested).

Half of this estimated V_{max} is $100/2 = 50$ μmol min^{-1}. Reading the table, $v = 50$ occurs exactly at $[S] = 4$ mM. Therefore $K_m \approx 4$ mM. Because this is a relatively small value, the enzyme shows a comparatively high affinity for its substrate – only a modest substrate concentration is required to drive the enzyme to half of its maximum rate.

VN **GIẢI THÍCH TIẾNG VIỆT**

V_{max} là tốc độ phản ứng tối đa, đạt được khi enzyme đã bão hoà cơ chất (mọi trung tâm hoạt động đều đang được sử dụng). K_m là nồng độ cơ chất tại đó tốc độ phản ứng bằng một nửa V_{max} – đây là chỉ số nghịch với **ái lực (affinity)** của enzyme với cơ chất: K_m càng **nhỏ** thì ái lực càng **cao** (chỉ cần ít cơ chất đã đạt nửa tốc độ tối đa); K_m càng **lớn** thì ái lực càng **thấp**. Cách đọc từ bảng số liệu: ước lượng V_{max} là giá trị mà tốc độ đang tiệm cận, sau đó tìm nồng độ cơ chất tương ứng với một nửa giá trị đó chính là K_m.

Enzyme inhibitors. An inhibitor is a molecule that reduces or blocks enzyme activity. Two contrasting mechanisms produce distinctly different effects on K_m and V_{max}:

- **Competitive inhibition**: the inhibitor's shape resembles the normal substrate closely enough that it can bind directly to the **active site**, physically blocking the substrate from binding there. Because inhibitor and substrate compete for the same site, the effect *can be overcome* by increasing substrate concentration sufficiently – given enough substrate, the enzyme can still eventually reach its original V_{max}, but only at a higher substrate concentration than before. The apparent K_m therefore **increases** (more substrate is needed to reach half-maximal rate), while V_{max} itself is **unchanged**.
- **Non-competitive inhibition**: the inhibitor binds at a site distinct from the active site (an **allosteric site**), causing a conformational change that is transmitted to and distorts the active site, impairing catalysis (or substrate binding) at that enzyme molecule regardless of substrate concentration. Because the inhibitor does not compete directly for the active site, the effect *cannot* be overcome by adding more substrate – a fraction of enzyme molecules are effectively taken out of action no matter how much substrate is present. V_{max} is therefore **reduced**, while K_m (the affinity of the still-functional active sites for substrate) is **unchanged**.

Ví dụ mẫu · Distinguishing competitive from non-competitive inhibition

The same enzyme is tested under three conditions, measuring rate v at a low and a high substrate concentration:

$[S]$ (mM)	No inhibitor	+ Inhibitor A	+ Inhibitor B
4	50	25	25
100	96	89	48

(All rates in μmol min^{-1}.) Identify which inhibitor is competitive and which is non-competitive, and justify your answer.

At low substrate concentration ($[S] = 4$ mM), both inhibitors reduce the rate identically (from 50 to 25), so the low-concentration data alone cannot distinguish them. The decisive comparison is at high substrate concentration ($[S] = 100$ mM, close to saturation): with Inhibitor A, the rate recovers to 89, close to the uninhibited value of 96 – consistent with the inhibitor being **out-competed** by the large excess of substrate. Inhibitor A is therefore **competitive**.

With Inhibitor B, the rate remains capped at 48 even at this high substrate concentration – roughly half the uninhibited rate, and no amount of additional substrate would raise it further, since the inhibitor's effect does not depend on substrate concentration at all. Inhibitor B is therefore **non-competitive**: it has permanently reduced the effective V_{max} of the enzyme population.

(!) Lỗi thường gặp: Do not decide competitive versus non-competitive inhibition from behaviour at a single, low substrate concentration – both types typically reduce the rate there, and the data can look identical (as in the worked example above). The distinguishing test is always behaviour **at high, near-saturating substrate concentration**: if the rate recovers toward the original (uninhibited) V_{max}, the inhibitor is competitive (raised apparent K_m, same V_{max}); if the rate remains capped well below the original V_{max} no matter how much substrate is added, the inhibitor is non-competitive (same K_m, reduced V_{max}).

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Đừng kết luận ức chế cạnh tranh hay không cạnh tranh chỉ dựa vào một nồng độ cơ chất thấp – ở nồng độ thấp, cả hai loại ức chế thường làm giảm tốc độ tương tự nhau. Phép thử quyết định là quan sát ở nồng độ cơ chất **cao, gần bão hoà**: nếu tốc độ phục hồi gần với V_{max} ban đầu (khi không có chất ức chế) → đó là **ức chế cạnh tranh** (chất ức chế gắn tại chính trung tâm hoạt động, có thể bị "lấn át" khi dư thừa cơ chất, làm K_m biểu kiến tăng nhưng V_{max} không đổi); nếu tốc độ vẫn bị giới hạn thấp hơn hẳn dù thêm bao nhiêu cơ chất → đó là **ức chế không cạnh tranh** (chất ức chế gắn tại vị trí dị lập thể khác, làm biến dạng trung tâm hoạt động, V_{max} giảm nhưng K_m không đổi).

Cofactors and coenzymes. Many enzymes require a non-protein helper molecule to be catalytically active. **Cofactors** are typically inorganic ions (e.g. Mg^{2+}, Zn^{2+}, Fe^{2+}/Fe^{3+}) that bind the enzyme and are often essential for maintaining the correct active-site conformation or for participating directly in catalysis. **Coenzymes** are organic helper molecules, frequently derived from vitamins, that typically carry chemical groups, electrons, or hydrogen atoms between different enzyme-catalysed reactions in a metabolic pathway – for example NAD^+ and $NADP^+$ (derived from niacin) and FAD (derived from riboflavin) act as electron/hydrogen carriers central to cell respiration and photosynthesis (see below), while coenzyme A (derived from pantothenic acid) carries acyl groups. Without its required cofactor or coenzyme, the protein portion of the enzyme (the apoenzyme) is usually catalytically inactive.

Metabolic pathways. A **metabolic pathway** is an ordered sequence of enzyme-catalysed reactions in which the product of one reaction becomes the substrate of the next, each step controlled by a specific enzyme. Organising metabolism into stepwise pathways (rather than single large reactions) allows energy to be released or captured gradually and in manageable, controllable amounts, and allows the cell to regulate flux through a pathway by controlling the activity of one or a few key enzymes (often the first, committing step) – for instance, many pathways are regulated by **feedback inhibition**, in which the pathway's own end product acts as an inhibitor of an early enzyme in the same pathway, automatically slowing production once enough end product has accumulated.

Allosteric regulation. Feedback inhibition depends on **allosteric enzymes**, which possess a regulatory (allosteric) site in addition to the active site. A regulatory molecule binding this allosteric site changes the enzyme's conformation, which is transmitted to and alters the shape of the active site – either reducing (an **allosteric inhibitor**) or increasing (an **allosteric activator**) the enzyme's affinity for substrate or its catalytic efficiency. Because binding occurs away from the active site itself, allosteric regulators do not need to resemble the substrate at all, unlike a competitive inhibitor; this is the same general mechanism described earlier for non-competitive inhibition, but applied here to endogenous molecules (often a pathway's own end product) that regulate flux through a metabolic pathway as part of normal cell control, rather than to an external toxin or drug.

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Enzyme dị lập thể (allosteric enzyme) có thêm một vị trí điều hoà (allosteric site) ngoài trung tâm hoạt động. Phân tử điều hoà gắn vào vị trí này làm thay đổi hình dạng enzyme, từ đó ảnh hưởng đến trung tâm hoạt động – có thể là **chất hoạt hoá dị lập thể** (tăng ái lực/hiệu quả xúc tác) hoặc **chất ức chế dị lập thể** (giảm ái lực/hiệu quả xúc tác), ví dụ điển hình là chính sản phẩm cuối của con đường chuyển hoá quay lại ức chế enzyme đầu tiên (ức chế ngược/feedback inhibition).

Denaturation. Denaturation is the loss of an enzyme's (or any protein's) native three-dimensional structure, caused by disruption of the weak, non-covalent interactions (hydrogen bonds, ionic bonds, and some hydrophobic interactions) that hold its tertiary and quaternary structure in shape – commonly triggered by excessive heat, extreme pH, or exposure to heavy metals/certain chemicals. The protein's primary structure (the sequence of peptide bonds linking amino acids) is not broken, but the loss of precise three-dimensional folding destroys the active site's shape, so the enzyme can no longer bind its substrate or catalyse the reaction. Denaturation is generally **irreversible** under physiological conditions.

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Cofactor (thường là ion vô cơ, VD Mg^{2+}, Zn^{2+}) và **coenzyme** (phân tử hữu cơ, thường có nguồn gốc từ vitamin, VD NAD^{+}, FAD) là các "trợ thủ" không phải protein mà nhiều enzyme cần có để hoạt động – coenzyme thường đóng vai trò vận chuyển điện tử/nguyên tử hydro giữa các phản ứng trong con đường chuyển hoá. **Biến tính (denaturation)** là sự phá vỡ cấu trúc không gian ba chiều của enzyme (do nhiệt độ cao, pH cực đoan...) làm hỏng hình dạng trung tâm hoạt động – quá trình này thường **không thể đảo ngược**, khác với ức chế (inhibition), vốn chỉ tạm thời ngăn cản hoạt động của enzyme mà không phá huỷ cấu trúc bậc ba.

Ví dụ mẫu · Interpreting temperature-activity curves for two enzymes

Relative activity was measured for two enzymes across a range of temperatures:

Temperature (°C)	10	20	30	37	45	55	65
Human salivary amylase (% activity)	15	40	75	100	60	10	0
Taq polymerase, hot-spring bacterium (% activity)	5	12	25	45	65	80	100

Identify the optimum temperature of each enzyme, and explain why they differ so much.

Human salivary amylase shows a clear optimum at $37°$C (its activity peaks there, at 100%, then falls sharply by 55–$65°$C) – consistent with the normal internal body temperature of the human host in which it evolved to function. *Taq* polymerase (from bacteria living in hot springs) is still increasing in activity at every temperature tested up to $65°$C, showing no sign yet of denaturing; its optimum lies at a much higher temperature (in reality close to 75–$80°$C), reflecting the fact that its tertiary structure is stabilised by additional/stronger bonding interactions that allow it to resist the thermal disruption that would denature the human enzyme at the same temperature. Both curves follow the same underlying logic (rising phase = increasing kinetic energy and collision frequency; falling phase = progressive denaturation) but are shifted according to the normal temperature of each organism's natural environment.

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Hình dạng đường cong hoạt tính enzyme theo nhiệt độ luôn gồm hai pha: pha **tăng** (do động năng phân tử tăng, tần suất va chạm thành công giữa cơ chất và trung tâm hoạt động tăng) và pha **giảm mạnh** sau nhiệt độ tối ưu (do biến tính enzyme). Nhiệt độ tối ưu của mỗi enzyme phản ánh môi trường sống bình thường của sinh vật mang enzyme đó – enzyme người thường tối ưu quanh $37°$C, trong khi enzyme của vi khuẩn ưa nhiệt (sống ở suối nước nóng) có thể tối ưu ở 70–$80°$C vì cấu trúc bậc ba của chúng được ổn định bởi các liên kết bền hơn, chịu nhiệt tốt hơn.

Temperature coefficient (Q_{10}). The sensitivity of an enzyme-catalysed reaction (or any biological rate process) to temperature can be expressed quantitatively using the **temperature coefficient,** Q_{10}: the factor by which the rate increases for a $10°$C rise in temperature.

$$Q_{10} = \frac{\text{rate at } (T + 10°\text{C})}{\text{rate at } T}$$

Over a range in which the enzyme is well below its optimum temperature (and not yet being denatured), Q_{10} typically lies between about 2 and 3 for biological reactions – rate roughly doubles or triples for every $10°$C rise, reflecting the increased kinetic energy and collision frequency of enzyme and substrate molecules. Once temperature approaches and then exceeds the optimum, the observed Q_{10} falls sharply, and becomes less than 1 once the rate itself is falling with rising temperature – a sign that progressive denaturation, not simple kinetic speed-up, now dominates.

Ví dụ mẫu · Calculating Q_{10}

The rate of an enzyme-catalysed reaction was measured at two temperatures, both known to be well below the enzyme's optimum: 12 μmol min^{-1} at $15°$C, and 24 μmol min^{-1} at $25°$C. (a) Calculate Q_{10} for this interval. (b) Predict the rate at $35°$C if the same Q_{10} continued to apply, and explain why this prediction might not hold in practice.

(a)

$$Q_{10} = \frac{\text{rate at } 25°\text{C}}{\text{rate at } 15°\text{C}} = \frac{24}{12} = 2.0$$

(b) If $Q_{10} = 2.0$ continued to apply from $25°$C to $35°$C, the predicted rate would be $24 \times 2.0 = 48$ μmol min^{-1}. This prediction may well fail in practice: as temperature keeps rising, the enzyme is increasingly likely to approach or exceed its optimum temperature, at which point additional heat progressively disrupts the weak bonds maintaining tertiary structure (denaturation) rather than simply increasing the frequency of successful collisions – so the true rate at $35°$C could be well below 48 μmol min^{-1}, and might even be lower than the rate already

measured at 25°C if 35°C lies well past the optimum.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hệ số nhiệt độ Q_{10} = tốc độ phản ứng ở nhiệt độ $(T + 10^{\circ}\text{C})$ chia cho tốc độ ở nhiệt độ T – cho biết tốc độ tăng bao nhiêu lần khi nhiệt độ tăng thêm 10°C. Với hầu hết phản ứng sinh học (khi còn cách xa nhiệt độ tối ưu), Q_{10} thường trong khoảng 2–3. Khi vượt qua nhiệt độ tối ưu, Q_{10} giảm mạnh (có thể nhỏ hơn 1) vì enzyme bắt đầu biến tính, chứ không còn đơn thuần do động năng phân tử tăng.

(!) Lỗi thường gặp: Do not treat Q_{10} as a fixed, universal constant for a given enzyme across all temperatures. Q_{10} describes the ratio of rates over one *particular* 10°C interval; because activity does not increase indefinitely with temperature, a Q_{10} calculated near or above the optimum will be much lower (or even below 1, once rate is falling) than a Q_{10} calculated well below the optimum, where kinetic energy alone still governs the rate.

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Đừng cho rằng Q_{10} là một hằng số cố định áp dụng cho enzyme ở mọi mức nhiệt độ. Q_{10} chỉ mô tả tỉ lệ tốc độ trong MỘT khoảng 10°C cụ thể; vì hoạt tính enzyme không tăng vô hạn theo nhiệt độ, Q_{10} tính gần hoặc vượt quá nhiệt độ tối ưu sẽ thấp hơn nhiều (thậm chí nhỏ hơn 1) so với Q_{10} tính ở vùng nhiệt độ thấp hơn nhiều so với tối ưu, nơi động năng phân tử vẫn là yếu tố chi phối tốc độ.

3.1.2 C1.2 Cell Respiration

Cell respiration is the controlled release of chemical energy from organic molecules (respiratory substrates) to produce ATP, the immediate energy currency usable for cellular work. **Aerobic respiration** requires oxygen and occurs in four linked stages.

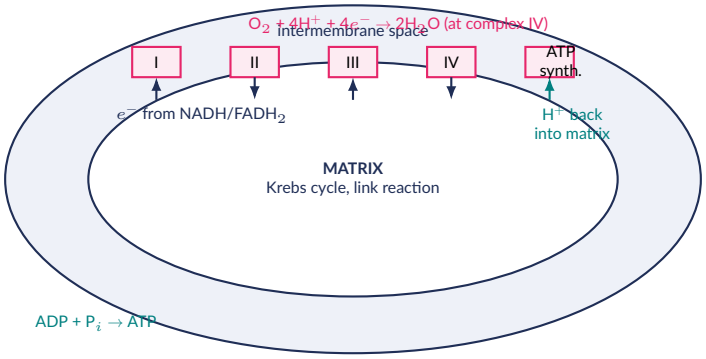
1. Glycolysis takes place in the **cytoplasm (cytosol)** of every cell and does not require oxygen. A single molecule of glucose (6-carbon) is split, via a sequence of enzyme-catalysed steps, into two molecules of **pyruvate** (3-carbon). The pathway invests 2 ATP early on but generates 4 ATP by **substrate-level phosphorylation** (direct enzymatic transfer of a phosphate group to ADP), for a **net yield of 2 ATP** per glucose, plus 2 molecules of NADH (formed as NAD^+ is reduced, carrying high-energy electrons onward).

2. The link reaction occurs in the **mitochondrial matrix**. Each pyruvate molecule (there are two per original glucose) is transported into the mitochondrion, decarboxylated (losing one carbon as CO_2) and oxidised, and the remaining 2-carbon fragment is attached to coenzyme A to form **acetyl coenzyme A (acetyl CoA)**, with NAD^+ reduced to NADH in the process. Because this happens once per pyruvate, the link reaction runs twice per original glucose molecule.

3. The Krebs cycle (citric acid cycle) also takes place in the **mitochondrial matrix**. The 2-carbon acetyl group of acetyl CoA condenses with a 4-carbon molecule (oxaloacetate) to form the 6-carbon citrate, which is then progressively oxidised and decarboxylated through a cyclical series of reactions, releasing 2 molecules of CO_2 per turn and regenerating oxaloacetate so the cycle can continue. Each turn (i.e. per acetyl CoA, so twice per original glucose) yields 1 ATP (by substrate-level phosphorylation), 3 NADH, and 1 $FADH_2$.

4. Oxidative phosphorylation, comprising the **electron transport chain (ETC)** and **chemiosmosis**, occurs at the **inner mitochondrial membrane** and accounts for the large majority of ATP produced in aerobic respiration. NADH and $FADH_2$ generated in the earlier stages donate their high-energy electrons to a series of protein complexes embedded in the inner membrane (the electron transport chain). As electrons pass from complex to complex, energy is progressively released and used to

actively pump H^+ ions from the matrix into the intermembrane space, building up a steep **proton (electrochemical) gradient** across the inner membrane. Oxygen serves as the **final electron acceptor** at the end of the chain, combining with electrons and H^+ to form water – this is the reason aerobic respiration requires oxygen: without a final acceptor, electrons would back up and the whole chain would stall. The accumulated protons then flow back down their gradient, from the intermembrane space into the matrix, through the enzyme **ATP synthase**, a channel-like rotary protein embedded in the inner membrane; this flow (**chemiosmosis**) drives the phosphorylation of ADP to ATP.



Simplified cross-section of a mitochondrion. Electron transport chain complexes (I–IV, pink) in the inner membrane pump H^+ into the intermembrane space as electrons from NADH/$FADH_2$ pass along the chain to O_2; H^+ flows back through ATP synthase (chemiosmosis), driving ATP synthesis.

Net ATP yield of aerobic respiration. Only a small amount of ATP is produced directly by substrate-level phosphorylation (2 from glycolysis $+ 2$ from the Krebs cycle $= 4$ ATP per glucose). The great majority of ATP – roughly 28 further molecules – is produced indirectly via oxidative phosphorylation, as the 10 NADH and 2 $FADH_2$ generated per glucose donate electrons to the ETC and drive chemiosmotic ATP synthesis. The overall net yield is therefore commonly cited as approximately 30–32 ATP per glucose molecule (older textbooks cite up to $\approx$ 36–38, using a simpler assumed conversion factor per NADH/$FADH_2$; the lower modern estimate accounts for the energy cost of shuttling cytosolic NADH into the mitochondrion).

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Hô hấp hiếu khí gồm bốn giai đoạn: **đường phân (glycolysis)** tại tế bào chất (glucose → 2 pyruvate, tạo 2 ATP ròng); **phản ứng liên kết (link reaction)** tại chất nền ty thể (pyruvate → acetyl CoA, giải phóng CO_2); **chu trình Krebs** tại chất nền ty thể (tạo CO_2, ATP, và các chất mang điện tử NADH/$FADH_2$); và **phosphoryl hoá oxy hoá** (chuỗi chuyền điện tử + hoá thẩm thấu) tại màng trong ty thể – đây là nguồn tạo ra phần lớn ATP. Oxy là chất nhận điện tử cuối cùng của chuỗi chuyền điện tử, kết hợp với H^+ tạo thành nước; dòng H^+ chảy ngược qua ATP synthase (hoá thẩm thấu) chính là động lực tổng hợp ATP.

Modern ATP-yield accounting per electron carrier. Using widely accepted modern (non-integer) conversion factors, each NADH that donates electrons to the ETC drives the synthesis of approximately 2.5 ATP, while each $FADH_2$ (which enters the chain at a later point, bypassing the first proton-pumping complex, and so contributes to a smaller proton gradient) drives approximately 1.5 ATP. Per glucose molecule: 10 NADH $\times$ $2.5 = 25$ ATP, plus 2 $FADH_2$ $\times$ $1.5 = 3$ ATP, giving 28 ATP from oxidative phosphorylation – plus the 4 ATP already produced by substrate-level phosphorylation (glycolysis and the Krebs cycle) – for a total of approximately 32 ATP overall, consistent with the commonly cited modern estimate of 30–32 ATP per glucose molecule.

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Theo hệ số quy đổi hiện đại: mỗi NADH tạo ra khoảng 2.5 ATP, mỗi $FADH_2$ tạo ra khoảng 1.5 ATP (vì đi vào chuỗi chuyền điện tử muộn hơn, bỏ qua phức hệ bơm proton đầu tiên). Với mỗi phân tử glucose: 10 NADH $\times 2.5 = 25$ ATP, cộng 2 $FADH_2$ $\times 1.5 = 3$ ATP, tổng cộng 28 ATP từ phosphoryl hoá oxy hoá, cộng thêm 4 ATP từ phosphoryl hoá mức cơ chất, cho tổng khoảng 32 ATP mỗi glucose – phù hợp với ước tính hiện đại thường dùng là 30–32 ATP.

Anaerobic respiration (fermentation) in eukaryotes. When oxygen is absent or insufficient, the electron transport chain cannot operate (there is no final electron acceptor to keep it running), so oxidative phosphorylation – the source of the great majority of ATP – stops. Without a way to reoxidise NADH back to NAD^+, glycolysis itself would also grind to a halt (it requires a continuous supply of NAD^+). **Fermentation** solves this by using pyruvate itself (rather than oxygen) as the final electron acceptor, regenerating NAD^+ so that glycolysis can continue, but capturing no further ATP beyond the 2 ATP net already produced in glycolysis.

- **Lactic acid fermentation** (animals, some bacteria): pyruvate is reduced directly to **lactate** using the electrons carried by NADH, regenerating NAD^+. In vertebrates, this occurs in skeletal muscle during intense exercise, when oxygen delivery cannot keep pace with the muscle's demand for ATP. Accumulating lactate contributes to the burning sensation and fatigue associated with intense exercise; it is later transported to the liver and reconverted to glucose/pyruvate once oxygen supply is restored.
- **Alcoholic fermentation** (yeast and some other microorganisms): pyruvate is first decarboxylated to acetaldehyde (releasing CO_2), and the acetaldehyde is then reduced to **ethanol** using the electrons from NADH, again regenerating NAD^+. This pathway is exploited industrially in brewing, winemaking, and bread-making (the released CO_2 makes bread dough rise).

Because both pathways regenerate only the 2 ATP produced directly in glycolysis (with none of the further ≈ 28–30 ATP that oxidative phosphorylation would otherwise supply), anaerobic respiration yields roughly an order of magnitude less ATP per glucose molecule than aerobic respiration – which is why sustained, intense muscular activity cannot be maintained anaerobically for long, and why facultative anaerobes such as yeast grow far more slowly without oxygen than with it.

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Khi thiếu oxy, chuỗi chuyền điện tử không thể hoạt động (không có chất nhận điện tử cuối cùng), nên hô hấp kỵ khí chỉ có thể tái tạo lại NAD^+ bằng cách dùng chính pyruvate làm chất nhận điện tử – ở động vật tạo ra **lactate (lên men lactic)**, ở nấm men tạo ra **ethanol + CO_2 (lên men rượu)**. Vì cả hai con đường này chỉ thu được 2 ATP từ đường phân (không có thêm ATP từ chuỗi chuyền điện tử), năng lượng thu được thấp hơn hô hấp hiếu khí khoảng **10 lần** – đây là lý do cơ bắp không thể duy trì hoạt động cường độ cao kéo dài nếu thiếu oxy.

Respiratory substrates and the respiratory quotient (RQ). Cells can respire carbohydrates, lipids, or proteins as fuel, depending on availability. Because these molecules differ in their relative proportions of carbon, hydrogen, and oxygen, complete oxidation of each requires a different ratio of oxygen consumed to carbon dioxide produced.

$$\text{RQ} = \frac{\text{volume of } CO_2 \text{ produced}}{\text{volume of } O_2 \text{ consumed}}$$

(measured under the same conditions of temperature and pressure, over the same time interval – equal volumes of gas contain equal numbers of moles, so this is equivalent to a mole ratio). Typical values: **carbohydrate** RQ ≈ 1.0 (exactly 1.0 for glucose, since $C_6H_{12}O_6 + 6O_2 \rightarrow 6CO_2 + 6H_2O$ consumes and produces equal moles of gas); **lipid** RQ ≈ 0.7 (fats contain proportionally more hydrogen and less oxygen than carbohydrates, so more O_2 is required to oxidise the extra hydrogen to water, lowering the $CO_2 : O_2$ ratio); **protein** RQ ≈ 0.8–0.9 (intermediate, and complicated by the fact that the nitrogen-containing amino group is excreted as nitrogenous waste rather than fully oxidised).

Ví dụ mẫu · Calculating RQ and identifying the respiratory substrate

Germinating sunflower seeds are placed in a respirometer at constant temperature. Over 10 minutes, the seeds consume 80 mm^3 of O_2 and produce 56 mm^3 of CO_2. Calculate the RQ and identify the most likely respiratory substrate.

$$\text{RQ} = \frac{CO_2 \text{ produced}}{O_2 \text{ consumed}} = \frac{56 \text{ mm}^3}{80 \text{ mm}^3} = 0.70$$

An RQ of approximately 0.7 corresponds to **lipid** as the respiratory substrate. This is biologically consistent with sunflower seeds, whose endosperm stores energy mainly as oil (lipid) rather than starch, and which mobilise this stored lipid as their primary fuel during early germination before photosynthetic leaves develop.

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Hệ số hô hấp (RQ) = thể tích CO_2 sinh ra / thể tích O_2 tiêu thụ (đo cùng điều kiện nhiệt độ, áp suất). Giá trị RQ giúp suy ra loại cơ chất hô hấp: **carbohydrate** ≈ 1.0; **lipid** ≈ 0.7 (chất béo có tỉ lệ hydro cao hơn so với oxy nên cần nhiều O_2 hơn để oxy hoá hoàn toàn); **protein** ≈ 0.8–0.9. Ví dụ hạt hướng dương nảy mầm có RQ ≈ 0.7 vì dự trữ năng lượng chủ yếu dưới dạng dầu (lipid) trong nội nhũ.

Measuring respiration rate with a respirometer. A simple respirometer allows the rate of oxygen consumption of small organisms (e.g. germinating seeds, small invertebrates) to be measured directly. The respiring organisms are sealed in a chamber connected to a capillary tube containing a coloured manometer fluid; **soda lime (or KOH solution)** placed in the chamber absorbs all CO_2 produced, so any pressure change – and hence any movement of the manometer fluid – reflects only the volume of O_2 consumed, regardless of the organism's RQ. A parallel **control (thermobarometer)** – an identical, sealed apparatus containing inert material (e.g. glass beads) instead of living organisms – corrects the reading for any fluid movement caused by changes in atmospheric temperature or pressure during the experiment, rather than by respiration.

Ví dụ mẫu · Calculating respiration rate from respirometer data

A respirometer containing germinating pea seeds, and a control thermobarometer containing an equal volume of glass beads, are connected to identical capillary tubes of cross-sectional area 2.0 mm^2. Over 10 minutes, the manometer fluid in the experimental tube moves 35 mm towards the seeds (indicating gas uptake), while the fluid in the control tube moves 3 mm in the same direction. Calculate the rate of oxygen consumption of the seeds, in mm^{3}min^{-1}.

The control's 3 mm movement reflects a change in atmospheric conditions alone (not respira-

tion), so it must be subtracted from the experimental reading to isolate the movement due to O_2 uptake by the seeds:

$$\text{corrected distance} = 35\ \text{mm} - 3\ \text{mm} = 32\ \text{mm}$$

Volume of O_2 consumed = corrected distance $\times$ cross-sectional area:

$$V = 32\ \text{mm} \times 2.0\ \text{mm}^2 = 64\ \text{mm}^3$$

This volume was taken up over 10 minutes, so the rate of oxygen consumption is:

$$\text{rate} = \frac{64\ \text{mm}^3}{10\ \text{min}} = 6.4\ \text{mm}^3\text{min}^{-1}$$

VN **GIẢI THÍCH TIẾNG VIỆT**

Trong thí nghiệm hô hấp kế (respirometer), **vôi tôi xút (soda lime)** hấp thụ toàn bộ CO_2 sinh ra, nên sự di chuyển của giọt chất lỏng trong ống mao dẫn chỉ phản ánh thể tích O_2 đã tiêu thụ. Ống đối chứng (thermobarometer, chứa vật liệu trơ thay vì sinh vật sống) giúp hiệu chỉnh sai số do thay đổi nhiệt độ/áp suất khí quyển (không phải do hô hấp) – khoảng dịch chuyển ở ống đối chứng cần được trừ khỏi ống thí nghiệm trước khi tính thể tích O_2 tiêu thụ (= khoảng cách hiệu chỉnh $\times$ tiết diện ống mao dẫn), sau đó chia cho thời gian để ra tốc độ hô hấp.

3.1.3 C1.3 Photosynthesis

Photosynthesis is the process by which photosynthetic organisms (plants, algae, cyanobacteria) convert light energy into chemical energy stored in organic molecules, using carbon dioxide and water as raw materials and releasing oxygen as a byproduct:

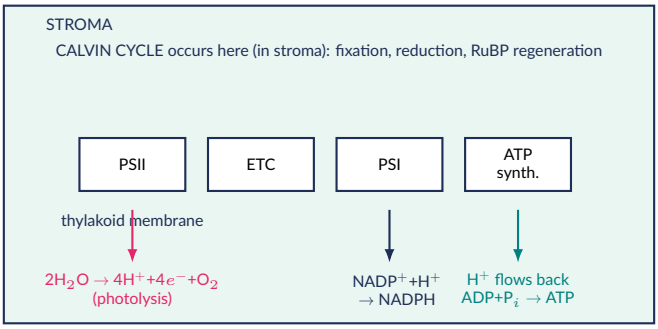
$$6\,CO_2 + 6\,H_2O \xrightarrow{\text{light energy}} C_6H_{12}O_6 + 6\,O_2$$

This overall equation summarises two linked sets of reactions that occur in different compartments of the **chloroplast**: the **light-dependent reactions** in the **thylakoid membrane** and the **light-independent reactions (Calvin cycle)** in the **stroma**.

Light-dependent reactions (thylakoid membrane). Light energy is absorbed by chlorophyll and accessory pigments organised into two distinct pigment-protein complexes, **Photosystem II (PSII)** and **Photosystem I (PSI)**, embedded in the thylakoid membrane.

- At **PSII**, absorbed light energy excites electrons in chlorophyll to a higher energy level; these high-energy electrons are passed into an electron transport chain in the thylakoid membrane. PSII replaces its lost electrons by splitting water molecules – **photolysis**: $2H_2O \rightarrow 4H^+ + 4e^- + O_2$ – which is the source of the O_2 released during photosynthesis, and also adds H^+ to the thylakoid lumen.
- Electrons pass along the electron transport chain from PSII towards PSI, releasing energy that is used to actively pump further H^+ ions into the thylakoid lumen, building a steep proton gradient across the thylakoid membrane – directly analogous to the mitochondrial ETC. This proton gradient drives **chemiosmosis**: H^+ flows back out of the lumen into the stroma through **ATP synthase** embedded in the thylakoid membrane, synthesising ATP from ADP and P_i (**photophosphorylation**).
- At **PSI**, the (now lower-energy) electrons are re-excited by further absorbed light, then passed via the carrier ferredoxin to reduce $NADP^+$ to **NADPH** (using an H^+ from the stroma).

Both products of the light-dependent reactions, **ATP** and **NADPH**, are then used to power the light-independent reactions in the stroma.



Simplified thylakoid membrane cross-section. PSII splits water (photolysis) and feeds electrons through an ETC to PSI, pumping H^+ into the thylakoid lumen; H^+ flows back through ATP synthase (chemiosmosis); PSI reduces $NADP^+$ to NADPH. Both ATP and NADPH then power the Calvin cycle in the surrounding stroma.

VN **GIẢI THÍCH TIẾNG VIỆT**

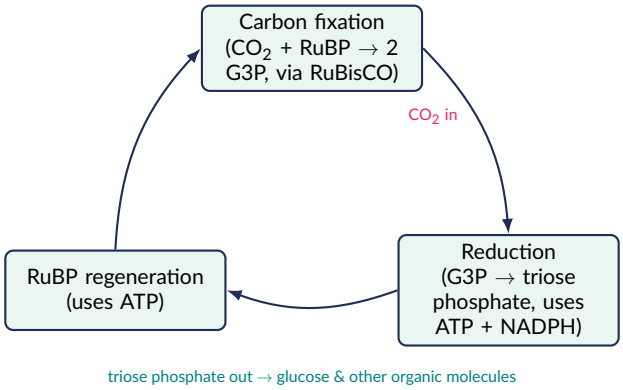
Phản ứng phụ thuộc ánh sáng xảy ra tại **màng thylakoid**: **PSII** hấp thụ ánh sáng, kích thích điện tử, và thực hiện **quang phân li nước (photolysis)** để bù lại điện tử đã mất, đồng thời giải phóng O_2; điện tử di chuyển qua chuỗi chuyền điện tử tới **PSI**, trên đường đi bơm H^+ vào xoang thylakoid tạo građien proton, sau đó H^+ chảy ngược qua ATP synthase (hoá thẩm thấu) để tổng hợp ATP; PSI tái kích thích điện tử để khử $NADP^+$ thành **NADPH**. Cả ATP và NADPH sinh ra đều được dùng để cung cấp năng lượng cho chu trình Calvin.

Light-independent reactions: the Calvin cycle (stroma). The Calvin cycle uses the ATP and NADPH generated by the light-dependent reactions to convert CO_2 into organic carbon compounds, in three stages:

- **Carbon fixation**: CO_2 combines with the 5-carbon sugar **RuBP (ribulose bisphosphate)**, catalysed by the enzyme **RuBisCO** (ribulose bisphosphate carboxylase/oxygenase – widely considered the most abundant enzyme on Earth). The resulting unstable 6-carbon intermediate immediately splits into two molecules of the 3-carbon compound **glycerate 3-phosphate (G3P)**.
- **Reduction**: each glycerate 3-phosphate is phosphorylated (using **ATP**) and then reduced (using **NADPH**) to form **triose phosphate**. This is the step that actually incorporates the chemical energy captured in the light-dependent reactions into a carbon-based product.
- **Regeneration of RuBP**: most of the triose phosphate produced is recycled, using further ATP, through a series of reactions that regenerate RuBP, allowing the cycle to continue fixing more CO_2. A fraction of the triose phosphate is instead drawn off from the cycle to synthesise glucose and other organic molecules (carbohydrates, lipids, amino acids) via further metabolic pathways.

VN **GIẢI THÍCH TIẾNG VIỆT**

Chu trình Calvin diễn ra tại **chất nền (stroma)**, gồm ba giai đoạn: **cố định carbon** (CO_2 kết hợp với RuBP nhờ enzyme **RuBisCO**, tạo ra glycerate 3-phosphate); **khử** (glycerate 3-phosphate được phosphoryl hoá bằng ATP và khử bằng NADPH thành triose phosphate); và **tái tạo RuBP** (hầu hết triose phosphate được dùng để tái tạo lại RuBP, một phần nhỏ được rút ra để tổng hợp glucose và các phân tử hữu cơ khác).



The Calvin cycle (stroma): carbon fixation (CO_2 + RuBP → glycerate 3-phosphate, via RuBisCO) → reduction (glycerate 3-phosphate → triose phosphate, powered by ATP and NADPH from the light-dependent reactions) → regeneration of RuBP (using further ATP), allowing the cycle to continue. A fraction of triose phosphate is drawn off at each turn to synthesise glucose and other organic molecules.

Factors limiting the rate of photosynthesis. At any given moment, the overall rate of photosynthesis is set by whichever input is in shortest supply relative to the others – the **limiting factor**.

- **Light intensity**: at low light intensity, rate increases roughly linearly as intensity rises (more photons drive more excitation events in the light-dependent reactions), then plateaus at higher intensities once light is no longer the scarcest input and some other factor (typically CO_2 concentration or temperature) becomes limiting instead.
- CO_2 **concentration**: similarly, rate rises with increasing CO_2 concentration while CO_2 (the substrate for carbon fixation) is scarce, then plateaus once CO_2 is no longer limiting.
- **Temperature**: because the Calvin cycle reactions are enzyme-catalysed (notably by RuBisCO), rate increases with temperature up to an optimum (faster enzyme kinetics), then falls sharply beyond the optimum as enzymes begin to denature – the same general shape as any enzyme-controlled process.

Ví dụ mẫu · Interpreting a limiting-factor graph

The rate of photosynthesis in a plant was measured across a range of light intensities, at two different atmospheric CO_2 concentrations (temperature held constant):

Light intensity (units)	0	10	20	30	40	50	60
Rate at 0.04% CO_2	0	8	14	18	19	19	19
Rate at 0.4% CO_2	0	8	15	21	27	32	36

(a) Explain why the two curves overlap at low light intensity. (b) Explain why the 0.04% curve plateaus while the 0.4% curve keeps rising. (c) Predict what a further increase in temperature might do to the 0.4% curve's eventual plateau.

(a) At low light intensity (0–20 units), both curves rise together because **light**, not CO_2, is the limiting factor at both CO_2 concentrations – since neither culture has enough light to use the available CO_2 fully, increasing CO_2 concentration makes no difference yet.

(b) Beyond about 20–30 units of light, the 0.04% CO_2 curve plateaus at 19: light is no longer scarce, so CO_2 concentration has become the limiting factor, and no further increase in light can raise the rate. At 0.4% CO_2 (ten times more CO_2 available), CO_2 is not yet limiting at these light intensities, so the rate continues climbing as light intensity increases.

(c) Since the 0.4% curve is still rising at 60 units, light or CO_2 may still be limiting, or the Calvin-cycle enzymes may be approaching their maximum turnover rate. A moderate increase in temperature (below the enzymes' optimum) would likely raise the eventual plateau further,

since RuBisCO and other Calvin-cycle enzymes would catalyse the fixation and reduction steps faster – but too large a temperature increase, beyond the enzymes' optimum, would instead lower the rate as the enzymes begin to denature.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tại một thời điểm, tốc độ quang hợp bị giới hạn bởi **yếu tố nào đang khan hiếm nhất** so với các yếu tố còn lại – đây gọi là **yếu tố giới hạn**. Trên đồ thị, khi một yếu tố (VD cường độ ánh sáng) tăng lên, tốc độ quang hợp tăng theo cho đến khi đạt ngưỡng (plateau) – lúc này một yếu tố KHÁC (VD nồng độ CO_2 hoặc nhiệt độ) đã trở thành yếu tố giới hạn mới, nên tăng thêm yếu tố ban đầu không còn làm tăng tốc độ nữa.

Action spectrum versus absorption spectrum. An **absorption spectrum** shows how strongly a pigment absorbs light of each wavelength: chlorophyll strongly absorbs blue-violet (≈ 430–450 nm) and red (≈ 640–680 nm) light, while reflecting green light (≈ 500–550 nm) – which is why leaves appear green. An **action spectrum** shows the *rate of photosynthesis* produced by light of each wavelength (e.g. measured via the rate of O_2 output). Because photosynthetic rate depends on how much light energy the pigments actually capture, the action spectrum closely parallels the combined absorption spectrum of chlorophylls and accessory pigments (e.g. carotenoids): wavelengths strongly absorbed (blue-violet, red) drive high rates of photosynthesis, while poorly absorbed wavelengths (green) drive comparatively low rates, even where the incident light energy is similar across the spectrum.

VN **GIẢI THÍCH TIẾNG VIỆT**

Phổ hấp thụ (absorption spectrum) cho biết sắc tố hấp thụ mạnh ở bước sóng nào (diệp lục hấp thụ mạnh ánh sáng xanh lam-tím và đỏ, phản xạ ánh sáng lục – vì vậy lá cây có màu xanh lục). **Phổ hoạt động (action spectrum)** cho biết tốc độ quang hợp ở mỗi bước sóng. Vì tốc độ quang hợp phụ thuộc vào lượng ánh sáng thực sự được sắc tố hấp thụ, hai phổ này có hình dạng gần như trùng khớp nhau.

Net (apparent) versus gross photosynthesis; the compensation point. What is actually measured in a typical photosynthesis experiment (e.g. counting oxygen bubbles from a submerged aquatic plant, or recording the change in dissolved oxygen concentration) is the *net* exchange of gas with the surroundings – because the plant is simultaneously photosynthesising (producing O_2, consuming CO_2) and respiring (consuming O_2, producing CO_2) at the same time. **Net (apparent) photosynthesis** is this directly measured rate; **gross photosynthesis** is the true, total rate of photosynthesis, before subtracting the plant's own respiration:

$$\text{Gross photosynthesis} = \text{Net (apparent) photosynthesis} + \text{Respiration rate}$$

Respiration rate can be measured directly by keeping the same organism in darkness, where net gas exchange is due to respiration alone (photosynthesis cannot occur without light). The **light compensation point** is the light intensity at which gross photosynthesis rate exactly equals respiration rate, so net gas exchange is zero: O_2 produced by photosynthesis is entirely reabsorbed by the plant's own respiration, with no net O_2 or CO_2 exchange with the environment detectable at that light intensity.

Ví dụ mẫu · Net and gross photosynthesis, and the compensation point

Net O_2 exchange for an aquatic plant was measured at several light intensities (positive = net O_2 production; negative = net O_2 consumption):

Light intensity (units)	0	5	10	15	20
Net O_2 exchange ($mm^3\ min^{-1}$)	-9	-4	0	6	12

(a) State the respiration rate of the plant. (b) Identify the light compensation point. (c) Calculate the gross photosynthesis rate at a light intensity of 20 units.

(a) At light intensity 0 (complete darkness), no photosynthesis can occur, so the measured net exchange is due entirely to respiration: the plant consumes O_2 at 9 mm^3min^{-1}, so the **respiration rate** $= 9$ mm^3min^{-1}.

(b) The **compensation point** occurs where net exchange $= 0$, i.e. at a light intensity of 10 **units**: at this point O_2 produced by photosynthesis is being consumed by respiration at exactly the same rate, so gross photosynthesis rate equals respiration rate.

(c) Gross photosynthesis $=$ net exchange $+$ respiration $= 12 + 9 = 21$ mm^3min^{-1} at a light intensity of 20 units.

VN **GIẢI THÍCH TIẾNG VIỆT**

Những gì đo được trực tiếp trong thí nghiệm quang hợp (VD đếm bọt khí, đo nồng độ O_2 hoà tan) là **trao đổi khí ròng (net/apparent)**, vì cây vừa quang hợp (tạo O_2) vừa hô hấp (tiêu thụ O_2) cùng lúc. **Quang hợp thực (gross) = quang hợp ròng (net) + tốc độ hô hấp**. Tốc độ hô hấp được đo bằng cách đặt cây trong bóng tối (không có quang hợp). **Điểm bù ánh sáng (compensation point)** là cường độ ánh sáng mà tại đó quang hợp thực đúng bằng tốc độ hô hấp, nên trao đổi khí ròng bằng 0.

Comparing chemiosmosis in mitochondria and chloroplasts. Aerobic respiration and photosynthesis both generate the great majority of their ATP by the same underlying mechanism: an electron transport chain embedded in a membrane pumps H^+ to build a proton gradient, and ATP synthase then uses the flow of H^+ back down this gradient to synthesise ATP (chemiosmosis) – but the two organelles differ in several structural and functional details.

Feature	Mitochondrion (respiration)	Chloroplast (photosynthesis)
Membrane bearing the ETC	Inner mitochondrial membrane	Thylakoid membrane
Source of high-energy electrons	NADH, $FADH_2$ (from glycolysis, the link reaction, and the Krebs cycle)	Chlorophyll, excited by absorbed light energy (at PSII and PSI)
Where H^+ accumulates	Intermembrane space	Thylakoid lumen
Final electron acceptor	O_2 (forming H_2O)	$NADP^+$ (forming NADPH)
Direction of H^+ flow through ATP synthase	Into the matrix	Into the stroma

VN **GIẢI THÍCH TIẾNG VIỆT**

Hô hấp hiếu khí và quang hợp đều dùng chung một cơ chế hoá thẩm thấu: chuỗi chuyền điện tử trên màng bơm H^+ tạo gradien proton, sau đó H^+ chảy qua ATP synthase để tổng hợp ATP. Điểm khác biệt chính: ở ty thể, điện tử đến từ NADH/$FADH_2$, chất nhận điện tử cuối cùng là O_2 (tạo nước), H^+ tích tụ ở khoang gian màng và chảy vào chất nền; ở lục lạp, điện tử đến từ

diệp lục được ánh sáng kích thích, chất nhận điện tử cuối cùng là $NADP^+$ (tạo NADPH), H^+ tích tụ trong xoang thylakoid và chảy vào chất nền (stroma).

3.2 C2 Cells: Chemical and Neural Signalling

3.2.1 C2.1 Chemical Signalling

HL only. *(Nội dung phần này thuộc chương trình mở rộng – HL only.)*

The **endocrine system** is a collection of ductless glands that secrete **hormones** directly into the bloodstream, rather than through a duct (contrast: exocrine glands, such as salivary or sweat glands, secrete their product through a duct). Hormones are chemical messengers that, once released, travel via the blood and are distributed throughout essentially the entire body – but only **target cells**, which possess a complementary receptor for that particular hormone, actually respond, exactly as in any other ligand-receptor signalling system.

Khái niệm cốt lõi

Because hormones circulate throughout the whole body via the blood, specificity of hormonal signalling depends entirely on which cells happen to express the matching receptor – the same hormone can therefore have completely different, tissue-specific effects depending on which receptor-bearing cells it encounters.

Insulin and glucagon: blood glucose regulation. The **islets of Langerhans** in the pancreas contain two hormone-secreting cell types with opposing effects. When blood glucose rises (e.g. after a meal), β **cells** secrete **insulin**, which stimulates liver, muscle, and fat cells to take up glucose from the blood and stimulates the liver to convert glucose into glycogen for storage (glycogenesis) – lowering blood glucose back toward normal. When blood glucose falls (e.g. between meals or during fasting), α **cells** secrete **glucagon**, which stimulates the liver to break down stored glycogen and release glucose into the blood (glycogenolysis) – raising blood glucose back toward normal. Together, insulin and glucagon form a **negative feedback** system that keeps blood glucose oscillating within a narrow range around a stable set point.

Adrenaline (epinephrine): the fight-or-flight response. Secreted by the adrenal medulla in response to stress or perceived danger (via sympathetic nervous system stimulation), adrenaline rapidly increases heart rate and the force of heart contraction, dilates the airways (bronchodilation) to increase oxygen intake, redirects blood flow toward skeletal muscles and away from the digestive system, and stimulates the breakdown of stored glycogen in liver and muscle to rapidly mobilise glucose – collectively preparing the body for immediate, intense physical action.

Thyroxine: metabolic rate. Secreted by the thyroid gland (itself regulated by thyroid-stimulating hormone, TSH, from the pituitary, which is in turn regulated by thyrotropin-releasing hormone, TRH, from the hypothalamus), thyroxine increases the basal metabolic rate of virtually all body cells – increasing oxygen consumption, cellular respiration rate, and heat production. Thyroxine is also essential for normal growth and development, particularly of the nervous system.

Negative feedback control of hormone secretion. Hormone secretion is itself typically regulated by negative feedback: rising thyroxine levels feed back to suppress further TRH and TSH release (the classic hypothalamic-pituitary-target-gland axis), preventing overproduction; blood glucose concentration itself directly feeds back on insulin and glucagon secretion from the pancreatic islets, without requiring a separate regulatory hormone.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hệ nội tiết tiết **hormone** vào máu, hormone di chuyển khắp cơ thể nhưng chỉ tác động lên **tế bào đích** có thụ thể phù hợp. **Insulin** (khi đường huyết tăng) và **glucagon** (khi đường huyết giảm) là cặp hormone đối lập điều hoà đường huyết theo cơ chế **phản hồi âm**. **Adrenaline**

chuẩn bị cơ thể cho phản ứng "chiến đấu hay bỏ chạy" (tăng nhịp tim, giãn phế quản, huy động glucose). **Thyroxine** điều hoà tốc độ trao đổi chất cơ bản, được kiểm soát qua trục dưới đồi – tuyến yên – tuyến giáp theo cơ chế phản hồi âm (thyroxine tăng sẽ ức chế ngược lại TRH và TSH).

Ví dụ mẫu · Blood glucose negative feedback and Type 1 diabetes

A person's fasting blood glucose is 4.8 mmol/L. After a carbohydrate-rich meal it rises to 7.9 mmol/L. (a) Trace the negative feedback loop that returns blood glucose toward 4.8 mmol/L. (b) Predict this person's blood glucose pattern after the same meal if their pancreatic β cells have been destroyed by autoimmune attack (Type 1 diabetes).

(a) Rising blood glucose ($4.8 \rightarrow 7.9$ mmol/L) is detected directly by pancreatic β cells, which respond by secreting **insulin** into the blood. Insulin binds receptors on liver, muscle, and fat cells, stimulating glucose uptake from the blood and glycogen synthesis in the liver. As blood glucose falls back toward 4.8 mmol/L, the stimulus for insulin secretion itself diminishes, so less insulin is released – the falling variable shuts off its own trigger, completing the negative feedback loop and returning glucose to the set point.

(b) Without functional β cells, no insulin can be secreted no matter how high blood glucose rises. The feedback loop is broken at the response step: after the same meal, this person's blood glucose would rise sharply and remain **abnormally elevated**, failing to return to 4.8 mmol/L, because the tissues that depend on insulin signalling to increase glucose uptake never receive that signal.

VN **GIẢI THÍCH TIẾNG VIỆT**

Trong cơ chế phản hồi âm điều hoà đường huyết, chính sự **giảm** của biến số (đường huyết) sau khi có đáp ứng (tiết insulin) sẽ làm tắt luôn tín hiệu kích thích ban đầu – đây là bản chất của phản hồi âm. Ở bệnh nhân đái tháo đường type 1, tế bào β bị phá huỷ nên vòng phản hồi bị "đứt" ngay tại bước đáp ứng (không tiết được insulin), khiến đường huyết tăng cao sau ăn và không tự trở về mức bình thường được.

Comparing nervous and hormonal control. Although both are forms of cell signalling, the two systems differ sharply in speed, duration, specificity, and mechanism.

Feature	Nervous control	Hormonal (endocrine) control
Speed	Very fast (milliseconds) – electrical impulses	Much slower (seconds to hours) – limited by diffusion and blood circulation time
Duration	Brief, short-lived response	Longer-lasting; hormone may persist in blood for minutes to days
Specificity/range	Highly precise – a specific neuron connects to a specific target cell	Broadcast throughout the whole body via blood, but effective only on cells bearing the matching receptor – can affect many different tissues at once
Mechanism	Electrical signal (action potential) along a neuron, plus a brief chemical step (neurotransmitter) at synapses	Entirely chemical – a hormone secreted into and carried by the blood

VN **GIẢI THÍCH TIẾNG VIỆT**

So sánh điều hoà thần kinh và điều hoà nội tiết: thần kinh **nhanh** (mili giây, dẫn truyền điện), **ngắn**, tác động **chính xác** lên một tế bào đích cụ thể qua synap; nội tiết **chậm** (giây đến giờ, qua máu), **kéo dài** hơn, và tác động **lan rộng** tới mọi tế bào có thụ thể phù hợp trên khắp cơ thể. Cơ chế thần kinh chủ yếu là điện học (điện thế hoạt động) kèm một bước hoá học ngắn tại synap; cơ chế nội tiết hoàn toàn là hoá học.

Mechanisms of hormone action: lipid-soluble versus water-soluble hormones. Hormones fall into two broad classes according to their solubility, which determines both where their receptor is located and how quickly and how long their effect lasts.

- **Steroid hormones** (e.g. cortisol, oestrogen, testosterone), derived from cholesterol, are lipid-soluble and can diffuse directly across the phospholipid bilayer of the plasma membrane. They bind **intracellular (often nuclear) receptors**, and the resulting hormone-receptor complex acts directly as a **transcription factor**, binding DNA and altering the transcription of specific target genes. Because this pathway requires new gene transcription and protein synthesis, effects typically develop over hours and can persist for a long time.
- **Peptide/protein hormones** (e.g. insulin, glucagon, adrenaline) are water-soluble and cannot cross the lipid bilayer. They instead bind **cell-surface receptors** embedded in the target cell's plasma membrane, triggering an intracellular **signal transduction** cascade (often involving a second messenger such as cyclic AMP) that rapidly alters the activity of enzymes/proteins already present in the cell – producing effects within seconds to minutes, but typically shorter-lived than steroid hormone effects.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hormone **steroid** (VD cortisol, oestrogen, testosterone) tan trong lipid, khuếch tán trực tiếp qua màng tế bào, gắn vào thụ thể **nội bào**, phức hợp hormone-thụ thể hoạt động như yếu tố phiên mã, làm thay đổi biểu hiện gen – tác dụng chậm nhưng kéo dài. Hormone **peptide/protein** (VD insulin, glucagon, adrenaline) tan trong nước, không qua được màng tế bào, gắn vào thụ thể **bề mặt tế bào**, kích hoạt chuỗi truyền tin nội bào (thường qua chất truyền tin thứ hai như cAMP) làm thay đổi hoạt động của các protein/enzyme đã có sẵn – tác dụng nhanh nhưng thường ngắn hơn.

Signal amplification through a second-messenger cascade. Binding of a single peptide hormone molecule to its cell-surface receptor can trigger a cascade in which each activated protein in turn activates several molecules of the next protein in the sequence – so the number of activated molecules multiplies at every step, allowing a very small number of hormone molecules to produce a large, rapid intracellular response.

Ví dụ mẫu · Amplification through a signalling cascade

A single hormone molecule binds its receptor and activates 1 molecule of enzyme A. Each activated molecule of enzyme A activates 20 molecules of enzyme B; each activated molecule of enzyme B activates 20 molecules of the final target enzyme, which then breaks down substrate molecules. Calculate the total number of target enzyme molecules activated by the binding of a single hormone molecule, and comment on the significance of this result.

Each step multiplies the number of activated molecules by 20:

$$1\,(\text{hormone}) \rightarrow 1\times 20 = 20\,(\text{enzyme A}) \rightarrow 20\times 20 = 400\,(\text{enzyme B}) \rightarrow 400\times 20 = 8{,}000\,(\text{target enzyme})$$

A single hormone-receptor binding event therefore ultimately activates $8{,}000$ molecules of the target enzyme – illustrating how a signal transduction cascade **amplifies** an initial signal by

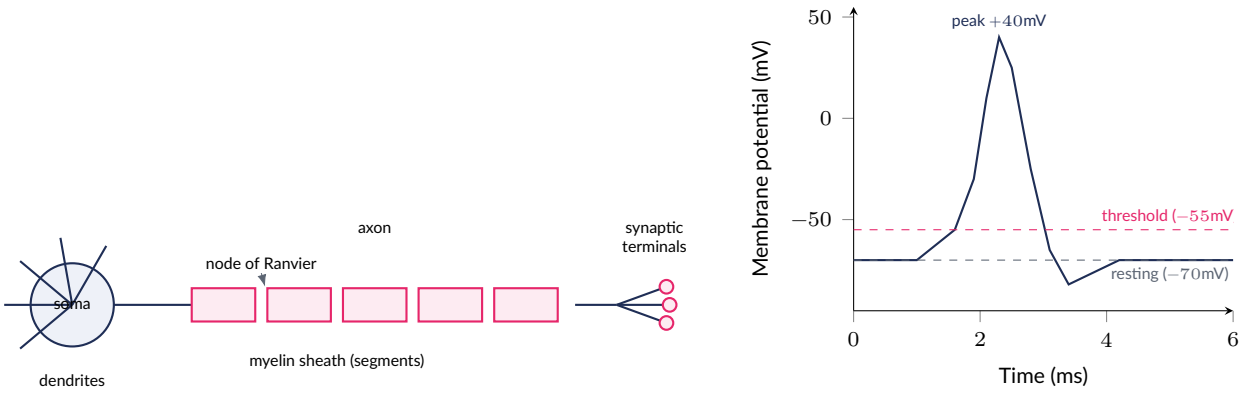
several orders of magnitude at each successive step, allowing a hormone present at extremely low blood concentration to still produce a large, fast, and easily detectable change in a target cell's activity.

VN **GIẢI THÍCH TIẾNG VIỆT**

Khi hormone peptide gắn vào thụ thể bề mặt tế bào, tín hiệu được **khuếch đại (amplification)** qua nhiều bước liên tiếp: mỗi protein được hoạt hoá lại hoạt hoá nhiều phân tử của protein tiếp theo, khiến số lượng phân tử được hoạt hoá tăng theo cấp số nhân qua từng bước. Nhờ vậy, chỉ một lượng rất nhỏ hormone trong máu cũng có thể tạo ra đáp ứng nội bào lớn và nhanh.

3.2.2 C2.2 Neural Signalling

Neuron structure. A neuron (nerve cell) is specialised for rapid, long-distance electrical signalling. **Dendrites** are branching extensions that receive signals from other neurons (or sensory receptors), increasing the surface area available for synaptic contact. The **cell body (soma)** contains the nucleus and most organelles, and integrates the incoming signals arriving from the dendrites. The **axon** is a long, thin extension that conducts the electrical impulse (action potential) away from the cell body toward the axon terminals. In many neurons the axon is wrapped in a **myelin sheath** – an insulating layer formed by Schwann cells (peripheral nervous system) or oligodendrocytes (central nervous system) – interrupted at regular intervals by small gaps, the **nodes of Ranvier**, where the axon membrane is exposed and voltage-gated ion channels are concentrated. At the end of the axon, **synaptic terminals** contain vesicles storing neurotransmitter, released when an impulse arrives.



Left: schematic neuron – dendrites, soma, myelinated axon with nodes of Ranvier, synaptic terminals. Right: an action potential trace – resting potential, threshold, rapid depolarisation, repolarisation, and a brief undershoot before returning to rest.

VN **GIẢI THÍCH TIẾNG VIỆT**

Cấu trúc neuron: **sợi nhánh (dendrite)** nhận tín hiệu; **thân tế bào (soma)** chứa nhân, tích hợp tín hiệu; **sợi trục (axon)** dẫn truyền điện thế hoạt động; **bao myelin** (do tế bào Schwann hoặc tế bào thần kinh đệm ít gai tạo thành) cách điện từng đoạn, xen giữa là **eo Ranvier** (nơi tập trung kênh ion cổng điện thế); **cúc synap** ở đầu tận cùng chứa túi chứa chất dẫn truyền thần kinh.

Resting potential. When not conducting an impulse, a neuron's plasma membrane maintains a stable electrical potential difference of approximately -70 **mV** (inside negative relative to outside) – the **resting potential**. Two mechanisms establish and maintain it: (1) the Na^+/K^+ **pump** (Na^+-K^+-ATPase) actively transports 3 Na^+ ions out of the cell for every 2 K^+ ions pumped in, using ATP,

against both ions' concentration gradients – establishing high extracellular Na^+ and high intracellular K^+; (2) at rest, the membrane is considerably more permeable to K^+ than to Na^+ (more K^+ leak channels are open), so K^+ diffuses out down its gradient more readily than Na^+ diffuses in, leaving the cell interior relatively negative.

Action potential. A stimulus must depolarise the membrane to a critical **threshold** (typically around -55 mV) to trigger an action potential; sub-threshold stimuli produce only small, local, decaying (graded) depolarisations that do not propagate. Once threshold is reached:

- **Depolarisation**: voltage-gated Na^+ channels open, and Na^+ rushes into the cell down its steep electrochemical gradient, rapidly driving the membrane potential from negative toward positive (up to roughly $+40$ mV). The opening of each channel further depolarises the membrane, opening still more Na^+ channels – a positive feedback loop that produces the sharp, rapid rising phase of the spike.
- **Repolarisation**: near the peak, voltage-gated Na^+ channels inactivate while voltage-gated K^+ channels open (with a short delay); K^+ flows out down its gradient, restoring a negative internal potential. A brief **undershoot** (hyperpolarisation) typically occurs as K^+ channels remain open slightly longer than strictly needed, before the resting potential is fully restored.

All-or-nothing principle: once threshold is reached, every action potential in a given neuron reaches the same maximum amplitude, regardless of how far above threshold the triggering stimulus was. Stimulus strength is instead encoded by the **frequency** of action potentials (a stronger or longer-lasting stimulus produces more action potentials per second, not larger ones). **Refractory period**: immediately after an action potential, a brief interval exists during which the membrane cannot fire again (or requires a much stronger stimulus), because Na^+ channels remain transiently inactivated – this ensures the impulse travels in one direction only and sets an upper limit on firing frequency.

(!) Lỗi thường gặp: Do not confuse the all-or-nothing action potential with a **graded (local) potential**. A sub-threshold stimulus produces only a small, local depolarisation whose *size varies continuously* with stimulus strength and which decays with distance without propagating – this is fundamentally different from an action potential, which, once threshold is crossed, always reaches the *same fixed amplitude* and actively propagates the full length of the axon without decrement. A "bigger" stimulus above threshold produces *more frequent*, not larger, action potentials.

VN **GIẢI THÍCH TIẾNG VIỆT**

Đừng nhầm điện thế hoạt động (all-or-nothing) với điện thế cục bộ (graded potential). Kích thích dưới ngưỡng chỉ tạo ra khử cực cục bộ nhỏ, có **biên độ thay đổi liên tục** theo cường độ kích thích và **tắt dần theo khoảng cách**, không lan truyền. Ngược lại, một khi đạt ngưỡng, điện thế hoạt động luôn đạt **cùng một biên độ cố định** và lan truyền trọn vẹn dọc sợi trục – kích thích mạnh hơn chỉ làm tăng **tần số** phát xung, không làm tăng biên độ từng xung.

Absolute versus relative refractory period. The refractory period following an action potential in fact comprises two distinguishable phases. During the **absolute refractory period** (typically around 1–2 ms), the voltage-gated Na^+ channels that opened during the preceding action potential remain transiently inactivated and structurally unable to reopen – no second action potential can be triggered here, no matter how strong the applied stimulus. This is followed by a brief **relative refractory period**, during which enough Na^+ channels have recovered from inactivation that a new action potential is possible again, but only if the stimulus is stronger than the normal threshold stimulus, since the membrane is still hyperpolarised (or not yet fully repolarised) by the continuing outward flow of K^+, so a larger depolarisation is needed to reach threshold. Together, these two phases set an

upper limit on the maximum frequency at which a neuron can generate action potentials, and ensure that an impulse normally propagates in one direction only along an axon, since the membrane region immediately behind a travelling impulse is briefly refractory and cannot be re-excited by the depolarisation passing through it.

VN **GIẢI THÍCH TIẾNG VIỆT**

Giai đoạn trơ (refractory period) thực ra gồm hai pha: **trơ tuyệt đối (absolute refractory period)** (khoảng 1–2 ms) – kênh Na^+ cổng điện thế vẫn đang bất hoạt, hoàn toàn không thể phát xung mới dù kích thích mạnh đến đâu; và **trơ tương đối (relative refractory period)** – một số kênh Na^+ đã hồi phục nên có thể phát xung mới, nhưng cần kích thích **mạnh hơn ngưỡng bình thường** vì màng vẫn đang tăng phân cực do dòng K^+ ra ngoài chưa kết thúc. Hai pha này giới hạn tần số phát xung tối đa của neuron và đảm bảo xung thần kinh chỉ lan truyền theo một chiều.

Ví dụ mẫu · Refractory period and maximum firing frequency

A sensory neuron has an absolute refractory period of 2 ms. (a) Calculate the theoretical maximum firing frequency this neuron could sustain, assuming a new action potential can be triggered the instant the absolute refractory period ends. (b) When a strong, sustained stimulus is actually applied, the neuron is found to fire at a maximum of only 350 action potentials per second. Suggest why this measured maximum is below the theoretical value from (a). (c) A local anaesthetic partially blocks voltage-gated Na^+ channels, extending the effective absolute refractory period to 4 ms. Calculate the new theoretical maximum firing frequency, and state what this predicts about the neuron's ability to encode stimulus intensity while the anaesthetic is present.

(a) If the absolute refractory period is the shortest possible interval between the start of one action potential and the next, the theoretical maximum firing frequency is the reciprocal of this interval, expressed in seconds:

$$f_{\text{max}} = \frac{1}{2\ \text{ms}} = \frac{1}{0.002\ \text{s}} = 500\ \text{impulses s}^{-1}\ (500\ \text{Hz})$$

(b) 500 Hz is a theoretical ceiling based only on the absolute refractory period. In practice, firing at this true maximum would additionally require every new stimulus to reach threshold again the instant the absolute refractory period ends – but the neuron is still in its **relative** refractory period at that instant, when the membrane is hyperpolarised and threshold is temporarily raised, so a larger-than-normal depolarisation is needed before the channels available at that moment can trigger another spike. This relative refractory period adds extra time beyond the strict 2 ms minimum before each successive action potential can actually fire, lowering the sustainable maximum frequency to a value (350 Hz) below the theoretical ceiling.

(c)

$$f_{\text{max}} = \frac{1}{4\ \text{ms}} = \frac{1}{0.004\ \text{s}} = 250\ \text{impulses s}^{-1}\ (250\ \text{Hz})$$

Halving the maximum firing frequency (from 500 to 250 Hz) would compress the range of frequencies available to encode stimulus intensity (recall that, by the all-or-nothing principle, stimulus strength is encoded by firing frequency, not spike amplitude); with a narrower range of possible frequencies, the neuron would be less able to signal fine differences in stimulus intensity through frequency alone, reducing the precision of the sensory information it can transmit.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tần số phát xung tối đa về mặt lý thuyết = 1 / (thời gian trơ tuyệt đối, tính bằng giây). Tuy nhiên tần số tối đa **thực tế đo được** thường thấp hơn giá trị lý thuyết này, vì ngay sau khi trơ tuyệt đối kết thúc, neuron vẫn đang trong pha **trơ tương đối** (cần kích thích mạnh hơn ngưỡng bình thường), nên xung tiếp theo thường xuất hiện muộn hơn một chút so với mức tối thiểu lý thuyết. Nếu thời gian trơ tuyệt đối bị kéo dài (VD do thuốc gây tê chặn kênh Na^+), tần số phát xung tối đa sẽ giảm, làm hẹp phạm vi tần số mà neuron có thể dùng để mã hoá cường độ kích thích.

Propagation and saltatory conduction. Local depolarisation at one point of the axon membrane spreads passively to the adjacent membrane region, bringing it to threshold and triggering a new action potential there, and so on along the axon – a self-propagating wave. In myelinated axons, the myelin sheath electrically insulates the membrane beneath it, and voltage-gated channels are concentrated almost exclusively at the nodes of Ranvier; the action potential therefore appears to "jump" from node to node (**saltatory conduction**) rather than being regenerated continuously at every point, dramatically increasing conduction speed (typically 10–$100\times$ faster than an unmyelinated axon of similar diameter) while also using less metabolic energy (fewer channels need to be reset per unit length).

Ví dụ mẫu · Calculating nerve impulse conduction speed

Two recording electrodes are placed 60 mm apart along a myelinated peripheral motor axon. A stimulus applied at the first electrode produces a recorded impulse at the second electrode 1.2 ms later. (a) Calculate the conduction speed. (b) An unmyelinated axon of similar diameter conducts at approximately 1.5 m/s; calculate how long the same 60 mm impulse would take along this unmyelinated axon, and state the speed ratio between the two.

(a) Convert to consistent units: distance $= 60$ mm $= 0.06$ m; time $= 1.2$ ms $= 0.0012$ s.

$$\text{speed} = \frac{\text{distance}}{\text{time}} = \frac{0.06\ \text{m}}{0.0012\ \text{s}} = 50\ \text{m s}^{-1}$$

(b) Time for the unmyelinated axon: $t = \dfrac{d}{v} = \dfrac{0.06\ \text{m}}{1.5\ \text{m s}^{-1}} = 0.04\ \text{s} = 40\ \text{ms}$. Speed ratio: $\dfrac{50}{1.5} \approx 33$, so the myelinated fibre conducts the impulse roughly 33 times faster – consistent with saltatory conduction between widely spaced nodes of Ranvier, compared with the continuous, point-by-point regeneration required along an unmyelinated membrane.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tốc độ dẫn truyền xung thần kinh = khoảng cách / thời gian (nhớ đổi đơn vị về mét và giây trước khi tính). Sợi trục có bao myelin dẫn truyền theo kiểu **nhảy cóc (saltatory conduction)** – điện thế hoạt động "nhảy" từ eo Ranvier này sang eo Ranvier khác thay vì phải tái tạo liên tục tại mọi điểm – nên tốc độ dẫn truyền nhanh hơn hẳn (có thể gấp hàng chục lần) so với sợi trục không có myelin cùng đường kính, đồng thời tiết kiệm năng lượng hơn.

Synaptic transmission. When an action potential arrives at the presynaptic (axon) terminal, it depolarises the terminal membrane, opening voltage-gated Ca^{2+} channels; the resulting influx of Ca^{2+} triggers synaptic vesicles to fuse with the presynaptic membrane and release their neurotransmitter content into the **synaptic cleft** by exocytosis. The neurotransmitter diffuses rapidly across the narrow cleft (only around 20 nm wide) and binds specific receptor proteins on the postsynaptic membrane, typically opening ligand-gated ion channels. This produces a local change in postsynaptic membrane potential – depolarisation (e.g. Na^+ influx) if excitatory, or hyperpolarisation (e.g. Cl^- influx or K^+ efflux) if inhibitory – and if the combined input from many synapses depolarises

the postsynaptic membrane to threshold, a new action potential is triggered. Finally, the neurotransmitter is removed from the cleft to terminate the signal and reset the synapse – either broken down enzymatically (e.g. acetylcholinesterase breaks down acetylcholine into acetate and choline) or taken back up into the presynaptic neuron (reuptake, e.g. for serotonin and dopamine).

VN **GIẢI THÍCH TIẾNG VIỆT**

Dẫn truyền qua synap: điện thế hoạt động tới cúc synap → mở kênh Ca^{2+} cổng điện thế → Ca^{2+} vào kích thích túi synap giải phóng chất dẫn truyền thần kinh vào khe synap (xuất bào) → chất dẫn truyền khuếch tán qua khe synap, gắn vào thụ thể trên màng sau synap → mở kênh ion, gây khử cực (kích thích) hoặc tăng phân cực (ức chế) → chất dẫn truyền được loại bỏ khỏi khe synap (bị enzyme phân giải hoặc tái hấp thu) để kết thúc tín hiệu, giúp synap sẵn sàng cho xung tiếp theo.

Excitatory and inhibitory neurotransmitters. Whether a neurotransmitter is excitatory or inhibitory depends on which ion channels its receptor opens on the postsynaptic membrane, not on any fixed property of the molecule itself. **Acetylcholine** and **glutamate** typically act as excitatory neurotransmitters (e.g. at the neuromuscular junction and at many excitatory synapses in the brain respectively), opening channels that admit Na^+ and depolarise the postsynaptic membrane. **GABA (gamma-aminobutyric acid)** and **glycine** typically act as inhibitory neurotransmitters, opening channels that admit Cl^- (or allow K^+ efflux), hyperpolarising the postsynaptic membrane and making it harder to reach threshold. The same neurotransmitter can occasionally have different effects at different receptor types, but at any single synapse the excitatory or inhibitory outcome is fixed by the particular receptor present there.

VN **GIẢI THÍCH TIẾNG VIỆT**

Một chất dẫn truyền thần kinh là **kích thích** hay **ức chế** phụ thuộc vào loại kênh ion mà thụ thể của nó mở ra ở màng sau synap, chứ không phải một tính chất cố định của bản thân phân tử. **Acetylcholine** và **glutamate** thường đóng vai trò kích thích (mở kênh Na^+, gây khử cực). **GABA** và **glycine** thường đóng vai trò ức chế (mở kênh Cl^- hoặc cho K^+ thoát ra, gây tăng phân cực, khó đạt ngưỡng hơn).

Summation at synapses. A single postsynaptic potential produced by one synapse is often too small, on its own, to bring the postsynaptic membrane to threshold. Two forms of **summation** allow multiple smaller signals to combine and reach threshold:

- **Spatial summation**: postsynaptic potentials arriving *simultaneously* from several different presynaptic neurons (at different synapses on the same postsynaptic cell) combine additively, since their individual depolarisations overlap in time and location on the postsynaptic membrane.
- **Temporal summation**: postsynaptic potentials arriving in *rapid succession* from the *same* presynaptic neuron combine additively, because each new potential arrives before the previous one has fully decayed.

Both excitatory and inhibitory postsynaptic potentials can summate; whether a postsynaptic neuron reaches threshold and fires depends on the net balance of all excitatory and inhibitory inputs it receives at a given moment, integrated over both space and time.

VN **GIẢI THÍCH TIẾNG VIỆT**

Cộng gộp không gian (spatial summation): nhiều tín hiệu sau synap đến **đồng thời** từ nhiều neuron trước synap khác nhau, cộng dồn lại với nhau. **Cộng gộp thời gian (temporal summation)**: nhiều tín hiệu đến **liên tiếp nhanh** từ cùng một neuron trước synap, cộng dồn trước khi tín hiệu trước kịp tắt hẳn. Neuron sau synap có đạt ngưỡng và phát xung hay không phụ thuộc vào tổng cân bằng giữa các tín hiệu kích thích và ức chế nhận được, tích hợp theo cả không gian và thời gian.

3.3 C3 Organisms: Integration and Defense

3.3.1 C3.1 Integration of Body Systems

No organ system in the body works alone. Maintaining a stable internal environment – **homeostasis** – and mounting an effective, coordinated response to changing conditions requires continuous cooperation between the nervous, endocrine, circulatory, respiratory, and other systems, each contributing sensing and/or effector capability to a shared physiological goal.

Khái niệm cốt lõi

Every homeostatic control system, regardless of the specific variable being regulated, follows the same three-part logic: a **receptor** detects a stimulus (a deviation of some internal variable from its normal range); a **coordinator (control centre)** processes this information and compares it against a reference value (**set point**); and an **effector** (a muscle or gland) carries out a response. When the response **opposes** (counteracts) the original deviation, the loop is a **negative feedback** loop, and this is the principal mechanism of homeostasis.

VN **GIẢI THÍCH TIẾNG VIỆT**

Mọi hệ thống kiểm soát cân bằng nội môi đều gồm ba thành phần: **thụ thể (receptor)** phát hiện sự thay đổi; **trung tâm điều phối (coordinator)** xử lý thông tin, so sánh với một **điểm chuẩn (set point)**; và **cơ quan đáp ứng (effector)** (cơ hoặc tuyến) thực hiện phản ứng. Nếu đáp ứng **ngược chiều** với sự lệch ban đầu, đó là **phản hồi âm (negative feedback)** – cơ chế chủ đạo của cân bằng nội môi.

Coordinated response during exercise: an integration example. During vigorous exercise, working skeletal muscles sharply increase their demand for O_2 and glucose and produce far more CO_2 and metabolic heat. No single organ system can meet this demand alone:

- The **nervous system** responds fastest: the autonomic (sympathetic) nervous system rapidly increases heart rate and breathing rate, driven both by direct signals from the motor cortex as movement begins and by chemoreceptors detecting rising blood CO_2 (falling pH) and signalling the cardiovascular and respiratory control centres in the medulla.
- The **endocrine system** reinforces and sustains the response: adrenaline, released from the adrenal medulla, further raises heart rate and mobilises stored glucose, with effects that persist longer than the initial nervous signal.
- The **circulatory system** redistributes blood flow – vasodilation increases blood flow to working muscle, while vasoconstriction reduces flow to the gut – increasing delivery of O_2 and glucose to muscle and increasing removal of CO_2 and heat.
- The **respiratory system** increases the rate and depth of ventilation, increasing O_2 uptake and CO_2 removal at the lungs to match the muscle's raised metabolic demand.

The nervous system provides the fast, immediate onset of this coordinated response; the endocrine system reinforces and sustains it. Without this integration, a rise in CO_2/fall in pH, a drop in blood glucose, or a dangerous rise in core temperature would quickly follow, illustrating why homeostatic regulation of exercise depends on multiple systems acting together rather than any single system alone.

VN **GIẢI THÍCH TIẾNG VIỆT**

Khi vận động mạnh, cơ xương cần nhiều O_2 và glucose hơn, tạo ra nhiều CO_2 và nhiệt hơn – cơ thể phải phối hợp **đồng thời** nhiều hệ cơ quan: hệ **thần kinh** (tăng nhanh nhịp tim, nhịp thở qua thụ thể hoá học phát hiện CO_2/pH máu), hệ **nội tiết** (adrenaline duy trì đáp ứng lâu hơn), hệ **tuần hoàn** (phân phối lại lưu lượng máu tới cơ đang hoạt động), và hệ **hô hấp** (tăng thông khí). Hệ thần kinh phản ứng nhanh, tức thời; hệ nội tiết củng cố và duy trì đáp ứng lâu dài hơn.

Positive feedback: a contrast. Not every physiological loop maintains stability. In **positive feedback**, the response **reinforces** (amplifies) the original stimulus rather than opposing it, driving a process rapidly and decisively toward a definite endpoint rather than toward a steady set point.

- **Childbirth**: pressure of the baby's head against the cervix stimulates stretch receptors, triggering release of **oxytocin**, which strengthens uterine contractions – pushing the baby further against the cervix, stretching it further, releasing still more oxytocin. This escalating cycle continues until the baby is delivered, at which point the stimulus (cervical stretch) disappears and the loop ends – not by returning to the starting condition, but by completing the process.
- **Blood clotting**: when a blood vessel is damaged, a small number of activated clotting factor molecules catalyse the activation of many more clotting factor molecules, which activate still more – each step reinforcing and amplifying clot formation, rapidly driving the process to completion (a stable clot) rather than to a steady state. The cascade is confined to the injury site and eventually halted by dilution of activated factors in flowing blood, circulating anticoagulant proteins, and the disappearance of the original stimulus once the wound is sealed.

Ví dụ mẫu · Classifying feedback loops

For each scenario, state whether it is an example of negative or positive feedback, and justify your answer: (i) a fall in core body temperature triggers shivering, which generates heat and raises body temperature back toward 37°C; (ii) during labour, increasing cervical stretch causes more oxytocin release, which causes stronger contractions and even more cervical stretch; (iii) a rise in blood pressure is detected by baroreceptors, triggering vasodilation that lowers blood pressure back toward normal.

(i) Negative feedback. The response (heat generation via shivering) **opposes** the original stimulus (falling temperature), driving the variable back toward its set point (37°C).

(ii) Positive feedback. The response (stronger contractions, more oxytocin) **reinforces** the original stimulus (cervical stretch) rather than reducing it, escalating the process toward a distinct endpoint (birth) rather than toward stability.

(iii) Negative feedback. The response (vasodilation, lowering blood pressure) **opposes** the original stimulus (rising blood pressure), returning the variable toward its normal set point.

VN **GIẢI THÍCH TIẾNG VIỆT**

Phản hồi dương (positive feedback) **khuếch đại** kích thích ban đầu thay vì đối kháng lại nó, đẩy quá trình đi nhanh đến một điểm kết thúc rõ ràng (VD sinh nở, đông máu) thay vì duy trì trạng thái ổn định. Khi phân loại một vòng phản hồi, hãy kiểm tra xem đáp ứng có **đối kháng** với kích thích (phản hồi âm) hay **củng cố/khuếch đại** kích thích đó (phản hồi dương) – không dựa vào việc kết quả "tốt" hay "xấu".

3.3.2 C3.2 Defense Against Disease

The body defends itself against pathogens (disease-causing organisms) using a layered system: physical/chemical barriers, a fast but non-specific innate response, and a slower but highly specific adaptive response.

Primary non-specific barriers. The **skin** forms a tough physical barrier of tightly packed, keratinised epidermal cells, and is also chemically hostile to microorganisms (sebum and sweat lower skin surface pH and contain antimicrobial compounds, e.g. lysozyme). **Mucous membranes** line body tracts that open to the external environment (respiratory, digestive, urogenital tracts); they secrete **mucus**, which traps pathogens and particles, and in the respiratory tract are equipped with cilia that continuously sweep trapped material away (the mucociliary escalator). Other chemical barriers include the strongly acidic stomach environment, which kills many ingested pathogens, and lysozyme

in tears and saliva.

Innate (non-specific) immune response. The innate response acts the same way regardless of which particular pathogen is involved, requires no prior exposure, and acts quickly.

- **Phagocytosis**: phagocytic white blood cells (e.g. macrophages, neutrophils) engulf pathogens and cell debris by endocytosis, then destroy the ingested material by fusing the resulting vesicle with lysosomes containing digestive enzymes.
- **Inflammation**: in response to tissue damage or infection, damaged cells and immune cells (e.g. mast cells) release histamine and other signalling molecules, causing local vasodilation (redness, warmth) and increased capillary permeability (allowing fluid, antimicrobial proteins, and phagocytes to move from blood into the affected tissue, producing swelling) – classically producing redness, heat, swelling, and pain, and recruiting phagocytes to the site.
- **Fever**: pathogens or immune signalling molecules (pyrogens) reset the hypothalamic temperature set point higher, raising core body temperature. Elevated temperature inhibits the growth of many pathogens (which often have a narrower optimal temperature range than the host) and enhances some aspects of immune cell activity.

Specific (adaptive) immune response. The adaptive response is slower to begin (days) but highly specific to a particular pathogen, and generates lasting immunological memory.

Antigens are molecules – typically proteins or polysaccharides on a pathogen's surface, or other foreign molecules – that the immune system recognises as non-self, triggering a response specific to that antigen. **Lymphocytes**, white blood cells responsible for the adaptive response, fall into two main classes:

- **B-lymphocytes (B-cells)**, which mature in the bone marrow. Once activated by binding a matching antigen (typically with helper T-cell assistance), a B-cell proliferates and differentiates into **plasma cells**, which secrete large quantities of soluble **antibodies** specific to that antigen – the **humoral (antibody-mediated) response**, effective mainly against extracellular pathogens such as bacteria and toxins, and against viruses before they enter host cells.
- **T-lymphocytes (T-cells)**, which mature in the thymus. **Helper T-cells** recognise antigen presented by antigen-presenting cells and, once activated, secrete cytokines that coordinate and activate both B-cells and cytotoxic T-cells – a central coordinating role in the adaptive response. **Cytotoxic T-cells** recognise antigen displayed on the surface of infected or abnormal (e.g. cancerous) body cells and, once activated, directly destroy that cell – the **cell-mediated response**, effective against intracellular pathogens (viruses) and cancer cells.

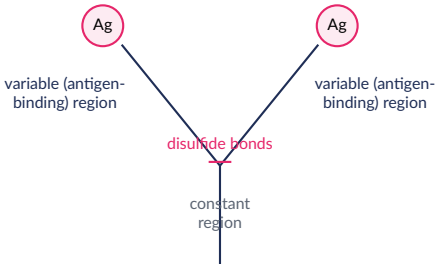
A subset of activated B- and T-cells persists long-term as **memory cells**, without further proliferating unless the same antigen is encountered again. Upon re-exposure, memory cells enable a much faster, larger **secondary immune response** than the original (primary) response – the molecular basis of long-term immunity.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hàng rào bảo vệ đầu tiên (da, niêm mạc) ngăn cản mầm bệnh xâm nhập; đáp ứng **miễn dịch không đặc hiệu (innate)** (thực bào, viêm, sốt) phản ứng nhanh nhưng không phân biệt loại mầm bệnh; đáp ứng **miễn dịch đặc hiệu (adaptive)** chậm hơn nhưng nhắm chính xác vào từng loại kháng nguyên, gồm **tế bào lympho B** (tiết kháng thể – đáp ứng dịch thể) và **tế bào lympho T** (**T hỗ trợ** điều phối đáp ứng miễn dịch; **T độc** tiêu diệt trực tiếp tế bào nhiễm bệnh – đáp ứng qua trung gian tế bào). **Tế bào nhớ (memory cells)** tồn tại lâu dài, giúp đáp ứng lần hai (khi gặp lại cùng kháng nguyên) nhanh và mạnh hơn hẳn lần đầu.

Antibody structure and specificity. An **antibody** (immunoglobulin) is a Y-shaped protein built from four polypeptide chains (two identical heavy chains, two identical light chains) held together by disulfide bonds. Each antibody has two identical **antigen-binding sites** (variable regions) whose precise three-dimensional shape is complementary to one specific antigen – the same logic of molecular

specificity seen in enzyme-substrate and receptor-ligand binding. Antibody binding can neutralise a pathogen directly (e.g. blocking a virus from entering a host cell), mark it for destruction by phagocytes (opsonisation), or cause pathogens to clump together (agglutination), aiding their clearance from the body.



Schematic antibody (immunoglobulin) structure: a Y-shaped protein of two heavy and two light polypeptide chains (held together by disulfide bonds, pink), with two identical variable (antigen-binding) regions – one at the tip of each arm – each complementary in shape to one specific antigen (Ag), and a constant region (stem) shared across antibodies of the same class.

Active versus passive immunity.

Feature	Active immunity	Passive immunity
Source of antibodies	Produced by the individual's own immune system	Transferred from an external source
Examples	Natural infection; vaccination	Maternal antibodies via placenta/breast milk; injected antiserum/antivenom
Onset	Slow (days to weeks – B/T cells must proliferate and differentiate)	Immediate
Duration	Long-lasting (memory cells persist)	Short-lived (weeks to months – antibodies gradually degrade, no memory cells are formed)

Natural versus artificial immunity. Both active and passive immunity can be further classified according to how they are acquired: **natural** immunity arises through ordinary life events, without deliberate medical intervention, while **artificial** immunity results from deliberate medical intervention. Combining both classifications gives four categories: **natural active** immunity (antibodies produced by the individual's own immune system following an actual infection); **artificial active** immunity (antibodies produced by the individual's own immune system following vaccination); **natural passive** immunity (antibodies transferred from another individual by natural physiological means, e.g. across the placenta or in breast milk); and **artificial passive** immunity (antibodies transferred by medical injection, e.g. antivenom or antiserum).

VN **GIẢI THÍCH TIẾNG VIỆT**

Miễn dịch chủ động và bị động còn có thể phân theo cách có được: **tự nhiên** (không qua can thiệp y tế) hoặc **nhân tạo** (qua can thiệp y tế). Kết hợp lại có bốn loại: **chủ động tự nhiên** (kháng thể tự tạo ra sau khi nhiễm bệnh thật); **chủ động nhân tạo** (kháng thể tự tạo ra sau khi tiêm vắc-xin); **bị động tự nhiên** (kháng thể nhận từ người khác qua nhau thai hoặc sữa mẹ); **bị động nhân tạo** (kháng thể được tiêm vào, VD huyết thanh kháng nọc độc/antiserum).

Vaccination. A vaccine introduces a harmless form or component of a pathogen (an attenuated/weakened whole pathogen, a killed pathogen, a purified antigen or subunit, or genetic material such as mRNA encoding an antigen) into the body. This is sufficient to trigger a primary adaptive immune response – antibody production, activation of B- and T-cells – and, critically, the formation

of **memory cells** specific to that antigen, **without** causing the actual disease, since the vaccine component cannot produce a full infection. If the vaccinated individual is later exposed to the real, live pathogen, memory cells enable a rapid, strong secondary response that typically clears the pathogen before symptoms or disease can develop.

VN **GIẢI THÍCH TIẾNG VIỆT**

Vắc-xin đưa vào cơ thể một dạng vô hại của mầm bệnh (đã làm suy yếu, đã chết, hoặc chỉ một thành phần kháng nguyên/mARN) để kích hoạt đáp ứng miễn dịch nguyên phát và hình thành **tế bào nhớ** mà **không** gây bệnh thật. Khi gặp lại mầm bệnh thật sau này, tế bào nhớ giúp cơ thể tạo đáp ứng thứ phát nhanh và mạnh, thường loại trừ mầm bệnh trước khi kịp gây triệu chứng.

Case study: HIV and the immune system. **HIV** (human immunodeficiency virus) specifically infects and progressively destroys **helper T-cells**, which display the CD4 receptor that HIV uses to enter the cell. Because helper T-cells play the central coordinating role in adaptive immunity – activating both B-cells (humoral response) and cytotoxic T-cells (cell-mediated response) – their progressive depletion over the course of untreated HIV infection steadily cripples both arms of the adaptive immune response. The resulting severe immunodeficiency (**AIDS**, acquired immunodeficiency syndrome – the late stage of untreated HIV infection) leaves the individual highly vulnerable to opportunistic infections and cancers that a healthy immune system would normally control or eliminate; these opportunistic conditions, rather than HIV itself, are typically the ultimate cause of death in untreated AIDS.

VN **GIẢI THÍCH TIẾNG VIỆT**

HIV tấn công đặc hiệu **tế bào T hỗ trợ** (qua thụ thể CD4), làm suy giảm dần khả năng phối hợp cả đáp ứng dịch thể (tế bào B) lẫn đáp ứng qua trung gian tế bào (tế bào T độc). Khi số lượng tế bào T hỗ trợ giảm quá thấp (giai đoạn **AIDS**), cơ thể mất khả năng chống lại các nhiễm trùng cơ hội và một số loại ung thư mà hệ miễn dịch khoẻ mạnh vốn có thể kiểm soát được – đây thường là nguyên nhân tử vong thực sự ở bệnh nhân AIDS, chứ không phải bản thân virus HIV.

Ví dụ mẫu · Primary versus secondary immune response

Antibody concentration against antigen X was measured in a person's blood after a first exposure (day 0) and again after a second exposure to the same antigen (introduced at day 60):

Days after 1st exposure	0	5	10	15	20	25	30
Antibody level (units)	0	0	2	8	10	7	4
Days after 2nd exposure	0	2	4	6	8	10	–
Antibody level (units)	0	1	20	60	90	95	–

Compare the two responses and explain the difference in terms of the cells involved. Relate your answer to how vaccination protects against future infection.

The **primary response** (first exposure) shows a long lag (roughly 7–10 days before antibody is detectable), a modest peak (around 10 units near day 20), and a gradual decline. The **secondary response** (second exposure) begins rising almost immediately, reaches a peak roughly **ten times higher** (95 vs. 10 units), and does so in a fraction of the time (within about 10 days rather than 20).

This difference occurs because the first exposure activates B-cells for the first time, requiring several days for clonal selection, proliferation, and differentiation into antibody-secreting plasma cells. A subset of the activated B-cells instead persists as long-lived **memory cells**. On

the second exposure, these memory cells are already present in large numbers and can differentiate into plasma cells almost immediately, without needing to be activated and expanded from scratch – producing a faster, larger, more effective response.

This is precisely the mechanism exploited by **vaccination**: the first (vaccine) exposure deliberately induces a primary response and memory cell formation without causing disease, so that if the real pathogen is encountered later, the body mounts an immediate secondary-style response, typically clearing the pathogen before it can cause illness.

VN **GIẢI THÍCH TIẾNG VIỆT**

Đáp ứng miễn dịch **lần đầu (primary)** có thời gian trễ dài, đỉnh kháng thể thấp, vì tế bào B phải được hoạt hoá, tăng sinh và biệt hoá lần đầu tiên. Đáp ứng **lần hai (secondary)** nhanh hơn nhiều và đạt đỉnh cao hơn hẳn vì đã có sẵn một lượng lớn **tế bào nhớ** từ lần tiếp xúc trước, chỉ cần biệt hoá thành tương bào (plasma cell) ngay lập tức. Đây chính là nguyên lý mà vắc-xin khai thác: tạo ra đáp ứng "lần đầu" an toàn (không gây bệnh) để khi gặp mầm bệnh thật, cơ thể phản ứng theo kiểu "lần hai" – nhanh và mạnh.

Herd immunity. A pathogen's **basic reproduction number (R_0)** is the average number of further individuals that one infected person will go on to infect in a population that is entirely susceptible (nobody immune). If a sufficiently large proportion of the population is immune (through vaccination or prior infection), an infected individual is statistically unlikely to encounter enough susceptible contacts to sustain the same rate of spread, so the effective spread of the pathogen through the population declines even though not every single individual is immune – protecting even those who cannot be vaccinated (e.g. for medical reasons) or in whom vaccination does not induce full immunity. This population-level protection is **herd immunity**, and the minimum proportion of the population that must be immune to achieve it can be estimated as:

$$\text{herd immunity threshold} = 1 - \frac{1}{R_0}$$

Ví dụ mẫu · Calculating the herd immunity threshold

A newly emerging respiratory pathogen is estimated to have a basic reproduction number $R_0 = 3$ (each infected person, in an entirely susceptible population, infects on average 3 further people). Calculate the minimum proportion of the population that must be immune to achieve herd immunity against this pathogen.

$$\text{herd immunity threshold} = 1 - \frac{1}{R_0} = 1 - \frac{1}{3} = 1 - 0.333 = 0.667$$

At least approximately 66.7% of the population would need to be immune (via vaccination or prior infection) to achieve herd immunity against this pathogen. Note that a pathogen with a higher R_0 (more transmissible) requires a higher immune proportion of the population to achieve the same protective effect.

VN **GIẢI THÍCH TIẾNG VIỆT**

Số tái sinh cơ bản (R_0) là số người trung bình mà một người nhiễm bệnh sẽ lây tiếp trong một quần thể hoàn toàn chưa có miễn dịch. **Miễn dịch cộng đồng (herd immunity)** xảy ra khi tỉ lệ đủ lớn dân số có miễn dịch (qua tiêm vắc-xin hoặc từng nhiễm bệnh), khiến mầm bệnh khó lan truyền hơn, gián tiếp bảo vệ cả những người không thể tiêm vắc-xin. Ngưỡng miễn dịch cộng

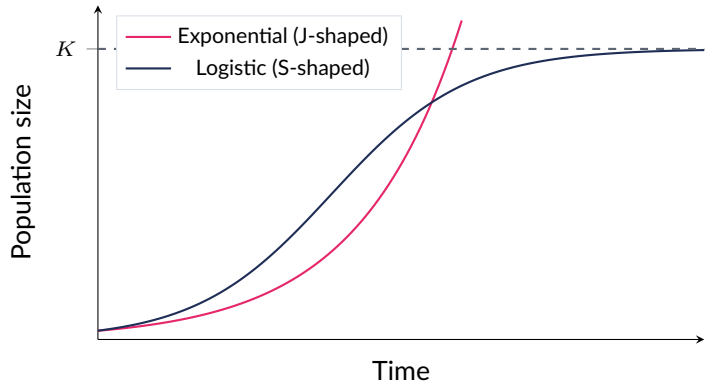
đồng tối thiểu ước tính bằng $1 - \frac{1}{R_0}$ – R_0 càng cao (mầm bệnh càng dễ lây) thì cần tỉ lệ miễn dịch trong dân số càng cao.

3.4 C4 Ecosystems: Populations and Energy Flow

3.4.1 C4.1 Populations and Communities

Population growth models. **Exponential growth** occurs when resources are effectively unlimited relative to population size: the population grows at a rate proportional to its current size, producing an accelerating, J-shaped curve when population size is plotted against time. This pattern is typical of a small population colonising a new, resource-rich environment, or of the early phase of growth in any population. **Logistic growth** occurs when resources (food, space, and other necessities) are limited: growth rate slows as population size approaches the **carrying capacity** (K) of the environment, producing an S-shaped (sigmoid) curve – an initial, near-exponential phase, followed by a decelerating phase as resources become scarcer, finally levelling off at K, where births balance deaths and population size stabilises.

Carrying capacity (K) is the maximum population size that a given environment can sustainably support in the long term, set by the availability of resources such as food, water, and space, and by other constraints such as waste accumulation and disease transmission.



Exponential growth (pink) produces an accelerating, J-shaped curve when resources are effectively unlimited relative to population size. Logistic growth (navy) produces an S-shaped curve that decelerates and levels off at the carrying capacity K (dashed line) as resources become limiting.

Factors affecting population size. **Density-dependent factors** have an effect that intensifies as population density increases – for example, competition for food, space, or other resources intensifies; predation may increase as prey become easier to find; disease and parasites spread more readily in a dense population. These factors are the principal mechanism producing logistic growth and regulating population size around carrying capacity, acting as a form of negative feedback on population size. **Density-independent factors** affect a population similarly regardless of its density – for example, a severe frost, a flood, or a wildfire – and can cause sharp population crashes irrespective of how crowded the population was beforehand.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tăng trưởng theo hàm mũ (exponential) tạo đường cong hình chữ J, xảy ra khi tài nguyên gần như không giới hạn. **Tăng trưởng logistic** tạo đường cong hình chữ S, tốc độ tăng trưởng chậm dần khi quần thể tiến gần **sức chứa môi trường (K)** – mức quần thể tối đa mà môi trường có thể duy trì lâu dài. **Yếu tố phụ thuộc mật độ** (cạnh tranh, dịch bệnh, thú ăn thịt) có tác động mạnh hơn khi mật độ quần thể tăng, là cơ chế chính điều chỉnh quần thể quanh K; **yếu tố**

không phụ thuộc mật độ (thiên tai, thời tiết cực đoan) tác động tương tự bất kể mật độ quần thể.

Predator-prey population cycles. In some predator-prey systems, the two populations show recurring oscillations over time, linked by a time lag: an increase in prey population (abundant food, low predation pressure) supports growth of the predator population somewhat later; the resulting rise in predator numbers increases predation pressure, causing the prey population to decline; the declining prey supply (food shortage) then causes the predator population to decline in turn, with its own time lag; reduced predation pressure then allows the prey population to recover, and the cycle repeats. A classic example, documented from Hudson's Bay Company fur-trapping records, is the roughly 9–10-year cycle of the snowshoe hare (prey) and Canada lynx (predator) populations in North America, in which lynx population peaks consistently lag behind hare population peaks.

Interspecific relationships.

Relationship	Species 1	Species 2	Example
Competition	harmed	harmed	Two barnacle species competing for space on a rocky shore
Predation	benefits	harmed (killed)	Lions preying on wildebeest
Mutualism	benefits	benefits	*Rhizobium* bacteria (fixed nitrogen for the plant) and legume roots (carbohydrates, protected niche for the bacteria)
Parasitism	benefits	harmed (not usually killed)	Tapeworm living in a vertebrate's intestine
Commensalism	benefits	unaffected	Egrets feeding on insects disturbed by grazing cattle

VN **GIẢI THÍCH TIẾNG VIỆT**

Chu kỳ quần thể vật ăn thịt – con mồi (VD linh miêu và thỏ rừng Bắc Mỹ) dao động có **độ trễ thời gian**: con mồi tăng → vật ăn thịt tăng theo (trễ) → áp lực săn mồi tăng làm con mồi giảm → vật ăn thịt giảm theo (trễ) → con mồi phục hồi, chu kỳ lặp lại. Năm kiểu quan hệ khác loài: **cạnh tranh** (cả hai bị hại), **quan hệ vật ăn thịt – con mồi** (một bên lợi, một bên bị hại/chết), **cộng sinh/hỗ sinh (mutualism)** (cả hai cùng lợi), **kí sinh (parasitism)** (một bên lợi, một bên bị hại nhưng thường không chết), **hội sinh (commensalism)** (một bên lợi, bên kia không ảnh hưởng).

Estimating population size. Quadrat sampling, used for plants and other sessile or slow-moving organisms, involves placing a frame of known, fixed area (the quadrat) at multiple *randomly* chosen locations within the study area (random placement avoids sampling bias), counting or estimating abundance (or percentage cover) within each quadrat, and using the mean density per quadrat to estimate total population size across the whole study area. A larger number of quadrat samples generally improves the reliability of the estimate.

Mark-release-recapture, used for mobile animal populations, proceeds in two stages: (1) capture a sample of individuals, mark them in a way that does not harm them or alter their behaviour or survival, and release them back into the population, allowing time for them to mix thoroughly back into the wider population; (2) after sufficient time, capture a second sample and record how many individuals in this second sample bear a mark from the first capture.

Lincoln index: $N = \dfrac{n_1 \times n_2}{m_2}$, where N = estimated total population size, n_1 = number marked and released in the first sample, n_2 = total number captured in the second sample, and m_2 = number of marked individuals recaptured in the second sample. This estimate assumes: population size does not change substantially between sampling occasions (negligible births, deaths, immigration, emigration, or a short enough interval that these are negligible); marked individuals redistribute randomly and have the same probability of capture as unmarked individuals; and marks are not lost and remain identifiable throughout the study.

Ví dụ mẫu · Lincoln index mark-release-recapture

Ecologists studying a population of freshwater snails capture, mark, and release 80 individuals. One week later, they capture a second sample of 100 individuals, of which 20 bear a mark from the first capture. (a) Estimate the total population size. (b) State two assumptions this estimate relies on.

(a) Using the Lincoln index with $n_1 = 80$, $n_2 = 100$, $m_2 = 20$:

$$N = \frac{n_1 \times n_2}{m_2} = \frac{80 \times 100}{20} = \frac{8000}{20} = 400$$

The estimated total population size is 400 **snails**.

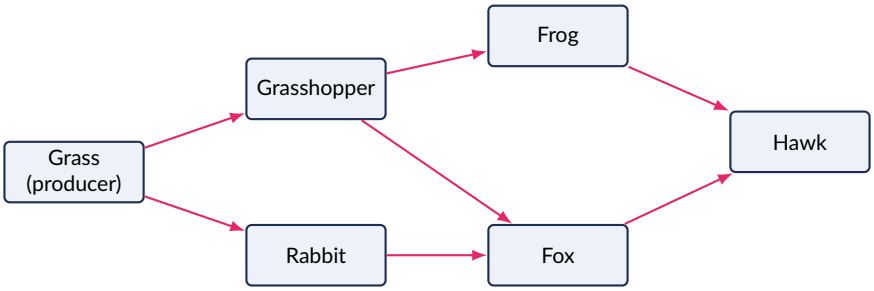
(b) For example: (i) the population must not have changed substantially (through births, deaths, immigration, or emigration) between the two sampling occasions; (ii) marked snails must have mixed randomly back into the population and been just as likely to be recaptured as unmarked snails (the mark itself must not affect survival, behaviour, or detectability).

VN **GIẢI THÍCH TIẾNG VIỆT**

Chỉ số Lincoln (Lincoln index): $N = \dfrac{n_1 \times n_2}{m_2}$, trong đó n_1 = số cá thể được đánh dấu và thả ở lần bắt đầu tiên, n_2 = tổng số cá thể bắt được ở lần hai, m_2 = số cá thể có dấu trong lần bắt thứ hai. Phương pháp này giả định quần thể không đổi đáng kể giữa hai lần bắt, và cá thể đã đánh dấu phân bố ngẫu nhiên trở lại quần thể (không có xu hướng dễ/khó bắt lại hơn cá thể chưa đánh dấu).

3.4.2 C4.2 Transfers of Energy and Matter

A **food chain** shows a single linear sequence of feeding relationships from a producer through successive consumers; a **food web** shows the fuller, interconnected network of feeding relationships within a community, since most organisms feed at more than one point (omnivory), making food webs a more realistic representation of how energy actually flows through an ecosystem. Each feeding level is a **trophic level**: producers (autotrophs that fix their own energy, chiefly by photosynthesis) form trophic level 1; primary consumers (herbivores) form trophic level 2; secondary consumers (carnivores/omnivores eating primary consumers) form trophic level 3; tertiary consumers form trophic level 4; and so on. Decomposers and detritivores break down dead organic matter and waste at every level, recycling matter, but are conventionally shown separately from the main trophic pyramid since they draw energy from all levels at once.



A simple food web. Arrows point from an organism being consumed toward the organism that consumes it, showing the direction of energy flow – most consumers here feed at more than one point, illustrating why a web is more realistic than a single linear food chain.

VN **GIẢI THÍCH TIẾNG VIỆT**

Chuỗi thức ăn là một trình tự ăn – bị ăn tuyến tính duy nhất; **lưới thức ăn** là mạng lưới các mối quan hệ dinh dưỡng đan xen trong một quần xã, phản ánh thực tế chính xác hơn vì hầu hết sinh vật ăn nhiều loại thức ăn khác nhau. **Bậc dinh dưỡng**: sinh vật sản xuất (bậc 1) → sinh vật tiêu thụ bậc 1 (động vật ăn cỏ) → sinh vật tiêu thụ bậc 2 → sinh vật tiêu thụ bậc 3, v.v. Sinh vật phân giải hoạt động ở mọi bậc, tái chế vật chất trở lại hệ sinh thái.

Gross and net productivity. **Gross primary productivity (GPP)** is the total rate at which producers convert light energy into chemical energy stored in organic molecules via photosynthesis, usually expressed per unit area per unit time (e.g. kJ $\text{m}^{-2}\text{yr}^{-1}$). Producers use part of this fixed energy for their own cellular respiration (R); the remainder, stored as new biomass and available to the next trophic level, is **net primary productivity (NPP)**.

$$\text{NPP} = \text{GPP} - R$$

The equivalent relationship applies at higher (consumer) trophic levels: net production (NP) equals the energy actually consumed and assimilated by that trophic level, minus the energy that trophic level loses to its own respiration:

$$\text{NP} = \text{energy consumed/assimilated} - \text{respiratory loss}$$

Ví dụ mẫu · Calculating GPP, NPP, and net production

In a grassland ecosystem, producers fix energy at a gross primary productivity of $18{,}000$ kJ $\text{m}^{-2}\text{yr}^{-1}$. Producer respiration accounts for $6{,}500$ kJ $\text{m}^{-2}\text{yr}^{-1}$. Primary consumers in this ecosystem assimilate $1{,}150$ kJ $\text{m}^{-2}\text{yr}^{-1}$ of energy from feeding on the producers, of which they lose 800 kJ $\text{m}^{-2}\text{yr}^{-1}$ to their own respiration. (a) Calculate NPP. (b) Calculate the net production (NP) of the primary consumer trophic level. (c) What percentage of NPP was assimilated by primary consumers?

(a) $\text{NPP} = \text{GPP} - R = 18{,}000 - 6{,}500 = 11{,}500$ kJ $\text{m}^{-2}\text{yr}^{-1}$.

(b) NP = energy assimilated − respiratory loss $= 1{,}150 - 800 = 350$ kJ $\text{m}^{-2}\text{yr}^{-1}$. This 350 kJ $\text{m}^{-2}\text{yr}^{-1}$ represents the energy actually available to primary consumers' own growth and reproduction (and, in turn, to be passed on to secondary consumers).

(c) $\dfrac{1{,}150}{11{,}500} \times 100\% = 10\%$ – consistent with the typical ecological efficiency of energy transfer between trophic levels (see the 10% rule, below).

VN **GIẢI THÍCH TIẾNG VIỆT**

NPP = GPP − hô hấp của sinh vật sản xuất: GPP là tổng năng lượng cố định được qua quang hợp; NPP là phần còn lại sau khi trừ đi năng lượng sinh vật sản xuất tự sử dụng cho hô hấp – đây chính là phần năng lượng thực sự tích luỹ thành sinh khối mới và có thể chuyển cho bậc dinh dưỡng kế tiếp. Ở các bậc tiêu thụ cao hơn, công thức tương tự: **sản lượng ròng (NP) = năng lượng đồng hoá được − năng lượng mất qua hô hấp**.

(!) Lỗi thường gặp: Do not treat "gross" and "net" productivity as interchangeable, and do not forget *whose* respiration is being subtracted at each level. **GPP** is the total energy fixed by producers, *before* any losses. **NPP** subtracts only the *producers'* own respiratory loss – it is the energy available to primary consumers, not the energy those consumers actually receive. At a consumer trophic level, **NP** similarly subtracts that consumer level's *own* respiratory loss from what *it* assimilated – not from the NPP of the level below. Always identify which trophic level's respiration is being subtracted before calculating.

VN **GIẢI THÍCH TIẾNG VIỆT**

Đừng nhầm lẫn "gross" (tổng) và "net" (ròng): **GPP** là tổng năng lượng cố định được, TRƯỚC khi trừ hao hụt; **NPP** chỉ trừ đi hô hấp của CHÍNH sinh vật sản xuất. Ở bậc tiêu thụ, **NP** trừ đi hô hấp của CHÍNH bậc tiêu thụ đó từ lượng năng lượng bậc đó đã đồng hoá được – không phải trừ từ NPP của bậc dưới. Luôn xác định rõ đang tính hô hấp của bậc dinh dưỡng nào trước khi trừ.

The 10% rule and reasons for energy loss between trophic levels. On average, only around 10% of the energy available at one trophic level is successfully transferred into the biomass of the next trophic level (the true figure varies, commonly cited in the range 5–20%, with 10% used as a typical working estimate). The remaining $\approx 90\%$ is lost at each step for several reasons:

- **Respiratory heat loss**: a large share of the energy an organism assimilates is used to power cellular respiration (movement, active transport, maintaining body temperature, and other life processes) and is ultimately released as metabolic heat rather than stored as biomass.
- **Egestion and non-consumption**: not all available biomass at one trophic level is actually eaten by the next (some prey escape predation, some parts such as bone or wood are inedible); and even of what is eaten, some passes through the digestive tract undigested and is egested as faeces rather than assimilated into the consumer's own tissue.

Because only around 10% of energy is transferred at each step, the total energy available decreases sharply (roughly tenfold) at each successive trophic level – placing a fundamental limit on food chain length, since very few natural food chains extend beyond about four or five trophic levels before the remaining energy becomes too little to support a further viable population.

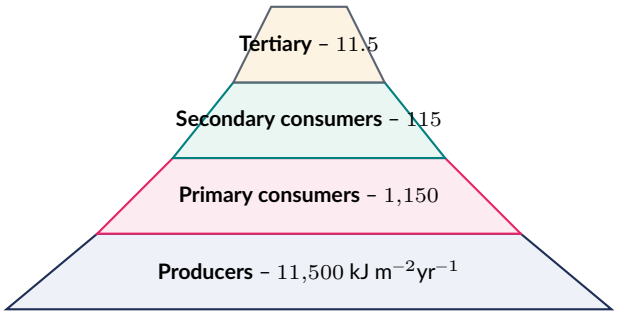
10% rule: energy transferred to trophic level $n+1 \approx 10\%$ of the energy available at trophic level n. Energy is lost at each transfer mainly as **respiratory heat** and through **egestion/incomplete consumption**.

Ví dụ mẫu · Constructing an energy pyramid using the 10% rule

Using the grassland ecosystem's NPP from the previous worked example ($11{,}500$ kJ m^{-2}yr^{-1} available to primary consumers), assume energy transfer efficiency between each successive trophic level is approximately 10%. Calculate the energy available to primary, secondary, and tertiary consumers, and comment on the shape of the resulting energy pyramid.

$$\text{Producers (NPP)} = 11{,}500 \text{ kJ m}^{-2}\text{yr}^{-1}$$
$$\text{Primary consumers} = 11{,}500 \times 0.10 = 1{,}150 \text{ kJ m}^{-2}\text{yr}^{-1}$$
$$\text{Secondary consumers} = 1{,}150 \times 0.10 = 115 \text{ kJ m}^{-2}\text{yr}^{-1}$$
$$\text{Tertiary consumers} = 115 \times 0.10 = 11.5 \text{ kJ m}^{-2}\text{yr}^{-1}$$

Across four trophic levels, available energy falls from $11{,}500$ to just 11.5 kJ m^{-2}yr^{-1} – a thousand-fold decrease overall (0.10^3). The pyramid narrows sharply and continuously at every level, since an energy pyramid, unlike a pyramid of numbers or biomass, can never be inverted: energy transfer efficiency between trophic levels is always well below 100%.



A pyramid of energy across four trophic levels, narrowing sharply at each transfer, consistent with the 10% rule.

Pyramids of energy, biomass, and numbers. A **pyramid of energy** sizes each trophic level by the *rate* of energy flow through it; because transfer efficiency between levels is always well below 100%, an energy pyramid is *always* a smoothly narrowing shape going up – there are no genuine exceptions. A **pyramid of biomass** sizes each level by the total mass of living organic material present at a single point in time (a "standing crop" snapshot, not a flow rate); it usually also narrows upward, but can occasionally appear inverted – for example, in some aquatic ecosystems, phytoplankton (producers) may have very low standing biomass at any instant despite extremely high productivity and turnover, since they are consumed and reproduce very rapidly, so a smaller producer biomass than consumer biomass can be measured at one moment even though energy flow itself is never actually reversed. A **pyramid of numbers** sizes each level by the number of individual organisms; its shape can vary considerably with organism size – for instance, one large tree (producer) may support a huge number of small herbivorous insects, making the "producer" level narrower than the herbivore level in a pyramid of numbers, even though the tree alone still represents far more biomass and energy than all the insects combined.

VN **GIẢI THÍCH TIẾNG VIỆT**

Tháp năng lượng luôn thu hẹp dần lên trên (không có ngoại lệ) vì hiệu suất chuyển hoá năng lượng giữa các bậc luôn thấp hơn 100%. **Tháp sinh khối** thường cũng thu hẹp dần nhưng đôi khi có thể **đảo ngược** tại một thời điểm chụp nhanh (VD thực vật phù du có sinh khối tức thời thấp nhưng tốc độ sinh sản/thay thế rất nhanh). **Tháp số lượng** có hình dạng thay đổi tuỳ kích thước sinh vật (VD một cây lớn có thể "nuôi" rất nhiều côn trùng nhỏ, khiến bậc sản xuất trông "hẹp" hơn bậc tiêu thụ trên tháp số lượng dù sinh khối/năng lượng của cây vẫn lớn hơn nhiều).

Biomagnification of persistent pollutants. Some pollutants – notably fat-soluble, chemically stable (persistent) substances such as certain pesticides and heavy metals – are not readily broken down

or excreted by the organisms that ingest them, and instead accumulate in fatty tissue over an organism's lifetime (**bioaccumulation**). Because a consumer must eat many times its own body mass of prey biomass to grow (since, by the 10% rule, only a small fraction of the prey's biomass/energy is converted into consumer biomass), nearly all of the persistent pollutant present in that large mass of prey is retained and concentrated into the much smaller mass of consumer tissue. Repeating this at each successive trophic level causes the concentration of the pollutant (measured per unit body mass) to increase sharply up the food chain – **biomagnification** – even though the total quantity of available energy is simultaneously decreasing at each level. Top predators, at the end of long food chains, can therefore accumulate concentrations many thousands of times higher than those in the surrounding environment or in producers, sometimes reaching harmful levels even when environmental concentrations alone appear negligible.

Ví dụ mẫu · Calculating a biomagnification factor

The concentration of a persistent, fat-soluble pesticide was measured in the tissues of organisms at each trophic level of an aquatic food chain:

Trophic level	Pesticide concentration (ppm, wet tissue mass)
Producers (phytoplankton)	0.002
Primary consumers (small fish)	0.02
Secondary consumers (medium fish)	0.25
Tertiary consumers (fish-eating birds)	4.0

(a) Calculate the overall biomagnification factor from producers to tertiary consumers. (b) Explain why concentration increases up the food chain even though the 10% rule means less energy is available at each successive trophic level.

(a)

$$\text{biomagnification factor} = \frac{4.0}{0.002} = 2000$$

The pesticide is roughly $2{,}000$ **times** more concentrated in the tissues of the tertiary consumers than in the producers.

(b) These two trends are not contradictory because they describe different quantities. Energy is lost at each trophic transfer (mainly as respiratory heat and through egestion), so the *total* energy/biomass available shrinks roughly tenfold at each level (the 10% rule). The pesticide, however, is fat-soluble and resistant to breakdown or excretion, so it is retained almost entirely rather than lost; each consumer must eat a large mass of prey (containing a large total quantity of pesticide) to obtain enough energy to grow, and nearly all of that ingested pesticide accumulates in the consumer's own much smaller body mass. The pollutant's concentration *per unit body mass* therefore rises at each level even as the total energy available keeps falling.

GIẢI THÍCH TIẾNG VIỆT

VN Một số chất ô nhiễm bền, tan trong lipid (VD một số thuốc trừ sâu, kim loại nặng) không bị phân giải/đào thải dễ dàng mà tích luỹ dần trong mô mỡ của sinh vật (**tích luỹ sinh học – bioaccumulation**). Vì mỗi bậc tiêu thụ phải ăn một lượng sinh khối con mồi lớn hơn nhiều so với sinh khối cơ thể mình (do quy tắc 10%), gần như toàn bộ chất ô nhiễm có trong lượng con mồi đó bị giữ lại và cô đặc vào khối lượng nhỏ hơn của bậc tiêu thụ – gọi là **khuếch đại sinh học (biomagnification)**. Do đó nồng độ chất ô nhiễm (tính trên một đơn vị khối lượng cơ thể) tăng dần lên các bậc dinh dưỡng cao hơn, dù tổng năng lượng sẵn có lại giảm dần theo quy tắc 10% – hai xu hướng này không mâu thuẫn vì chúng mô tả hai đại lượng khác nhau (nồng độ trên một đơn vị khối lượng, so với tổng năng lượng).

Outline of the carbon cycle. Atmospheric/dissolved CO_2 is fixed into organic carbon by photosynthesis; this organic carbon passes through food chains via feeding, and is returned to the atmosphere as CO_2 mainly through **respiration** (by producers, consumers, and decomposers alike) and through **decomposition** of dead organic matter. Some carbon is stored long-term in sinks such as ocean-dissolved bicarbonate, calcium carbonate shells/skeletons and limestone, and (over geological time) fossil fuels; combustion of fossil fuels returns some of this long-stored carbon rapidly to the atmosphere.

Outline of the nitrogen cycle. Atmospheric nitrogen gas (N_2) is largely unavailable to most organisms directly. **Nitrogen-fixing bacteria** (free-living, or symbiotic in legume root nodules) convert N_2 into ammonia/ammonium (**nitrogen fixation**), which plants can use to build amino acids and nucleic acids. **Nitrifying bacteria** convert ammonium into nitrite and then nitrate (**nitrification**), the form most readily absorbed by plant roots. Nitrogen passes through food chains via consumption; **decomposers** break down dead organic matter and waste, releasing ammonium back into the soil (**ammonification**). Under low-oxygen conditions, **denitrifying bacteria** convert soil nitrate back to atmospheric N_2 (**denitrification**), completing the cycle.

VN **GIẢI THÍCH TIẾNG VIỆT**

Chu trình carbon (tóm tắt): CO_2 được cố định qua quang hợp → đi qua chuỗi thức ăn → trở lại khí quyển qua hô hấp và phân giải; một phần được lưu trữ dài hạn (đá vôi, nhiên liệu hoá thạch). **Chu trình nitơ (tóm tắt)**: vi khuẩn cố định đạm chuyển N_2 thành amoni; vi khuẩn nitrat hoá chuyển amoni thành nitrat (dạng cây hấp thụ được); sinh vật phân giải trả amoni về đất khi phân giải xác hữu cơ (amon hoá); vi khuẩn phản nitrat hoá chuyển nitrat trở lại thành N_2 trong điều kiện thiếu oxy, khép kín chu trình.

3.5 Theme C Practice Bank

Bài tập luyện tập

Which statement correctly describes the induced-fit model of enzyme action?

(A) The active site is a rigid shape that never changes on substrate binding

(B) The active site changes shape slightly as the substrate binds, improving the fit and straining substrate bonds

(C) The substrate changes its own shape to match a fixed active site

(D) Induced fit only applies to enzymes that require a cofactor

Lời giải chi tiết

In the induced-fit model, the active site is flexible and moulds around the substrate as it binds, improving the fit and helping to strain bonds within the substrate to lower activation energy. **(B)**.

Bài tập luyện tập

An enzyme assay is carried out at $[S] = 6$ mM (equal to the enzyme's K_m) and again at a saturating substrate concentration. If $V_{\text{max}} = 80$ μmol min^{-1}, calculate the rate at $[S] = K_m$, and explain why this value is diagnostic of K_m.

Lời giải chi tiết

By definition, K_m is the substrate concentration at which reaction rate equals half of V_{max}. At $[S] = K_m$, the rate is therefore $\frac{V_{\text{max}}}{2} = \frac{80}{2} = 40$ μmol min^{-1}. This is diagnostic because it is the defining property of K_m: whichever substrate concentration produces exactly half the maximal rate, on a rate-versus-$[S]$ curve, is by definition equal to K_m.

Bài tập luyện tập

A student adds a fixed amount of a competitive inhibitor to an enzyme reaction. Which of the following would restore the reaction rate closest to the original (uninhibited) V_{max}?

(A) Lowering the temperature

(B) Adding a large excess of substrate

(C) Adding more inhibitor

(D) Raising the pH far above the enzyme's optimum

Lời giải chi tiết

A competitive inhibitor competes with substrate for the same active site; because this competition can be overcome by mass action, adding a large excess of substrate out-competes the inhibitor for binding, allowing the rate to approach the original V_{max} (at a higher apparent K_m). **(B)**.

Bài tập luyện tập

Which of the following correctly pairs a stage of aerobic respiration with its location in the cell?

(A) Glycolysis – mitochondrial matrix

(B) Krebs cycle – cytoplasm

(C) Oxidative phosphorylation – inner mitochondrial membrane

(D) Link reaction – thylakoid membrane

Lời giải chi tiết

Oxidative phosphorylation (electron transport chain and chemiosmosis) occurs at the inner mitochondrial membrane. Glycolysis occurs in the cytoplasm, and both the link reaction and the Krebs cycle occur in the mitochondrial matrix – not the thylakoid membrane, which is a chloroplast structure. **(C)**.

Bài tập luyện tập

A respirometer study of a small insect records O_2 consumption of 250 mm^3 and CO_2 production of 225 mm^3 over one hour, under constant temperature and pressure. Calculate the RQ and identify the most likely respiratory substrate.

Lời giải chi tiết

$$\text{RQ} = \frac{\text{CO}_2 \text{ produced}}{\text{O}_2 \text{ consumed}} = \frac{225}{250} = 0.90$$

An RQ of approximately 0.9 is consistent with **protein** as the primary respiratory substrate.

Bài tập luyện tập

Three organisms are tested in a respirometer, giving the following data:

Organism	O_2 consumed (mm^3/min)	CO_2 produced (mm^3/min)	RQ
P	40	40	?
Q	60	42	?
R	50	45	?

Calculate the RQ for each organism and state the most likely primary respiratory substrate in each case.

Lời giải chi tiết

P: $\frac{40}{40} = 1.0 \rightarrow$ **carbohydrate**. Q: $\frac{42}{60} = 0.70 \rightarrow$ **lipid**. R: $\frac{45}{50} = 0.90 \rightarrow$ **protein**. These values match the typical RQ ranges: carbohydrate ≈ 1.0, lipid ≈ 0.7, protein ≈ 0.8–0.9.

Bài tập luyện tập

After a 400 m sprint, an athlete's leg muscles ache and feel fatigued well before their breathing returns to normal. Explain, in terms of respiratory pathways and ATP yield, why intense sprinting relies heavily on anaerobic respiration, and why this cannot be sustained for long.

Lời giải chi tiết

During an all-out sprint, the demand for ATP in leg muscle rises far faster than the circulatory and respiratory systems can deliver oxygen. Muscle cells therefore rely heavily on **lactic acid fermentation**: pyruvate from glycolysis is reduced directly to lactate, regenerating NAD^+ so glycolysis can continue producing ATP even without oxygen. However, this pathway yields only the 2 ATP produced directly by glycolysis (substrate-level phosphorylation) per glucose, since without oxygen as a final electron acceptor the electron transport chain cannot run and the far larger ATP yield of oxidative phosphorylation (≈ 28 further ATP per glucose) is unavailable. Because roughly ten times less ATP is generated per glucose molecule anaerobically, and because accumulating lactate contributes to muscle fatigue, this pathway can only supply the muscle's enormous ATP demand for a short burst before performance must fall or aerobic respiration must resume (explaining the elevated breathing rate that persists after the sprint, as the body repays its oxygen debt).

Bài tập luyện tập

In the light-dependent reactions of photosynthesis, the splitting of water (photolysis) occurs at:

(A) Photosystem I, releasing CO_2
(B) Photosystem II, releasing O_2
(C) The stroma, releasing ATP
(D) RuBisCO, releasing NADPH

Lời giải chi tiết

Photolysis occurs at Photosystem II, where water is split to replace electrons lost from chlorophyll to the electron transport chain, releasing O_2 as a byproduct and adding H^+ to the thylakoid lumen. **(B)**.

Bài tập luyện tập

List, in order, the three stages of the Calvin cycle, and state which molecule from the light-dependent reactions is used at each stage that requires one.

Lời giải chi tiết

(1) **Carbon fixation**: CO_2 combines with RuBP, catalysed by RuBisCO, forming two molecules of glycerate 3-phosphate (no ATP/NADPH used here). (2) **Reduction**: glycerate 3-phosphate is phosphorylated using **ATP** and then reduced using **NADPH** to form triose phosphate. (3) **Regeneration of RuBP**: most triose phosphate is converted back into RuBP using further **ATP**, allowing the cycle to continue; a fraction of triose phosphate is drawn off to build glucose and other organic molecules.

Bài tập luyện tập

Photosynthetic rate was measured across a range of CO_2 concentrations, at two light intensities:

CO_2 concentration (%)	0.01	0.02	0.04	0.08	0.16	0.32
Rate at low light (units)	3	6	9	10	10	10
Rate at high light (units)	3	7	13	20	24	25

(a) At 0.16% CO_2, what is the limiting factor for the low-light culture? Justify your answer. (b) What is the limiting factor for the high-light culture at 0.01% CO_2?

Lời giải chi tiết

(a) At low light, the rate has already plateaued at 10 units by 0.08% CO_2 and stays at 10 even as CO_2 rises further – so at 0.16%, adding more CO_2 makes no difference, meaning **light intensity** (not CO_2) is now the limiting factor for the low-light culture.

(b) At 0.01% CO_2, both cultures give the same low rate (3 units) regardless of light intensity – showing that at this very low CO_2 level, CO_2 **concentration** is the limiting factor even for the high-light culture, since extra light cannot be used without enough CO_2 substrate for carbon fixation.

Bài tập luyện tập

A pigment extract absorbs strongly at 430 nm and 675 nm, and weakly at 550 nm. Based on the relationship between absorption and action spectra, predict at which of these three wavelengths the rate of photosynthesis (e.g. O_2 output) would be lowest, and explain why.

Lời giải chi tiết

The rate of photosynthesis would be **lowest at 550 nm** (green light). Because the action spectrum closely follows the absorption spectrum of the photosynthetic pigments, wavelengths that are poorly absorbed (here, 550 nm, in the green region, which is largely reflected rather than absorbed by chlorophyll) drive correspondingly low rates of photosynthesis, even though the incident light energy may be similar across all three wavelengths – only absorbed light energy can be used to excite electrons in the photosystems.

Bài tập luyện tập

Which comparison between nervous and hormonal control is correct?

(A) Nervous control is generally slower but more specific than hormonal control

(B) Hormonal control is generally faster but shorter-lasting than nervous control

(C) Nervous control is generally faster and more precisely targeted than hormonal control

(D) Both systems use identical electrical signalling mechanisms

Lời giải chi tiết

Nervous signals travel as fast electrical impulses along specific neuron-to-target connections (fast, highly precise, short-lived), while hormonal signals travel more slowly through the blood to any cell bearing the matching receptor (slower, broader reach, often longer-lasting). **(C)**.

Bài tập luyện tập

Explain, using the hypothalamic-pituitary-thyroid axis, how thyroxine secretion is controlled by negative feedback, and predict what would happen to TSH levels if a person's thyroid gland were surgically removed.

Lời giải chi tiết

The hypothalamus secretes TRH, which stimulates the pituitary to secrete TSH, which stimulates the thyroid gland to secrete thyroxine. Rising thyroxine levels feed back to **suppress** further TRH and TSH release, preventing overproduction – a classic negative feedback axis. If the thyroid gland is removed, no thyroxine can be secreted regardless of TSH level, so the negative feedback signal that would normally suppress TSH/TRH release is permanently absent; consequently, TSH (and TRH) levels would be expected to rise and remain **chronically elevated**, as the hypothalamus and pituitary continue signalling for more thyroxine that can never be produced.

Bài tập luyện tập

Which structure is responsible for saltatory conduction of an action potential along a myelinated axon?

(A) Continuous depolarisation along the entire length of the myelin sheath

(B) Voltage-gated channels concentrated at the nodes of Ranvier, with the action potential "jumping" between them

(C) The cell body integrating multiple dendritic inputs

(D) The synaptic cleft

Lời giải chi tiết

Myelin insulates the axon membrane beneath it, so voltage-gated ion channels are effectively active only at the exposed nodes of Ranvier; the action potential is regenerated at each node in turn, appearing to jump from node to node, which greatly increases conduction speed. **(B)**.

Bài tập luyện tập

Two electrodes are placed 45 mm apart along an unmyelinated axon. A stimulus at the first electrode produces a recorded impulse at the second electrode 30 ms later. Calculate the conduction speed in m/s.

Lời giải chi tiết

Convert units: distance $= 45$ mm $= 0.045$ m; time $= 30$ ms $= 0.030$ s.

$$\text{speed} = \frac{0.045\ \text{m}}{0.030\ \text{s}} = 1.5\ \text{m s}^{-1}$$

This is a typical conduction speed for an unmyelinated axon, much slower than the tens of metres per second typical of myelinated fibres of similar diameter.

Bài tập luyện tập

Place the following events of synaptic transmission in the correct order: (i) neurotransmitter binds postsynaptic receptors; (ii) action potential arrives at the presynaptic terminal; (iii) voltage-gated Ca^{2+} channels open and Ca^{2+} enters the terminal; (iv) synaptic vesicles fuse with the presynaptic membrane, releasing neurotransmitter; (v) neurotransmitter is broken down or taken back up, terminating the signal.

Lời giải chi tiết

Correct order: **(ii)** → **(iii)** → **(iv)** → **(i)** → **(v)**. The action potential arrives and depolarises the presynaptic terminal (ii), opening voltage-gated Ca^{2+} channels (iii); Ca^{2+} influx triggers vesicle fusion and neurotransmitter release into the cleft (iv); neurotransmitter diffuses across and binds postsynaptic receptors, potentially triggering a new signal (i); finally the neurotransmitter is removed to reset the synapse (v).

Bài tập luyện tập

Immediately after firing an action potential, a neuron's membrane briefly cannot fire another action potential even in response to a very strong stimulus. This period is called the:

(A) Resting potential
(B) Threshold period
(C) Refractory period
(D) Graded potential

Lời giải chi tiết

The refractory period follows an action potential; voltage-gated Na^{+} channels remain briefly inactivated, preventing immediate re-firing regardless of stimulus strength. This ensures one-directional propagation and limits maximum firing frequency. **(C)**.

Bài tập luyện tập

During a fever, a patient's body temperature rises from 37°C to 39.5°C and stays elevated for two days before returning to normal. Using the receptor-coordinator-effector model of a control system, outline how the hypothalamus would act to *lower* the temperature back toward 37°C once the fever begins to resolve, and name the effectors involved.

Lời giải chi tiết

Receptor: thermoreceptors (in the hypothalamus and skin) detect that body temperature (39.5°C) is above the (now-restored) set point (37°C). **Coordinator**: the hypothalamus compares the detected temperature to the set point and initiates heat-loss responses. **Effectors**: sweat glands increase sweat secretion (evaporative cooling), and blood vessels in the skin dilate (vasodilation), increasing blood flow near the skin surface and heat radiation to the environment. As body temperature falls back toward 37°C, these responses are reduced – a negative feedback loop.

Bài tập luyện tập

Which of the following is the best example of positive, rather than negative, feedback?

(A) Falling blood glucose stimulating glucagon release, raising blood glucose back to normal

(B) Rising blood CO_2 triggering faster, deeper breathing that lowers blood CO_2 back toward normal

(C) Activated clotting factors catalysing the activation of further clotting factors, rapidly amplifying clot formation

(D) A rise in blood pressure triggering vasodilation that lowers blood pressure back toward normal

Lời giải chi tiết

In (C), each activated clotting factor reinforces and amplifies the process of clot formation rather than opposing it, driving the cascade rapidly to completion – the defining pattern of positive feedback. The other three options all show the response opposing and reversing the original stimulus (negative feedback). **(C)**.

Bài tập luyện tập

Which of the following is an example of the innate (non-specific), rather than the adaptive (specific), immune response?

(A) A plasma cell secreting antibodies specific to a particular viral antigen

(B) A macrophage engulfing and digesting a bacterium by phagocytosis

(C) A memory B-cell rapidly differentiating into plasma cells upon re-exposure to an antigen

(D) A cytotoxic T-cell recognising and destroying a virus-infected cell

Lời giải chi tiết

Phagocytosis by a macrophage does not depend on recognising one specific antigen and occurs the same way regardless of which pathogen is present – the hallmark of the innate response. The other three options all depend on recognition of a specific antigen and involve lymphocytes – the adaptive response. **(B)**.

Bài tập luyện tập

Explain how the structure of an antibody relates to its function, and explain the key difference between the humoral and cell-mediated branches of the adaptive immune response.

Lời giải chi tiết

An antibody is a Y-shaped protein made of two heavy and two light polypeptide chains; its two identical antigen-binding sites have a three-dimensional shape complementary to one specific antigen, allowing highly specific recognition and binding, analogous to enzyme-substrate specificity. This binding can neutralise a pathogen, mark it for phagocytosis (opsonisation), or cause agglutination.

The **humoral response** is mediated by B-cells, which differentiate into plasma cells that secrete soluble antibodies into the blood/lymph, acting mainly against extracellular pathogens and toxins. The **cell-mediated response** is mediated by cytotoxic T-cells, which directly recognise and destroy infected or abnormal body cells displaying the antigen on their own surface, acting mainly against intracellular pathogens (such as viruses) and cancer cells – rather than secreting a diffusible antibody, cell-mediated immunity requires direct cell-to-cell contact and destruction.

Bài tập luyện tập

A patient with untreated HIV infection shows a progressively falling helper T-cell count over several years and eventually develops a severe fungal lung infection that a healthy person's immune system would normally control easily. Explain the connection between the falling helper T-cell count and the patient's vulnerability to this opportunistic infection.

Lời giải chi tiết

HIV specifically infects and destroys helper T-cells (via the CD4 receptor). Helper T-cells play a central coordinating role in adaptive immunity: they activate B-cells to differentiate into antibody-secreting plasma cells (humoral response) and activate cytotoxic T-cells to destroy infected cells (cell-mediated response). As the helper T-cell count falls, the immune system progressively loses its ability to mount effective antibody and cell-mediated responses against new pathogens, since both depend on helper T-cell activation and coordination. This severe immunodeficiency (AIDS) leaves the patient unable to mount an effective defence against pathogens (such as this fungal infection) that a person with a normal helper T-cell count would readily control – explaining why opportunistic infections, rather than HIV itself, are the direct cause of illness at this stage.

Bài tập luyện tập

A population of bacteria is introduced into a flask of fresh nutrient broth. Population size is recorded over time:

Time (h)	0	2	4	6	8	10	12
Population (millions/mL)	1	4	16	45	78	92	95

(a) Which growth model best describes the population between 0 and 4 hours? Justify your answer. (b) Which growth model best describes the whole 12-hour dataset? (c) Estimate the carrying capacity (K) of this culture.

Lời giải chi tiết

(a) Between 0 and 4 hours, the population is roughly quadrupling every 2 hours ($1 \to 4 \to 16$) – a constant multiplicative (proportional) rate of increase, consistent with **exponential growth**, as would be expected while nutrients are still abundant relative to the small population.

(b) Across the full 12 hours, growth is rapid at first but then clearly slows (from 45 to 78 to 92 to 95, smaller absolute increases each time) and appears to be levelling off toward a plateau – consistent with **logistic growth**, as nutrients become limiting and density-dependent factors (e.g. nutrient depletion, waste accumulation) increasingly restrain further growth.

(c) The population is levelling off at approximately 95–100 **million/mL**, so $K \approx 95$–100 million cells/mL is a reasonable estimate of the carrying capacity of this culture.

Bài tập luyện tập

Conservationists mark and release 150 tagged deer in a reserve. Three weeks later, they observe a sample of 120 deer, of which 18 carry a tag. Estimate the total deer population using the Lincoln index.

Lời giải chi tiết

Using $N = \dfrac{n_1 \times n_2}{m_2}$ with $n_1 = 150$, $n_2 = 120$, $m_2 = 18$:

$$N = \frac{150 \times 120}{18} = \frac{18{,}000}{18} = 1{,}000$$

The estimated total population is $1{,}000$ **deer**.

Bài tập luyện tập

A sudden, severe frost kills a large proportion of an insect population regardless of how crowded or sparse the population was beforehand. This is best classified as a:

(A) Density-dependent factor
(B) Density-independent factor
(C) Form of interspecific competition
(D) Form of mutualism

Lời giải chi tiết

Because the frost's effect does not depend on population density – it kills a similar proportion whether the population is crowded or sparse – it is a density-independent factor, unlike competition, predation, or disease, whose impact intensifies with increasing density. **(B)**.

Bài tập luyện tập

Hare (prey) and lynx (predator) populations were monitored over 12 years:

Year	1	2	3	4	5	6	7	8	9	10	11	12
Hare (thousands)	20	55	90	70	30	15	25	60	95	65	25	15
Lynx (hundreds)	10	15	35	55	45	25	12	18	40	60	42	20

Describe the relationship shown by these data, and explain the mechanism that produces it.

Lời giải chi tiết

Both populations rise and fall cyclically, and the lynx (predator) population peaks consistently **after** the hare (prey) population peaks – e.g. the hare peak at year 3 ($90{,}000$) is followed by the lynx peak at year 4 (55 hundred); the hare peak at year 9 ($95{,}000$) is followed by the lynx

peak at year 10 (60 hundred). This lagged relationship is the signature of a predator-prey cycle: as hares increase (abundant food, low predation pressure), the lynx population grows in response, but with a delay (time is needed for increased food supply to translate into more lynx survival/reproduction); the growing lynx population then increases predation pressure, causing the hare population to decline; the declining hare population (reduced food) then causes the lynx population to decline in turn, again with a delay; reduced predation pressure then allows hares to recover, and the cycle repeats.

Bài tập luyện tập

A species of small fish cleans parasites off the skin of a much larger fish; the small fish obtains food (the parasites) while the large fish is relieved of harmful parasites and suffers no cost. This interspecific relationship is best classified as:

(A) Parasitism
(B) Commensalism
(C) Mutualism
(D) Competition

Lời giải chi tiết

Both species benefit here: the small fish gains food, and the large fish benefits from parasite removal – the defining pattern of mutualism, not commensalism (which requires one species to be unaffected) or parasitism (which requires one species to be harmed). **(C)**.

Bài tập luyện tập

In a lake ecosystem, phytoplankton (producers) have a gross primary productivity of $9{,}000$ kJ m^{-2}yr^{-1} and lose $3{,}200$ kJ m^{-2}yr^{-1} to their own respiration. Zooplankton (primary consumers) assimilate 850 kJ m^{-2}yr^{-1} from feeding on the phytoplankton and lose 560 kJ m^{-2}yr^{-1} to their own respiration. (a) Calculate NPP of the phytoplankton. (b) Calculate the net production of the zooplankton trophic level. (c) What percentage of the phytoplankton's NPP was assimilated by the zooplankton?

Lời giải chi tiết

(a) NPP $=$ GPP $- R = 9{,}000 - 3{,}200 = 5{,}800$ kJ m^{-2}yr^{-1}.
(b) NP $= 850 - 560 = 290$ kJ m^{-2}yr^{-1}.
(c) $\dfrac{850}{5{,}800} \times 100\% \approx 14.7\%$ – somewhat higher than the typical 10% estimate, but within the commonly observed 5–20% range for ecological efficiency between trophic levels.

Bài tập luyện tập

A food chain has the following energy values: producers $NPP = 24{,}000$ kJ m^{-2}yr^{-1}; primary consumers $= 2{,}300$ kJ m^{-2}yr^{-1}; secondary consumers $= 210$ kJ m^{-2}yr^{-1}; tertiary consumers $= 19$ kJ m^{-2}yr^{-1}. Calculate the percentage transfer efficiency between each successive pair of trophic levels, and state whether each is consistent with the 10% rule.

Lời giải chi tiết

Producers → primary consumers: $\frac{2{,}300}{24{,}000} \times 100\% \approx 9.6\%$ – consistent with the 10% rule.

Primary → secondary consumers: $\frac{210}{2{,}300} \times 100\% \approx 9.1\%$ – consistent with the 10% rule.

Secondary → tertiary consumers: $\frac{19}{210} \times 100\% \approx 9.0\%$ – consistent with the 10% rule.

All three transfer efficiencies fall close to 10%, illustrating that although the true efficiency at each specific transfer varies somewhat, 10% remains a reasonable typical working estimate across this food chain.

Bài tập luyện tập

In a particular aquatic ecosystem, a pyramid of biomass constructed from a single sampling date shows a smaller standing biomass of phytoplankton (producers) than of the zooplankton (primary consumers) that feed on them, even though the phytoplankton clearly support the zooplankton population. Which of the following best explains this apparent inversion, without contradicting the 10% rule of energy transfer?

(A) The 10% rule does not apply to aquatic ecosystems

(B) Phytoplankton reproduce and are consumed so rapidly that their standing biomass at a single moment can be low even though their productivity (rate of biomass production) is high

(C) Energy flows from zooplankton to phytoplankton in this ecosystem

(D) Zooplankton are actually producers in this ecosystem

Lời giải chi tiết

A pyramid of biomass is a snapshot of standing stock at one moment, not a measure of the flow of energy over time. Fast-reproducing, rapidly turned-over producers such as phytoplankton can have a small standing biomass at any instant while still supplying a high rate of energy/biomass production (high productivity) to support a larger, slower-turnover consumer biomass – this does not contradict the 10% rule, which governs the flow of energy (a pyramid of energy for the same ecosystem would still narrow normally going up). **(B)**.

Bài tập luyện tập

Explain, in outline, the roles of nitrogen-fixing bacteria, nitrifying bacteria, and denitrifying bacteria in the nitrogen cycle.

Lời giải chi tiết

Nitrogen-fixing bacteria (free-living or symbiotic in legume root nodules) convert atmospheric N_2, which most organisms cannot use directly, into ammonia/ammonium – a biologically usable form of nitrogen (nitrogen fixation). **Nitrifying bacteria** in the soil convert ammonium into nitrite and then into nitrate (nitrification), the form of nitrogen most readily absorbed by plant roots. **Denitrifying bacteria**, active mainly under low-oxygen (anaerobic) soil conditions, convert nitrate back into atmospheric N_2 (denitrification), returning nitrogen to the atmosphere and completing the cycle.

Bài tập luyện tập

An enzyme reaction is carried out with substrate present in large excess (non-limiting) throughout, at constant temperature and pH. If the enzyme concentration is doubled while all other conditions are held constant, what happens to the initial reaction rate?

(A) It stays the same
(B) It approximately doubles
(C) It approximately halves
(D) It becomes zero

Lời giải chi tiết

Provided substrate is non-limiting, every additional enzyme molecule adds one more active site available to bind substrate at any instant, so rate is directly proportional to enzyme concentration – doubling enzyme concentration approximately doubles the rate. **(B)**.

Bài tập luyện tập

The rate of a plant enzyme-catalysed reaction was measured at two temperatures, both known to be well below the enzyme's optimum: 8 μmol min^{-1} at 12°C, and 16 μmol min^{-1} at 22°C. Calculate Q_{10} for this interval, and state what this value indicates about the reaction's temperature sensitivity.

Lời giải chi tiết

$$Q_{10} = \frac{\text{rate at } 22^{\circ}\text{C}}{\text{rate at } 12^{\circ}\text{C}} = \frac{16}{8} = 2.0$$

A Q_{10} of 2.0 indicates that the reaction rate approximately doubles for every 10°C rise in temperature over this interval – a typical value for enzyme-catalysed biological reactions well below their optimum temperature, reflecting increased kinetic energy and collision frequency between enzyme and substrate.

Bài tập luyện tập

Which of the following is best classified as a coenzyme, rather than an inorganic cofactor?

(A) Mg^{2+}
(B) Zn^{2+}
(C) NAD^{+}
(D) Fe^{2+}

Lời giải chi tiết

NAD^{+} is an organic coenzyme, derived from the vitamin niacin, that carries electrons and hydrogen atoms between metabolic reactions. Mg^{2+}, Zn^{2+}, and Fe^{2+} are inorganic ions and are classified as cofactors, not coenzymes. **(C)**.

Bài tập luyện tập

Pepsin, a stomach protease with an optimum pH of approximately 1.5–2, is placed in a neutral (pH 7) solution together with its normal substrate. Explain, in terms of enzyme structure, why pepsin's activity would be very low under these conditions, and state whether this effect would be reversible if the solution were promptly returned to pH 1.5–2.

Lời giải chi tiết

At neutral pH, far from pepsin's optimum, the altered H^+ concentration changes the ionisation of acidic and basic side chains in and around the active site, disrupting some of the ionic bonds and hydrogen bonds that maintain the active site's precise three-dimensional shape. Substrate can therefore no longer bind effectively, and catalytic activity falls sharply. Provided exposure to neutral pH is not prolonged or extreme enough to cause full denaturation, this disruption is typically **reversible**: promptly returning the enzyme to its optimum pH restores the normal ionisation state of these side chains, and hence restores the active site's shape and catalytic activity, since the enzyme's primary structure (and its capacity to fold correctly) has not been permanently destroyed.

Bài tập luyện tập

Which of the following correctly identifies a direct product formed per turn of the Krebs cycle (i.e. per acetyl CoA entering the cycle)?

(A) 2 ATP and 4 NADH

(B) 1 ATP, 3 NADH, and 1 $FADH_2$

(C) 4 ATP and no NADH

(D) 2 $FADH_2$ and no CO_2

Lời giải chi tiết

Each turn of the Krebs cycle (per acetyl CoA) yields 1 ATP by substrate-level phosphorylation, 3 NADH, 1 $FADH_2$, and releases 2 molecules of CO_2. **(B)**.

Bài tập luyện tập

Explain why alcoholic fermentation, rather than lactic acid fermentation, is exploited industrially in bread-making and brewing, identifying the specific product of alcoholic fermentation responsible for each use.

Lời giải chi tiết

Alcoholic fermentation (in yeast) produces two industrially useful products from pyruvate: CO_2 gas, released when pyruvate is decarboxylated to acetaldehyde – this is the gas trapped within bread dough that causes it to rise, later escaping (or being baked off) to leave air pockets in the baked loaf; and **ethanol**, formed when acetaldehyde is reduced using electrons from NADH – this is the alcohol produced in brewing and winemaking. Lactic acid fermentation instead reduces pyruvate directly to lactate, without releasing CO_2 or producing ethanol, so it is not useful for leavening dough or producing alcoholic beverages; it is exploited industrially in a different context, such as the production of yoghurt and other fermented dairy products using lactic acid bacteria, where the acid produced (rather than gas or alcohol) curdles and preserves the milk.

Bài tập luyện tập

Germinating seeds of three crop species were tested in a respirometer at constant temperature:

Seed	O_2 consumed (mm^3/hr)	CO_2 produced (mm^3/hr)	RQ
Wheat	50	50	?
Peanut	80	56	?
Soybean	60	51	?

Calculate the RQ for each seed type and suggest the main respiratory substrate mobilised in each case.

Lời giải chi tiết

Wheat: $\frac{50}{50} = 1.0$ – consistent with **carbohydrate** (starch-rich endosperm) as the main substrate. Peanut: $\frac{56}{80} = 0.70$ – consistent with **lipid**, matching the oil-rich reserves typical of peanut seeds. Soybean: $\frac{51}{60} = 0.85$ – an intermediate value, consistent with soybean seeds' unusually high protein content (soybeans store substantial protein alongside oil), suggesting a mixed protein/lipid contribution to respiration rather than a single pure substrate.

Bài tập luyện tập

Net O_2 exchange for a potted plant's shoot was measured at several light intensities (positive = net production; negative = net consumption):

Light intensity (units)	0	5	10	15	20
Net O_2 exchange ($mm^3\ min^{-1}$)	-6	-2	0	7	14

(a) State the respiration rate. (b) Identify the light compensation point. (c) Calculate the gross photosynthesis rate at light intensities of 5 and 20 units.

Lời giải chi tiết

(a) In darkness (light intensity 0), net exchange reflects respiration alone: the plant consumes O_2 at 6 mm^3min^{-1}, so respiration rate $= 6$ mm^3min^{-1}.

(b) Net exchange $= 0$ at a light intensity of 10 **units** – the compensation point, where gross photosynthesis rate equals respiration rate.

(c) Gross photosynthesis $=$ net exchange $+$ respiration. At light intensity 5: $-2 + 6 = 4$ mm^3min^{-1}. At light intensity 20: $14 + 6 = 20$ mm^3min^{-1}.

Bài tập luyện tập

A leaf's absorption spectrum shows strong absorption of blue-violet and red light and weak absorption of green light. Which of the following best describes the expected action spectrum (rate of photosynthesis versus wavelength) for the same leaf?

(A) Uniformly high rate at all wavelengths, since all visible light carries similar energy

(B) Peaks in the blue-violet and red regions, with a trough in the green region, mirroring the absorption spectrum

(C) A peak only in the green region

(D) A single peak in the ultraviolet region

Lời giải chi tiết

Because photosynthetic rate depends on how much light energy the pigments actually absorb, the action spectrum closely follows the combined absorption spectrum of chlorophylls and accessory pigments: wavelengths strongly absorbed (blue-violet, red) drive high rates of photosynthesis, while poorly absorbed wavelengths (green) drive comparatively low rates. **(B)**.

Bài tập luyện tập

The rate of photosynthesis in a plant was measured across a range of temperatures, at fixed light intensity and CO_2 concentration:

Temperature (°C)	10	20	30	40	50
Rate (arbitrary units)	5	14	22	18	4

(a) Estimate the optimum temperature for photosynthesis in this plant. (b) Explain, in terms of enzyme structure, why the rate falls sharply beyond the optimum rather than simply levelling off, as a purely physical limiting factor (such as light intensity) would.

Lời giải chi tiết

(a) The rate rises from $10°$C to a peak of 22 units at $30°$C, then falls sharply – so the optimum temperature is approximately $30°$C.

(b) The Calvin cycle reactions (notably carbon fixation by RuBisCO) are enzyme-catalysed, so rising temperature initially increases rate by raising kinetic energy and collision frequency. Beyond the optimum, however, excess thermal energy disrupts the weak bonds maintaining these enzymes' tertiary structure, progressively denaturing them and destroying active site shape – an effect with no equivalent for a purely physical factor such as light intensity, whose limiting effect simply plateaus once enough light is available, rather than actively damaging the photosynthetic machinery the way excess heat denatures enzymes.

Bài tập luyện tập

Which of the following correctly describes a key difference between steroid and peptide hormone action?

(A) Steroid hormones bind cell-surface receptors; peptide hormones diffuse across the membrane to intracellular receptors

(B) Steroid hormones act as transcription factors after binding intracellular receptors; peptide hormones bind cell-surface receptors and trigger intracellular signal transduction

(C) Both hormone types always produce effects within milliseconds

(D) Peptide hormones always alter gene transcription directly; steroid hormones never affect gene expression

Lời giải chi tiết

Lipid-soluble steroid hormones diffuse across the plasma membrane and bind intracellular receptors, with the resulting complex acting as a transcription factor; water-soluble peptide hormones cannot cross the membrane and instead bind cell-surface receptors, triggering an intracellular signal transduction cascade. **(B)**.

Bài tập luyện tập

Cortisol (a steroid hormone) and adrenaline (a peptide-derived hormone) are both released in response to stress. Explain why adrenaline's effects (e.g. increased heart rate) appear within seconds, while cortisol's effects (e.g. altered metabolic enzyme gene expression) take much longer – often hours – to develop.

Lời giải chi tiết

Adrenaline is water-soluble and cannot cross the plasma membrane, so it binds cell-surface receptors on target cells, immediately triggering an intracellular signal transduction cascade that modifies the activity of enzymes/proteins already present in the cell – since no new protein needs to be synthesised, effects appear within seconds. Cortisol is lipid-soluble and diffuses across the plasma membrane to bind intracellular receptors; the hormone-receptor complex then acts as a transcription factor, altering which genes are transcribed. This pathway additionally requires transcription of the relevant genes into mRNA and translation into new protein before any functional effect (e.g. a changed level of a metabolic enzyme) can appear – a process that inherently takes much longer, typically hours, to produce a measurable effect.

Bài tập luyện tập

A pituitary tumour causes TSH to be secreted at an abnormally high, constant rate, independent of the normal negative feedback signal from thyroxine. Predict what would happen to (i) thyroxine levels and (ii) TRH levels, and explain your reasoning for each.

Lời giải chi tiết

(i) Thyroxine: because the tumour drives TSH secretion continuously regardless of thyroxine level, the thyroid gland is chronically over-stimulated, so thyroxine levels would be expected to become and remain **abnormally elevated**.

(ii) TRH: the hypothalamus's own negative feedback response to circulating thyroxine is not affected by the pituitary tumour – only the pituitary's TSH secretion has become independent of feedback. Since thyroxine levels are chronically high, the hypothalamus would still detect this and appropriately **suppress** TRH release; however, this suppression cannot lower TSH secretion in this case, because the tumour secretes TSH autonomously, illustrating how the feedback loop can be broken at one specific point (the pituitary's response) while an upstream component (the hypothalamus) continues to respond normally to the same signal.

Bài tập luyện tập

Which of the following best explains the role of the Na^+/K^+ pump in establishing a neuron's resting potential?

(A) It allows Na^+ and K^+ to diffuse passively down their concentration gradients

(B) It actively transports 3 Na^+ out and 2 K^+ in per cycle, using ATP, establishing the concentration gradients that the membrane's selective permeability then exploits

(C) It opens only during an action potential to allow Na^+ influx

(D) It actively transports Cl^- ions to hyperpolarise the membrane

Lời giải chi tiết

The Na^+/K^+ pump actively transports 3 Na^+ out of the cell for every 2 K^+ pumped in, using ATP, against both concentration gradients. This establishes high extracellular Na^+ and high intracellular K^+; because the resting membrane is more permeable to K^+ than Na^+, K^+ then diffuses out more readily, leaving the cell interior negative. **(B)**.

Bài tập luyện tập

Electrodes placed 90 mm apart along a myelinated sensory axon record a conduction time of 1.5 ms between them. (a) Calculate the conduction speed in m/s. (b) An unmyelinated axon of similar diameter conducts at 2.0 m/s; calculate how long the same 90 mm impulse would take along this unmyelinated axon, and state the speed ratio between the two axons.

Lời giải chi tiết

(a) Distance $= 90$ mm $= 0.09$ m; time $= 1.5$ ms $= 0.0015$ s.

$$\text{speed} = \frac{0.09\ \text{m}}{0.0015\ \text{s}} = 60\ \text{m s}^{-1}$$

(b) $t = \dfrac{d}{v} = \dfrac{0.09\ \text{m}}{2.0\ \text{m s}^{-1}} = 0.045\ \text{s} = 45\ \text{ms}$. Speed ratio $= \dfrac{60}{2.0} = 30$, so the myelinated axon conducts roughly 30 times faster, consistent with saltatory conduction between widely spaced nodes of Ranvier.

Bài tập luyện tập

A single excitatory postsynaptic potential produced by neuron A is too small, on its own, to bring neuron D to threshold. Explain two distinct ways, using the concepts of summation, in which neuron D could nonetheless be brought to threshold and fire an action potential.

Lời giải chi tiết

Spatial summation: if several other presynaptic neurons (in addition to neuron A) release neurotransmitter onto neuron D at approximately the same time, their individual postsynaptic potentials can combine additively, since they overlap in time and location on the postsynaptic membrane, together reaching threshold.

Temporal summation: if neuron A alone fires repeatedly in rapid succession, each new postsynaptic potential can arrive before the previous one has fully decayed, so successive potentials from the same presynaptic neuron add together, eventually reaching threshold without requiring any other presynaptic neuron to be involved.

Bài tập luyện tập

During breastfeeding, an infant's suckling stimulates the release of oxytocin, which causes milk ejection; continued suckling stimulates further oxytocin release and further milk ejection, until the infant stops feeding. This pattern is best classified as an example of:

(A) Negative feedback
(B) Positive feedback
(C) A density-dependent factor
(D) The innate immune response

Lời giải chi tiết

The response (oxytocin release, milk ejection) reinforces and is reinforced by the original stimulus (suckling) rather than opposing it, escalating the process until the stimulus itself ends (the infant stops feeding) – the defining pattern of positive feedback, directly analogous to the role of oxytocin in childbirth. **(B)**.

Bài tập luyện tập

Using the structure of an antibody – two identical variable (antigen-binding) regions and one constant region – explain how each region contributes to antibody function.

Lời giải chi tiết

The two **variable regions**, at the tip of each arm, have a unique three-dimensional shape complementary to one specific antigen, allowing highly specific recognition and binding – the same logic of molecular specificity seen in enzyme-substrate binding. This specific binding can neutralise a pathogen, mark it for phagocytosis (opsonisation), or cause agglutination. The **constant region** (the stem) has the same structure across all antibodies of a given class, regardless of which antigen the variable regions recognise; this constant region can be recognised by other immune components (e.g. phagocytes, complement proteins), allowing a consistent downstream effector response to be triggered once any antibody of that class has bound its target antigen.

Bài tập luyện tập

A pathogen has an estimated basic reproduction number $R_0 = 6$. Calculate the herd immunity threshold for this pathogen, and state what proportion of the population could remain non-immune while herd immunity is still maintained.

Lời giải chi tiết

$$\text{herd immunity threshold} = 1 - \frac{1}{R_0} = 1 - \frac{1}{6} \approx 0.833$$

Approximately 83.3% of the population would need to be immune. This leaves approximately $100\% - 83.3\% = 16.7\%$ of the population that could remain non-immune while herd immunity is still maintained.

Bài tập luyện tập

A person bitten by a venomous snake is immediately injected with pre-formed antibodies against the snake venom (antivenom), providing rapid but short-lived protection with no memory cells formed. This is best classified as:

(A) Natural active immunity
(B) Artificial active immunity
(C) Natural passive immunity
(D) Artificial passive immunity

Lời giải chi tiết

The antibodies are pre-formed (not produced by the patient's own immune system, so **passive**) and are administered by deliberate medical injection (so **artificial**, not acquired through an ordinary life event). **(D)**.

Bài tập luyện tập

A yeast culture is grown in fresh nutrient broth. Population size is recorded over time:

Time (h)	0	4	8	12	16	20	24
Population ($\times 10^6$ cells/mL)	2	8	30	70	110	125	128

(a) Which growth model best describes the population between 0 and 8 hours? Justify your answer. (b) Which growth model best describes the whole 24-hour dataset? (c) Estimate the carrying capacity (K) of this culture.

Lời giải chi tiết

(a) Between 0 and 8 hours, the population increases by a roughly constant multiplicative factor over each 4-hour interval ($2 \rightarrow 8$, a $4\times$ increase; $8 \rightarrow 30$, roughly a further $3.75\times$ increase) – consistent with **exponential growth**, as expected while nutrients remain abundant relative to the small population.

(b) Across the full 24 hours, growth is rapid at first but clearly decelerates later (from 70 to 110 to 125 to 128, ever smaller absolute increases), levelling off toward a plateau – consistent with **logistic growth**, as nutrients become limiting and density-dependent factors increasingly restrain further growth.

(c) The population is levelling off at approximately 128×10^6 **cells/mL**, so $K \approx 125$–130×10^6 cells/mL is a reasonable estimate.

Bài tập luyện tập

The concentration of mercury, a persistent pollutant, was measured in the tissues of organisms at each trophic level of a marine food chain:

Trophic level	Mercury concentration (ppm)
Producers (algae)	0.01
Primary consumers (small fish)	0.1
Secondary consumers (tuna)	1.2
Tertiary consumers (dolphins)	9.0

Calculate the biomagnification factor (a) from producers to dolphins, and (b) from small fish to tuna. (c) Explain briefly why mercury, specifically, biomagnifies in this way.

Lời giải chi tiết

(a) $\dfrac{9.0}{0.01} = 900$ – mercury is approximately 900 times more concentrated in dolphin tissue than in the producers.

(b) $\dfrac{1.2}{0.1} = 12$ – mercury is approximately 12 times more concentrated in tuna than in the small fish they feed on.

(c) Mercury (particularly in its organic form, methylmercury) is fat-soluble and poorly excreted, so it accumulates in an organism's tissue over its lifetime (bioaccumulation) rather than being broken down or eliminated. Because each consumer must eat a large mass of prey to obtain enough energy to grow (only a small fraction of prey biomass/energy is converted into consumer biomass, per the 10% rule), nearly all of the mercury present in that large prey mass is retained and concentrated into the smaller mass of consumer tissue – so concentration per

unit body mass rises sharply at each successive trophic level.

Theme D: Continuity and Change

Mục tiêu Unit: Giải thích cơ chế nhân đôi ADN bán bảo toàn cùng vai trò của các enzyme (helicase, DNA polymerase, primase, ligase) và bằng chứng thực nghiệm Meselson–Stahl; trình bày đầy đủ quá trình phiên mã, xử lý pre-mRNA (cắt intron, ghép exon), mã di truyền (bộ ba, tính suy biến, tính phổ quát) và dịch mã (ribosome, tRNA, aminoacyl-tRNA synthetase); phân loại các dạng đột biến điểm và đột biến dịch khung, giải thích đột biến hồng cầu hình lưỡi liềm và nguyên lý công nghệ chỉnh sửa gen CRISPR-Cas9. Mô tả chu kỳ tế bào, các pha nguyên phân, cấu trúc nhiễm sắc thể, và ứng dụng trong tăng trưởng/sửa chữa mô cũng như ung thư; trình bày điều hoà biểu hiện gen (operon, yếu tố phiên mã, epigenetics – chỉ dành cho HL) và khái niệm thế nước ($\psi = \psi_s + \psi_p$) cùng hiện tượng trương nước/co nguyên sinh ở tế bào thực vật. Phân biệt sinh sản vô tính và hữu tính, mô tả giảm phân và sự hình thành giao tử, cơ chế điều hoà hormone của chu kỳ kinh nguyệt; vận dụng thành thạo các quy luật di truyền Mendel (lai một tính, lai hai tính, phép lai phân tích, phả hệ, đồng trội, đa alen) và kiểm định khi bình phương (χ^2) để đánh giá độ phù hợp giữa số liệu quan sát và tỉ lệ kỳ vọng; giải thích cơ chế điều hoà ngược âm trong điều nhiệt và điều hoà đường huyết. Vận dụng định luật Hardy–Weinberg để tính tần số alen/kiểu gen của một quần thể, phân biệt các kiểu chọn lọc tự nhiên, phân tích diễn thế sinh thái và độ ổn định của hệ sinh thái, và giải thích cơ chế hiệu ứng nhà kính, chu trình carbon cùng các bằng chứng và hậu quả của biến đổi khí hậu do con người gây ra.

4.1 D1 Molecules: DNA Replication, Protein Synthesis and Mutation

4.1.1 D1.1 DNA Replication

Every time a cell divides, its entire genome must be copied with extremely high fidelity so that each daughter cell receives a complete, accurate set of genetic instructions. **DNA replication** is the process by which a cell produces an exact copy of its DNA before division.

The semi-conservative model

DNA replication is **semi-conservative**: the two strands of the parental double helix separate, and each original (parental) strand serves as a **template** for the synthesis of one new, complementary strand. The result is two daughter double helices, each composed of **one original (old) strand and one newly synthesized strand**. Genetic information is conserved because each new strand is built by strict complementary base pairing (A–T, C–G) against an intact template strand.

Ví dụ mẫu · The Meselson–Stahl experiment: evidence for semi-conservative replication

Before 1958, three competing hypotheses existed for how DNA replicates: **conservative** (the original double helix stays fully intact; an entirely new double helix is made alongside it), **semi-conservative** (each daughter helix is one old strand + one new strand), and **dispersive** (each daughter strand is a patchwork mixture of old and new segments). Meselson and Stahl grew *E. coli* in a medium containing only the heavy nitrogen isotope ^{15}N, so all of the bacteria's DNA became **fully heavy**. They then transferred the bacteria to normal, light-nitrogen (^{14}N) medium and used density-gradient centrifugation to separate DNA by mass after each round of replication.

Model	Predicted bands after 1 replication	Predicted bands after 2 replications
Conservative	Two bands: heavy (untouched original) + light (all-new), no intermediate band	Two bands: heavy ($1/4$ of DNA) + light ($3/4$ of DNA), still no intermediate band
Semi-conservative	One intermediate (hybrid) band only	Two bands: intermediate + light, in roughly equal (1:1) amounts
Dispersive	One intermediate band (indistinguishable from semi-conservative here)	Still only *one* band, but shifted to a density between intermediate and light

Observed result: after one round, all DNA formed a single band of intermediate density; after two rounds, DNA formed two distinct bands (intermediate and light) in roughly equal amounts. This immediately ruled out the **conservative** model (which predicts a heavy band persisting after round 1 — never observed) and the **dispersive** model (which predicts the DNA always stays as a single band, never splitting into two discrete bands — contradicted at round 2). Only the **semi-conservative** model correctly predicts both observations.

VN **GIẢI THÍCH TIẾNG VIỆT**

Mô hình nhân đôi **bán bảo toàn** (semi-conservative): hai mạch của ADN mẹ tách ra, mỗi mạch cũ làm khuôn để tổng hợp một mạch mới bổ sung, tạo ra hai ADN con, mỗi ADN con có một mạch cũ và một mạch mới. Thí nghiệm Meselson–Stahl (dùng đồng vị nitơ nặng ^{15}N rồi chuyển sang môi trường ^{14}N nhẹ, li tâm theo gradient tỉ trọng) là bằng chứng kinh điển: sau 1 lần nhân đôi chỉ có MỘT vạch tỉ trọng trung gian (bác bỏ mô hình bảo toàn — vốn dự đoán còn vạch nặng); sau 2 lần nhân đôi có HAI vạch (trung gian và nhẹ) tỉ lệ gần bằng nhau (bác bỏ mô hình phân tán — vốn dự đoán mãi chỉ có MỘT vạch dịch dần về nhẹ). Kết quả này chỉ phù hợp với mô hình bán bảo toàn.

Ví dụ mẫu · Extending the Meselson–Stahl logic to further replication rounds

Starting from a single fully-heavy (^{15}N/^{15}N) DNA duplex, predict the proportions of hybrid (heavy/light) and fully light DNA duplexes after 4 rounds of semi-conservative replication in ^{14}N medium.

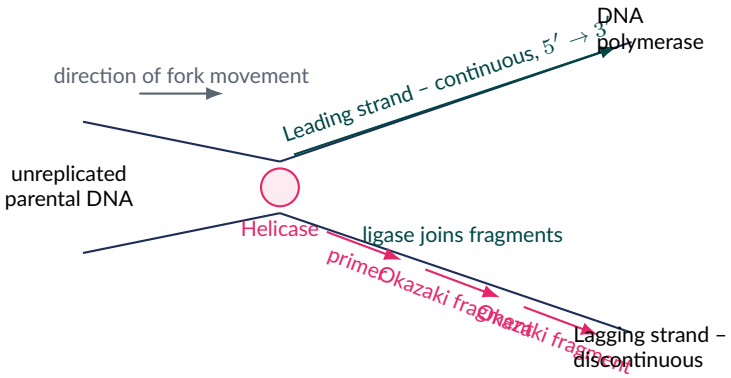
Reasoning. Only the two original heavy strands ever exist; each remains paired, in every subsequent generation, with one newly synthesized light strand, so there are always exactly **2** hybrid duplexes, however many rounds of replication occur. Every other duplex is built entirely from newly synthesized (light) strands.

Step 1 – total duplexes after $n = 4$ rounds: $2^n = 2^4 = 16$.
Step 2 – hybrid duplexes: always 2, regardless of n (as long as $n \geq 1$).
Step 3 – fully light duplexes: $2^n - 2 = 16 - 2 = 14$.

Result: after 4 rounds, $\frac{2}{16} = 12.5\%$ of duplexes are hybrid (intermediate density) and $\frac{14}{16} = 87.5\%$ are fully light – consistent with the semi-conservative model's prediction that the hybrid band never disappears but becomes a progressively smaller fraction of the total DNA as replication continues.

Key enzymes of DNA replication.

Enzyme	Role
Helicase	Unwinds and "unzips" the parental double helix at the **origin of replication**, breaking hydrogen bonds between base pairs to expose two single-stranded templates.
Primase	Synthesizes a short **RNA primer** complementary to the template, providing a free $3'$-OH group that DNA polymerase requires to begin adding nucleotides (DNA polymerase cannot start a new strand from scratch).
DNA polymerase	Synthesizes the new strand by adding free nucleotides complementary to the template strand, always in the $5' \to 3'$ direction; also performs **proofreading**.
DNA ligase	Joins ("seals") adjacent fragments of newly synthesized DNA — most importantly, joins the Okazaki fragments of the lagging strand into one continuous strand.



Replication fork. Helicase unwinds the parental helix at the origin of replication. On the **leading strand**, DNA polymerase synthesizes continuously in the $5' \to 3'$ direction, matching the direction the fork opens. On the **lagging strand**, synthesis must also occur $5' \to 3'$ but runs *away* from the fork, so it proceeds in short **Okazaki fragments**, each started by an RNA primer and later joined together by DNA ligase.

The two new strands are not synthesized in an identical way, because DNA polymerase can only add nucleotides in the $5' \to 3'$ direction and the two template strands are antiparallel.

Leading vs. lagging strand

On the **leading strand**, the template runs $3' \to 5'$ toward the fork, so DNA polymerase can synthesize the new strand **continuously** in the same direction that the fork is opening, needing only a single primer.

On the **lagging strand**, the template runs $5' \to 3'$ toward the fork, so the new strand would have to be synthesized *away* from the fork. DNA polymerase solves this by synthesizing the lagging strand in short, discontinuous stretches called **Okazaki fragments**, each initiated by its own RNA primer (laid down by primase) as more template is exposed; DNA ligase later joins the fragments into one continuous strand. (At SL, it is sufficient to know that the lagging strand is synthesized discontinuously via Okazaki fragments; the mechanistic reason follows directly from the $5' \to 3'$ rule and antiparallel strand structure.)

Origin of replication. Replication begins at a specific DNA sequence called the **origin of replication**, where helicase first binds and opens the double helix, creating one (in bacteria, typically a single origin) or many (in eukaryotic chromosomes, many origins along each chromosome, allowing the much larger eukaryotic genome to be copied within a practical time frame) replication forks.

Proofreading and fidelity

DNA polymerase has a built-in **proofreading** function: after adding each nucleotide, it checks whether the base just added is correctly paired with the template. If an incorrect nucleotide has been inserted, DNA polymerase can remove it and replace it with the correct one before continuing. This proofreading activity is a major reason why DNA replication is remarkably accurate, with an error rate before proofreading of roughly 1 in 10^4–10^5 nucleotides, reduced to roughly 1 in 10^9–10^{10} nucleotides after proofreading and additional post-replication repair mechanisms.

VN **GIẢI THÍCH TIẾNG VIỆT**

Bốn enzyme chính trong nhân đôi ADN: **helicase** (tháo xoắn/mở mạch kép tại điểm khởi đầu tái bản – origin of replication), **primase** (tổng hợp đoạn mồi ARN ngắn để DNA polymerase có điểm bắt đầu), **DNA polymerase** (tổng hợp mạch mới theo chiều $5' \to 3'$, đồng thời có khả năng **sửa lỗi/kiểm tra tính chính xác** – proofreading), và **DNA ligase** (nối liền các đoạn ADN, đặc biệt là nối các đoạn Okazaki của mạch chậm). Do hai mạch khuôn có chiều ngược nhau (đối song song) và enzyme chỉ tổng hợp theo chiều $5' \to 3'$, **mạch nhanh** (leading strand) được tổng hợp liên tục cùng chiều mở của chạc ba tái bản, còn **mạch chậm** (lagging strand) phải tổng hợp thành từng đoạn ngắn gọi là **đoạn Okazaki**, mỗi đoạn cần một đoạn mồi riêng, sau đó được ligase nối lại. Khả năng sửa lỗi của DNA polymerase là lý do chính giúp việc nhân đôi ADN có độ chính xác cực cao.

(!) Lỗi thường gặp: Học sinh thường nhầm lẫn **chức năng** của các enzyme tái bản. Helicase KHÔNG tổng hợp nucleotide – nó chỉ **tháo xoắn** mạch kép. DNA polymerase KHÔNG thể tự khởi đầu một mạch mới từ đầu – nó cần **primase** tạo mồi ARN trước. DNA ligase KHÔNG tổng hợp ADN mới – nó chỉ **nối** các đoạn ADN đã có sẵn (đặc biệt là các đoạn Okazaki) lại với nhau bằng liên kết phosphodiester. Ghi nhớ đúng trình tự: helicase mở mạch → primase đặt mồi → DNA polymerase kéo dài mạch → ligase nối các đoạn.

Telomeres and the end-replication problem

(HL only) DNA polymerase can only extend an existing $3'$-OH end and always requires a primer; this creates a problem at the very end of a linear chromosome's lagging-strand template. When the terminal RNA primer at the extreme end of the template is eventually removed, there is no upstream $3'$-OH available for DNA polymerase to fill the resulting short gap, so a small amount of sequence is lost from that end with every round of replication. **Telomeres** – long stretches of short, repetitive, non-coding DNA sequence found at both ends of linear eukaryotic chromosomes – protect the organism's actual genes from this progressive erosion by acting as an expendable buffer: telomeric sequence is shortened first, so coding genes remain intact for many divisions. Once telomeres become critically short, the cell typically stops dividing (or undergoes programmed cell death), which is one proposed mechanism limiting the number of times a normal somatic cell can divide. **Telomerase**, an enzyme that carries its own internal RNA template and can extend the very end of a chromosome, restores telomere length in germ-line cells, stem cells, and (problematically) in most cancer cells – al-

lowing these cell lineages to keep dividing indefinitely.

VN **GIẢI THÍCH TIẾNG VIỆT**

(Nội dung sau đây chỉ dành cho chương trình HL.) Vì DNA polymerase luôn cần mồi và chỉ kéo dài từ đầu $3'$-OH có sẵn, đầu mút của mạch chậm trên nhiễm sắc thể thẳng không thể được sao chép trọn vẹn – sau khi đoạn mồi ARN cuối cùng bị loại bỏ, không còn đầu $3'$-OH phía trước để lấp đầy khoảng trống, khiến ADN bị ngắn dần sau mỗi lần nhân đôi ("vấn đề đầu mút"). **Telomere** là các đoạn trình tự lặp lại, không mã hoá, nằm ở hai đầu nhiễm sắc thể, đóng vai trò như một vùng đệm bị hao mòn thay cho các gen chức năng. Khi telomere ngắn tới mức tới hạn, tế bào thường ngừng phân chia hoặc chết theo chương trình. Enzyme **telomerase** (mang theo khuôn ARN riêng) có thể kéo dài lại telomere – hoạt động mạnh ở tế bào mầm, tế bào gốc, và (một cách có vấn đề) ở hầu hết tế bào ung thư, giúp các dòng tế bào này phân chia gần như vô hạn.

4.1.2 D1.2 Protein Synthesis

Genetic information stored in DNA is expressed through two linked processes: **transcription** (DNA → mRNA) and **translation** (mRNA → polypeptide). Together, these constitute the central dogma of molecular biology.

Transcription

RNA polymerase binds to a specific DNA sequence called the **promoter**, marking the start of a gene, and unwinds the double helix locally. It then reads one DNA strand — the **template strand** — in the $3' \to 5'$ direction, and synthesizes a complementary, antiparallel strand of **messenger RNA (mRNA)** in the $5' \to 3'$ direction, using free ribonucleotides (A, U, C, G; uracil replaces thymine) and following the same complementary base-pairing rules as DNA (except A pairs with U instead of T). Transcription continues until RNA polymerase reaches a **terminator** sequence, at which point the newly made RNA transcript is released.

Eukaryotic pre-mRNA processing

In eukaryotes, the initial RNA transcript (**pre-mRNA**) contains both coding and non-coding regions. Non-coding segments called **introns** are removed, and the coding segments, called **exons**, are joined together — a process called **splicing**, carried out by a large RNA–protein complex called the spliceosome. Only after splicing (and, in eukaryotes, addition of a protective cap and tail) does the mature mRNA leave the nucleus for translation in the cytoplasm. (Prokaryotes lack a nucleus and generally lack introns, so their mRNA can be translated immediately, often while transcription is still in progress.)

VN **GIẢI THÍCH TIẾNG VIỆT**

Phiên mã (transcription): RNA polymerase bám vào vùng khởi động (promoter), đọc mạch khuôn ADN theo chiều $3' \to 5'$ và tổng hợp mRNA theo chiều $5' \to 3'$ (bổ sung, đối song song, dùng U thay cho T), dừng lại khi gặp vùng kết thúc (terminator). Ở sinh vật nhân thực, pre-mRNA sơ khai còn chứa các đoạn **intron** (không mã hoá) xen giữa các đoạn **exon** (mã hoá); bộ máy **cắt nối** (splicing) sẽ loại bỏ intron và ghép các exon lại với nhau để tạo mRNA trưởng thành trước khi mRNA đi ra tế bào chất để dịch mã.

Alternative splicing increases protein diversity

The spliceosome does not always remove and join exons in exactly the same pattern every time a given gene's pre-mRNA is processed. Through **alternative splicing**, some exons can be included in the final mature mRNA in one instance and skipped (spliced out along with the surrounding introns) in another, or exons can be joined in a different order or combination. This means a *single* gene can give rise to **multiple different mature mRNA transcripts**, and therefore multiple different (but related) protein products, depending on which exons are retained. Alternative splicing is a major reason why the human genome, with roughly only $20{,}000$ protein-coding genes, can nonetheless produce a far larger number of distinct proteins – and it is often regulated differently in different cell types or developmental stages, adding another layer of control beyond simply switching a gene on or off.

VN **GIẢI THÍCH TIẾNG VIỆT**

Cắt nối luân phiên (alternative splicing): bộ máy cắt nối không phải lúc nào cũng loại bỏ/giữ lại đúng những exon giống nhau – một exon có thể được giữ lại trong lần xử lý này nhưng bị cắt bỏ cùng intron xung quanh trong lần khác, hoặc các exon có thể được ghép nối theo trật tự khác nhau. Nhờ vậy, MỘT gen duy nhất có thể tạo ra NHIỀU loại mRNA trưởng thành khác nhau, và do đó nhiều loại protein khác nhau (nhưng có liên quan) – đây là lý do quan trọng giúp bộ gen người (chỉ khoảng 20.000 gen mã hoá protein) vẫn có thể tạo ra số lượng protein lớn hơn nhiều so với số gen, và cơ chế này thường được điều hoà khác nhau tuỳ loại tế bào hoặc giai đoạn phát triển.

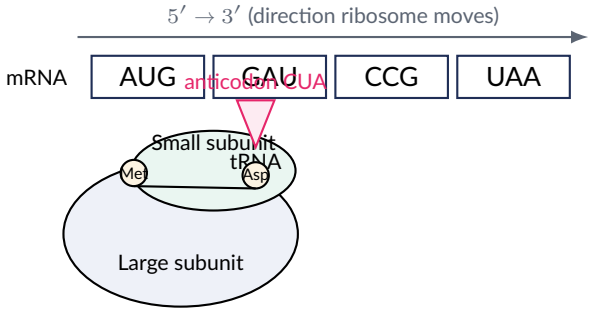
The genetic code

The genetic code translates a sequence of mRNA nucleotides into a sequence of amino acids, read in non-overlapping groups of three bases called **codons**.

- **Triplet code**: each codon consists of exactly 3 nucleotides, and each codon specifies one amino acid (or a stop signal). With 4 possible bases, there are $4^3 = 64$ possible codons.
- **Degeneracy (redundancy)**: since there are 64 codons but only 20 standard amino acids, most amino acids are specified by *more than one* codon (e.g., both GAA and GAG code for glutamic acid). This redundancy means a change in the third codon position often does not change the amino acid produced.
- **Universality**: with only minor exceptions, the same 64 codons specify the same amino acids in virtually every organism on Earth, from bacteria to humans — strong evidence for a single common ancestor of all life.
- **Start and stop signals**: the codon **AUG** both codes for methionine and signals the **start** of translation; the codons **UAA**, **UAG**, and **UGA** are **stop codons** that do not code for any amino acid but instead signal the end of translation.

Codon table excerpt (codons used in the worked examples and practice problems of this chapter).

Codon(s)	Amino acid	Codon(s)	Amino acid
AUG	Methionine (Met) – **START**	GUU, GUC, GUA, GUG	Valine (Val)
UAA, UAG, UGA	**STOP** (no amino acid)	CCU, CCC, CCA, CCG	Proline (Pro)
GAU, GAC	Aspartic acid (Asp)	GCU, GCC, GCA, GCG	Alanine (Ala)
GAA, GAG	Glutamic acid (Glu)	UGG	Tryptophan (Trp)
AGA, AGG	Arginine (Arg)	UCU, UCC, UCA, UCG	Serine (Ser)
UGU, UGC	Cysteine (Cys)	UAU, UAC	Tyrosine (Tyr)
AAA, AAG	Lysine (Lys)		



Translation overview. The ribosome (large + small subunit) moves along the mRNA in the $5' \to 3'$ direction, one codon at a time. Each incoming **tRNA** carries a specific amino acid (attached by an aminoacyl-tRNA synthetase) and exposes a three-base **anticodon** that base-pairs with the current mRNA codon; a peptide bond then forms between the new amino acid and the growing polypeptide chain.

Translation

Translation converts an mRNA sequence into a polypeptide, carried out by **ribosomes** (composed of a large and a small subunit, each built from ribosomal RNA and protein).

- **tRNA (transfer RNA)** molecules are folded into a characteristic clover-leaf/L shape; each tRNA exposes a three-base **anticodon** at one end that base-pairs with a complementary mRNA codon, and carries a specific amino acid attached at the other end.
- **Aminoacyl-tRNA synthetase** is the enzyme that "charges" each tRNA — it attaches the correct amino acid to the correct tRNA, using ATP, based on the tRNA's anticodon sequence. This charging step is what ultimately links a codon to the correct amino acid.
- **Initiation**: the small ribosomal subunit binds the mRNA and locates the start codon (AUG); an initiator tRNA carrying methionine binds, then the large subunit joins to complete the functional ribosome.
- **Elongation**: the ribosome moves codon by codon along the mRNA ($5' \to 3'$); at each step, a charged tRNA with a complementary anticodon enters, and a **peptide bond** forms between the new amino acid and the growing polypeptide chain (catalyzed by the ribosome's peptidyl transferase activity), after which the ribosome moves to the next codon and the used tRNA is released.
- **Termination**: when a stop codon (UAA, UAG, or UGA) enters the ribosome, no tRNA has a matching anticodon; instead, release factors bind, the completed polypeptide is released, and the ribosome dissociates from the mRNA.

Ví dụ mẫu · From DNA template to mRNA to polypeptide

A gene's template strand reads, $3' \to 5'$: `TAC CTA GGC ATT`. Determine the mRNA sequence and the resulting polypeptide (or termination signal) for each codon.

Step 1 – transcribe. mRNA is synthesized $5' \to 3'$, complementary and antiparallel to the template (each DNA base pairs with its RNA complement; T→A, A→U, C→G, G→C):

$$\text{Template } (3' \to 5') : \texttt{T A C C T A G G C A T T}$$

$$\text{mRNA } (5' \to 3') : \texttt{A U G G A U C C G U A A}$$

Step 2 – translate, using the codon table:

$$\texttt{AUG} = \text{Met (start)}, \quad \texttt{GAU} = \text{Asp}, \quad \texttt{CCG} = \text{Pro}, \quad \texttt{UAA} = \text{Stop}.$$

Result: the polypeptide begins Met–Asp–Pro, and translation terminates at the UAA stop codon (a 3-amino-acid peptide before release, ignoring any further downstream sequence not given here).

VN **GIẢI THÍCH TIẾNG VIỆT**

Bộ mã di truyền là mã **bộ ba** (triplet): mỗi codon gồm 3 nucleotide, có $4^3 = 64$ codon khả dĩ nhưng chỉ mã hoá cho 20 loại amino acid → mã có tính **suy biến/dư thừa** (nhiều codon cùng mã hoá một amino acid). Mã di truyền có tính **phổ quát** — hầu hết sinh vật dùng chung một bộ mã. AUG vừa mã hoá methionine vừa là codon **mở đầu**; UAA, UAG, UGA là các codon **kết thúc**, không mã hoá amino acid nào. Trong dịch mã, **tRNA** mang bộ ba đối mã (anticodon) khớp bổ sung với codon trên mRNA, còn **aminoacyl-tRNA synthetase** là enzyme gắn đúng amino acid vào đúng tRNA. Ribosome di chuyển theo chiều $5' \to 3'$ trên mRNA, hình thành liên kết peptide giữa các amino acid liên tiếp cho đến khi gặp codon kết thúc.

Post-translational modification. Many polypeptides are not immediately functional after translation. They may be folded into a specific three-dimensional shape (often assisted by chaperone proteins), have signal sequences or extra segments enzymatically cleaved off, or have chemical groups added (e.g., phosphate groups, sugar groups in glycosylation, or lipid groups) — collectively called **post-translational modification**. These modifications can affect a protein's final shape, location within or outside the cell, activity, and stability.

(!) Lỗi thường gặp: Học sinh thường nhầm lẫn giữa **mạch khuôn** (template strand) và **mạch mã hoá** (coding/sense strand). RNA polymerase chỉ đọc mạch KHUÔN (theo chiều $3' \to 5'$) để tổng hợp mRNA theo chiều $5' \to 3'$ – mRNA tạo ra có trình tự GIỐNG với mạch mã hoá (chỉ khác U thay T), KHÔNG giống mạch khuôn. Một lỗi khác thường gặp: nhầm chiều đọc bộ ba trên mRNA – ribosome luôn đọc mRNA theo chiều $5' \to 3'$, bắt đầu từ codon mở đầu AUG gần đầu $5'$, KHÔNG đọc từ đầu $3'$.

4.1.3 D1.3 Mutation and Gene Editing

A **mutation** is any permanent change in the nucleotide sequence of DNA. Mutations are the ultimate source of all new genetic variation, but most occur in non-coding DNA or are silent; only a minority directly alter protein structure or function.

Types of point mutation and frameshift mutation

A **point mutation** is a change to a single nucleotide (or a small number of nucleotides) that does not alter the overall length/reading frame of the gene.

- **Silent mutation**: the base change alters a codon, but — due to the degeneracy of the genetic code — the new codon still specifies the *same* amino acid. No change to the protein.
- **Missense mutation**: the base change alters a codon so that it specifies a *different* amino acid. The protein may function normally, less well, or (rarely) even better, depending on how important that amino acid position is to protein structure/function.
- **Nonsense mutation**: the base change converts a codon that specified an amino acid into a *premature stop codon*, causing translation to terminate early and producing a shortened (truncated), usually non-functional, protein.

A **frameshift mutation** results from the **insertion** or **deletion** of a number of nucleotides that is *not* a multiple of three. Because the ribosome reads mRNA in continuous, non-overlapping triplets, inserting or deleting nucleotides shifts the **reading frame** for every codon downstream of the mutation, typically scrambling the entire amino acid sequence from that point onward and often creating a new, premature stop codon. Frameshift mutations are usually far more disruptive to protein function than point substitutions.

Ví dụ mẫu · Classifying mutations with a codon table

The original mRNA reads: `AUG GAU CCG UGG UAA` (Met–Asp–Pro–Trp–Stop). Classify each altered sequence below.

(a) `AUG GAC CCG UGG UAA`. Codon 2 changes GAU→GAC. Both GAU and GAC code for Asp ⇒ **silent mutation** (protein unchanged: Met–Asp–Pro–Trp–Stop).

(b) `AUG GCU CCG UGG UAA`. Codon 2 changes GAU→GCU. GCU codes for Ala, not Asp ⇒ **missense mutation** (Met–**Ala**–Pro–Trp–Stop).

(c) `AUG GAU CCG UGA UAA`. Codon 4 changes UGG (Trp)→UGA (Stop) ⇒ **nonsense mutation**: translation now terminates early, producing a truncated peptide (Met–Asp–Pro, only 3 amino acids instead of 4).

(d) An adenine (A) is **inserted** immediately after the start codon: `AUGAGAUCCGUGGUAA`. Regrouping into new codons from the start: `AUG–AGA–UCC–GUG–GUA`… ⇒ Met–**Arg–Ser–Val–Val**…, a completely different amino acid sequence from position 2 onward, and the original stop codon is no longer in frame ⇒ **frameshift (insertion) mutation**.

Causes of mutation

Mutations arise from two broad sources: **spontaneous replication errors** (DNA polymerase occasionally inserts an incorrect base, or slippage occurs on repetitive sequences, even though proofreading corrects the vast majority of these), and exposure to **mutagens** — external agents that increase the mutation rate. Mutagens include **radiation** (ultraviolet light, which can cause adjacent thymine bases to bond abnormally; ionizing radiation such as X-rays and gamma rays, which can break DNA strands directly) and **chemical mutagens** (e.g., compounds in tobacco smoke, certain industrial chemicals, and some naturally occurring toxins, which can chemically alter bases or intercalate into the DNA helix and disrupt replication).

Ví dụ mẫu · The molecular basis of sickle-cell disease

The gene for the β-globin subunit of human haemoglobin normally contains the codon `GAG` at a particular position, coding for **glutamic acid (Glu)**, a polar, negatively-charged amino acid. In the sickle-cell allele, a single base substitution changes this codon to `GUG`, which codes for **valine (Val)**, a nonpolar, hydrophobic amino acid.

(a) Classify the mutation. A single base change (A→U at the mRNA level, corresponding to a T→A change in that position of the coding DNA strand) that changes the amino acid specified ⇒ this is a **missense point mutation** (not silent, since the amino acid changes; not nonsense, since the new codon still specifies an amino acid, not a stop signal).

(b) Explain the phenotypic consequence. The substituted valine is hydrophobic and sits at a position on the outer surface of the haemoglobin molecule. Under low-oxygen conditions, the exposed hydrophobic valine residues on adjacent haemoglobin molecules stick to one another, causing haemoglobin molecules to polymerize into long, rigid fibres. These fibres distort red blood cells into a characteristic sickle (crescent) shape, which are less flexible, tend to block small blood vessels, and are broken down more rapidly — producing the pain crises and chronic anaemia of sickle-cell disease. This is a clear example of how a single nucleotide substitution can alter one amino acid, which in turn alters protein folding/behaviour, which in turn produces a whole-organism phenotype.

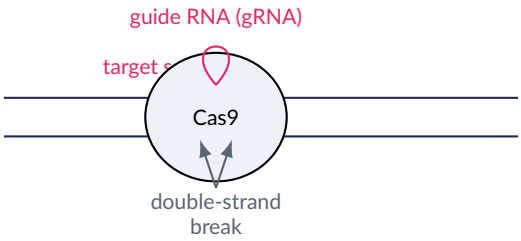
Gene editing: CRISPR-Cas9

CRISPR-Cas9 is a gene-editing technology adapted from a natural bacterial immune defence system against viruses.

- A short synthetic **guide RNA (gRNA)** is designed with a sequence complementary to the specific target DNA sequence a researcher wants to edit.
- The guide RNA associates with the **Cas9** enzyme (an endonuclease) and directs it to bind the target DNA sequence by complementary base pairing.
- Cas9 then cuts *both* strands of the DNA at that specific location, creating a double-strand break.
- The cell's own DNA repair machinery then repairs the break — either imprecisely (often disabling/"knocking out" the gene, useful for studying gene function or disabling a harmful gene) or precisely, if researchers also supply a corrected DNA template, allowing a specific mutation to be repaired or a new sequence to be inserted.

Applications include correcting disease-causing mutations (e.g., experimental gene therapies for sickle-cell disease and β-thalassaemia that edit blood stem cells), engineering crop plants for higher yield, disease resistance, or drought tolerance, and creating model organisms for research.

Ethical considerations include the distinction between editing **somatic cells** (affects only the treated individual, not inherited by offspring — generally viewed as comparable to other medical treatments) versus editing **germline cells or embryos** (changes would be inherited by all future descendants, raising concerns about consent of future generations, unequal access creating new forms of inequality, unintended **off-target** edits elsewhere in the genome, and the possibility of non-therapeutic "enhancement" uses).



The CRISPR-Cas9 system. The guide RNA (gRNA) is complementary to a specific target DNA sequence and directs the Cas9 enzyme to bind there; Cas9 then introduces a double-strand break at that precise location, which the cell's repair machinery subsequently repairs – either imprecisely (disabling the gene) or precisely, if a repair template is supplied.

Ví dụ mẫu · Reasoning about a CRISPR correction strategy for sickle-cell disease

A research team wants to use CRISPR-Cas9 to correct the sickle-cell mutation in a patient's bone-marrow stem cells (which produce red blood cells) before returning the corrected cells to the patient.

(a) What must the guide RNA sequence be complementary to? The region of the β-globin gene immediately surrounding the mutated codon (GTG at the DNA level), so that the Cas9-gRNA complex binds specifically at that site and nowhere else in the genome.

(b) What additional component is needed to *correct* the mutation, rather than simply disable the gene? A DNA **repair template** carrying the normal (GAG) sequence, supplied alongside the Cas9-gRNA complex, so that when the cell repairs the double-strand break, it uses the corrected template and restores the normal glutamic-acid codon.

(c) Why is editing bone-marrow stem cells *ex vivo* (outside the body) and returning only those cells considered a somatic, not a germline, gene therapy? The edit only affects the patient's own blood-forming cells; it will not be present in the patient's sperm or egg cells, so the correction cannot be passed on to any future offspring — it affects only the treated individual, avoiding the deeper ethical concerns raised by heritable germline editing.

VN **GIẢI THÍCH TIẾNG VIỆT**

Đột biến điểm gồm ba loại theo ảnh hưởng lên protein: **đột biến câm** (silent – amino acid không đổi do tính suy biến của mã di truyền), **đột biến sai nghĩa** (missense – đổi thành một amino acid khác), và **đột biến vô nghĩa** (nonsense – tạo ra codon kết thúc sớm, làm protein bị cắt ngắn). **Đột biến dịch khung** (frameshift) xảy ra khi thêm/mất số nucleotide KHÔNG chia hết cho 3, làm lệch toàn bộ khung đọc phía sau điểm đột biến – thường gây hậu quả nghiêm trọng hơn đột biến điểm. Nguyên nhân đột biến: lỗi sao chép tự phát hoặc tác nhân gây đột biến (mutagen) như tia UV, tia phóng xạ ion hoá, hoá chất. Bệnh hồng cầu hình lưỡi liềm là ví dụ kinh điển: đột biến điểm GAG→GTG đổi glutamic acid (ưa nước) thành valine (kỵ nước) trên chuỗi β-globin, khiến hemoglobin kết tụ thành sợi dài khi thiếu oxy, làm hồng cầu biến dạng hình lưỡi liềm. Công nghệ **CRISPR-Cas9** dùng một đoạn ARN dẫn đường (guide RNA) để đưa enzyme Cas9 đến đúng vị trí ADN cần cắt, mở ra khả năng sửa lỗi gen – nhưng đi kèm các vấn đề đạo đức quan trọng, đặc biệt là sự khác biệt giữa chỉnh sửa tế bào sinh dưỡng (không di truyền) và chỉnh sửa tế bào mầm/phôi (di truyền cho thế hệ sau).

4.2 D2 Cells: Division, Gene Expression and Water Potential

4.2.1 D2.1 Cell and Nuclear Division

The cell cycle

The **cell cycle** is the ordered sequence of growth and division that a eukaryotic cell passes through, divided into **interphase** (further divided into G_1, S, and G_2) and the **mitotic (M) phase**.

- **G_1 (first gap/growth phase)**: the cell grows, carries out its normal metabolic functions, and synthesizes proteins and organelles needed for eventual division.
- **S (synthesis phase)**: the entire genome is replicated (see D1.1); each chromosome, once a single DNA molecule, now consists of two identical **sister chromatids**.
- **G_2 (second gap phase)**: further growth and protein synthesis (e.g., proteins needed for the mitotic spindle), and final checks before division.
- **M (mitotic phase)**: nuclear division (mitosis) followed by cytokinesis (division of the cytoplasm into two separate cells).

Checkpoints are surveillance points (chiefly at the G_1/S boundary, the G_2/M boundary, and during metaphase — the spindle-assembly checkpoint) at which the cell checks for conditions such as adequate cell size, availability of nutrients, and absence of DNA damage before being allowed to proceed to the next stage. Checkpoints prevent a cell from dividing when conditions are unfavourable or when DNA damage has not yet been repaired.

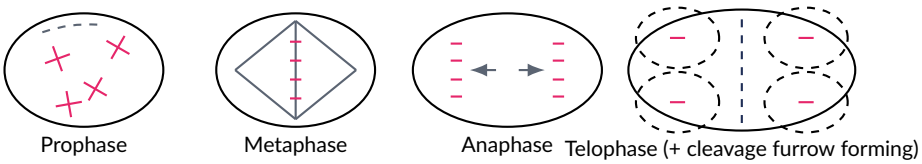
Chromosome structure. **Chromatin** is the loosely packed complex of DNA and histone proteins found in the nucleus during interphase. Before mitosis, chromatin condenses into visible, tightly coiled **chromosomes**. After S phase, each chromosome consists of two identical, genetically-equivalent **sister chromatids**, joined together at a constricted region called the **centromere**. During anaphase, sister chromatids are pulled apart and each becomes an independent chromosome in a daughter cell.

Stages of mitosis

Mitosis is nuclear division that produces two daughter nuclei genetically identical to the parent nucleus and to each other, each with the same (diploid, $2n$) chromosome number as the original cell.

- **Prophase**: chromatin condenses into visible chromosomes (each still composed of two sister chromatids); the mitotic spindle begins to form from opposite poles of the cell; the nuclear envelope breaks down.
- **Metaphase**: spindle fibres from each pole attach to the centromere of every chromosome and align all chromosomes along the cell's equator (the metaphase plate).
- **Anaphase**: sister chromatids separate and are pulled by shortening spindle fibres to opposite poles of the cell — from this point on, each chromatid is counted as its own chromosome.
- **Telophase**: a nuclear envelope re-forms around each set of chromosomes at the two poles, and the chromosomes decondense back into chromatin.

Cytokinesis then divides the cytoplasm into two separate daughter cells — via a pinching **cleavage furrow** in animal cells, or via a newly built **cell plate** that becomes a new cell wall in plant cells.



The four stages of mitosis. Prophase: chromosomes condense, spindle forms. Metaphase: chromosomes align at the equator. Anaphase: sister chromatids separate toward opposite poles. Telophase: two nuclear envelopes re-form as the cell begins to pinch into two (cytokinesis).

Ví dụ mẫu · Mitotic index and cell-cycle timing

A student examines a microscope slide of onion root-tip cells and counts 1000 cells in total: 920 in interphase, 42 in prophase, 14 in metaphase, 8 in anaphase, and 16 in telophase. Assume the total cell cycle for these cells takes 24 hours.

(a) Calculate the mitotic index. The **mitotic index** is the proportion of cells in mitosis (any M-phase stage) at a given moment:

$$\text{Mitotic index} = \frac{42 + 14 + 8 + 16}{1000} = \frac{80}{1000} = 0.08 = 8\%.$$

(b) Estimate the total time spent in mitosis. Since the proportion of cells observed in mitosis approximates the proportion of the cycle spent in mitosis:

$$0.08 \times 24 \text{ h} = 1.92 \text{ h} = 115.2 \text{ min} \approx 115 \text{ minutes}.$$

(c) Estimate the time spent in each mitotic stage. Within the 80 mitotic cells, prophase $= 42/80 = 52.5\%$, metaphase $= 14/80 = 17.5\%$, anaphase $= 8/80 = 10\%$, telophase $= 16/80 = 20\%$ of mitotic time:

$$\text{Prophase} \approx 0.525 \times 115.2 \approx 60.5 \text{ min}, \quad \text{Metaphase} \approx 0.175 \times 115.2 \approx 20.2 \text{ min},$$

$$\text{Anaphase} \approx 0.10 \times 115.2 \approx 11.5 \text{ min}, \quad \text{Telophase} \approx 0.20 \times 115.2 \approx 23.0 \text{ min}.$$

Check: $60.5 + 20.2 + 11.5 + 23.0 \approx 115.2$ min. ✓ Prophase is by far the longest mitotic stage here, consistent with the fact that chromosome condensation and spindle formation take considerable time, while anaphase (chromatid separation) is typically the shortest.

Ví dụ mẫu · Tracking chromosome and DNA content through mitosis

A species has a diploid chromosome number of $2n = 8$. For each stage below, state the number of chromosomes and the number of separate DNA molecules (chromatids) present in a single cell.

Stage	Chromosomes	DNA molecules (chromatids)
G_1 (before S phase)	8	8 (each chromosome unreplicated)
G_2 / prophase / metaphase (after S phase)	8	16 (each chromosome = 2 sister chromatids)
Immediately after anaphase (whole cell, both future daughter sets, before cytokinesis)	16	16 (each chromatid now counts as its own chromosome)
Each daughter cell after telophase/cytokinesis	8	8

Key reasoning: chromosome number is counted by the number of centromeres present; DNA

replication in S phase doubles the number of DNA molecules (chromatids) without changing the chromosome count, since sister chromatids stay joined at one centromere until anaphase. Only when sister chromatids separate in anaphase does the chromosome count itself double (transiently, within the still-undivided cell) – cytokinesis then restores each daughter cell to the original diploid number, with every chromosome unreplicated once again.

(!) Lỗi thường gặp: Một lỗi thường gặp: cho rằng nhân đôi ADN (pha S) làm TĂNG số lượng nhiễm sắc thể. SAI – pha S chỉ làm tăng số lượng **phân tử ADN/chromatid** (từ 1 thành 2 chromatid chị em trên mỗi NST), nhưng số lượng NST (tính theo số tâm động) vẫn giữ nguyên cho đến tận kỳ sau (anaphase), khi hai chromatid chị em mới thực sự tách rời và mỗi chromatid được tính là một NST độc lập.

Biological significance of mitosis; cancer as an application

Because mitosis produces daughter cells that are genetically identical (diploid, $2n$) to the parent cell, it is the basis of **growth** (increasing cell number in a developing organism), **tissue repair** (replacing damaged or worn-out cells), and **asexual reproduction** in many organisms (offspring genetically identical to the parent).

Cancer results from the loss of normal cell-cycle control: mutations in genes that regulate the cell cycle (e.g., proto-oncogenes that become overactive **oncogenes**, or tumour-suppressor genes such as $p53$ that lose their function) allow cells to bypass checkpoints and divide repeatedly and uncontrollably, even when signalled to stop. This uncontrolled division produces a mass of cells called a **tumour**. A **benign** tumour grows locally without invading surrounding tissue; a **malignant** tumour invades neighbouring tissue and can **metastasize** (spread to other parts of the body via the blood or lymphatic system), which is what makes cancer potentially life-threatening.

VN **GIẢI THÍCH TIẾNG VIỆT**

Chu kỳ tế bào gồm G_1 (tăng trưởng), S (nhân đôi ADN, mỗi nhiễm sắc thể thành 2 chromatid chị em), G_2 (chuẩn bị cuối), và M (nguyên phân + phân chia tế bào chất). Các **điểm kiểm soát** (checkpoint) tại G_1/S, G_2/M, và trong kỳ giữa (kiểm tra gắn thoi) đảm bảo tế bào chỉ phân chia khi điều kiện thuận lợi và ADN không bị hư hỏng. Bốn kỳ của nguyên phân: **kỳ đầu** (NST co xoắn, thoi phân bào hình thành, màng nhân biến mất) → **kỳ giữa** (NST xếp thành một hàng ở mặt phẳng xích đạo) → **kỳ sau** (chromatid chị em tách nhau, di chuyển về hai cực) → **kỳ cuối** (màng nhân tái hình thành ở hai cực, NST duỗi xoắn), sau đó là **phân chia tế bào chất** (cytokinesis). Nguyên phân tạo ra tế bào con **giống hệt** tế bào mẹ về mặt di truyền, là cơ sở của sinh trưởng, tái tạo mô, và sinh sản vô tính. **Ung thư** xuất hiện khi tế bào mất kiểm soát chu kỳ phân chia (đột biến gen tiền ung thư thành gen ung thư, hoặc mất chức năng gen ức chế u như $p53$), dẫn đến phân chia không kiểm soát và hình thành khối u.

4.2.2 D2.2 Gene Expression (HL only)

This subtopic (D2.2) is assessed only at Higher Level (HL); it is not required for the Standard Level (SL) course.

Every cell in a multicellular organism carries essentially the *same* genome, yet a liver cell, a neuron, and a skin cell look and function very differently. This is possible because cells express only a **subset** of their genes at any given time, and *which* genes are expressed is tightly regulated.

Regulation of transcription in prokaryotes: the operon model

In bacteria, genes involved in a single metabolic pathway are often organized into an **operon**: a cluster of genes transcribed together from a single promoter, allowing coordinated control. The classic example is the *lac* operon in *E. coli*, which contains genes needed to digest lactose.

- A **regulatory (repressor) protein** can bind to an **operator** sequence next to the promoter, physically blocking RNA polymerase from transcribing the structural genes.
- When lactose is present, a lactose derivative binds to the repressor protein, changing its shape so it can no longer bind the operator. The operator is now free, RNA polymerase can transcribe the genes, and the lactose-digesting enzymes are produced — this is called **induction**.
- When lactose is absent, the repressor binds the operator and transcription is blocked (**repression**) — the cell saves energy by not producing enzymes it does not currently need.

This is an efficient control strategy: genes are only expressed when their product is actually needed.

Ví dụ mẫu · Reasoning about a lac operon operator mutation

A mutation changes the DNA sequence of the *operator* region of the *lac* operon so severely that the repressor protein can no longer bind to it at all, even in the complete absence of lactose. Predict the effect on transcription of the lactose-digesting structural genes (a) when lactose is absent, and (b) when lactose is present.

(a) Lactose absent. Normally, with no lactose present, the repressor would bind the (intact) operator and block transcription. Here, however, the repressor *cannot* bind the mutated operator at all, so nothing physically blocks RNA polymerase – the structural genes are transcribed **continuously**, even though lactose is not available to be digested. This is called **constitutive expression**: the genes are expressed regardless of whether their product is actually needed, wasting cellular energy and resources.

(b) Lactose present. Transcription still proceeds continuously, exactly as in (a). Normally lactose acts by inactivating the repressor, but since the repressor already cannot bind this mutated operator, the presence or absence of lactose makes no additional difference to transcription of this operon.

Regulation of transcription in eukaryotes: transcription factors

Eukaryotic gene expression is regulated mainly by **transcription factors** — regulatory proteins that bind to specific DNA sequences (such as promoters and more distant regulatory sequences called enhancers) and either help recruit RNA polymerase (**activators**, increasing transcription) or block it (**repressors**, decreasing transcription). A given gene is typically controlled by the combined effect of *several* transcription factors acting together, allowing fine, combinatorial control over exactly when, where, and how strongly a gene is expressed. Different cell types express different combinations of transcription factors, which is a major reason why cells with an identical genome can express such different subsets of genes.

Epigenetics

Epigenetics refers to heritable changes in gene expression that do *not* involve any change to the underlying DNA sequence itself.

- **DNA methylation**: the addition of methyl ($-CH_3$) groups, typically to cytosine bases. Heav-

ily methylated regions of DNA are generally associated with reduced transcription (methylation can physically block transcription-factor binding or recruit proteins that compact the DNA).

- **Histone modification**: DNA is packaged around histone proteins; chemical modifications to histones (such as acetylation) can loosen chromatin packing, making genes more accessible and increasing expression, while other modifications promote tighter packing and silence genes.
- Epigenetic marks can be influenced by **environmental factors** (diet, stress, toxin exposure) and can be copied during DNA replication, allowing a particular pattern of gene expression to be maintained across many cell divisions — this is how a differentiated cell "remembers" which genes to keep switched on or off as it divides.

Why do differentiated cells with identical genomes express different genes? Every somatic cell in an organism inherited the same genome from the zygote, but during development, cells become exposed to different signalling molecules and combinations of transcription factors, which establish (and epigenetic marks then help maintain) a distinct, stable pattern of gene expression in each cell lineage. The result is **tissue-specific gene expression**: a pancreatic islet cell expresses the insulin gene at high levels and keeps most other tissue-specific genes (e.g., those for muscle contraction proteins) switched off, while a muscle cell does the reverse — despite carrying the very same DNA sequence.

VN **GIẢI THÍCH TIẾNG VIỆT**

(Nội dung D2.2 chỉ dành cho chương trình HL.) Điều hoà biểu hiện gen ở vi khuẩn thường theo mô hình **operon** – ví dụ operon lac: khi có lactose, chất cảm ứng làm protein ức chế (repressor) rời khỏi vùng operator, RNA polymerase phiên mã được (**cảm ứng/induction**); khi không có lactose, repressor gắn vào operator, chặn phiên mã (**ức chế/repression**). Ở sinh vật nhân thực, các **yếu tố phiên mã** (transcription factor) gắn vào ADN để hoạt hoá hoặc ức chế phiên mã một cách tổ hợp. **Epigenetics** là những thay đổi biểu hiện gen di truyền được nhưng KHÔNG làm thay đổi trình tự ADN, gồm **methyl hoá ADN** (thường làm im lặng gen) và **biến đổi histone** (ví dụ acetyl hoá làm lỏng cấu trúc nhiễm sắc thể, tăng biểu hiện gen); các dấu ấn này có thể bị ảnh hưởng bởi môi trường (chế độ ăn, stress, độc tố) và được duy trì qua các lần phân chia tế bào. Đây là lý do các tế bào biệt hoá có cùng bộ gen nhưng biểu hiện gen khác nhau theo từng loại mô.

4.2.3 D2.3 Water Potential

Defining water potential

Water potential (ψ, measured in kilopascals, kPa) is a measure of the tendency of water to move from one region to another — specifically, the potential energy of water relative to pure water at atmospheric pressure, which is defined as $\psi = 0$. Water always moves, by osmosis or bulk flow, from a region of **higher (less negative) water potential** to a region of **lower (more negative) water potential**. Because dissolved solutes always lower a solution's water potential, water potential values for solutions and cells are usually negative.

Components of water potential. Total water potential is the sum of two components:

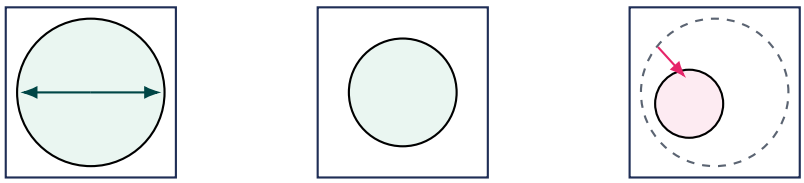
$$\psi = \psi_s + \psi_p,$$

where ψ_s is the **solute potential** (also called osmotic potential) — always ≤ 0, and more negative the higher the solute concentration, because dissolved solute particles reduce the free energy/movement of water molecules; and ψ_p is the **pressure potential** — usually positive in a walled plant cell (physical pressure exerted by the cell wall pushing back against the swelling protoplast, i.e., turgor pressure), but it can be zero (unconfined solution, or a fully flaccid cell) or even negative (e.g., tension in xylem vessels pulling water upward).

Water potential and plant cell states

- A cell placed in a solution with a *higher* (less negative) water potential than the cell will gain water: the protoplast swells against the cell wall, pressure potential rises, and the cell becomes **turgid**. Turgor pressure is essential for supporting non-woody plant tissue.
- A cell in equilibrium with its surroundings (no net water movement) is described as **flaccid** ($\psi_p \approx 0$).
- A cell placed in a solution with a *lower* (more negative) water potential than the cell will lose water: the protoplast shrinks and eventually pulls away from the cell wall entirely, a state called **plasmolysis**.

The same higher-to-lower water potential rule explains water movement into roots from soil (soil water, usually close to 0 kPa when moist, has a higher water potential than the solute-rich root cells) and the continued movement of water from root to shoot to leaf as each successive tissue maintains a slightly more negative water potential than the one before it.



Turgid (ψ_p large positive) | Flaccid ($\psi_p \approx 0$) | Plasmolyzed (protoplast shrunk, pulled from wall)

Three states of a walled plant cell placed in solutions of different water potential. **Turgid**: the cell has taken up water, the protoplast presses firmly against the cell wall, generating a large positive pressure potential. **Flaccid**: no net water movement; the protoplast just fills the wall with negligible pressure potential. **Plasmolyzed**: severe water loss to a strongly hypertonic (very negative ψ) external solution causes the protoplast to shrink and pull away from the cell wall (dashed outline shows the wall's original position).

Ví dụ mẫu · Calculating and comparing water potential

A sucrose solution has a concentration of $C = 0.3$ mol dm^{-3} at $T = 27°$C $= 300$ K. Sucrose does not ionize in solution, so $i = 1$. Use $\psi_s = -iCRT$, with $R = 8.31$ kPa · dm^3 · mol^{-1} · K^{-1} (numerically equal to the universal gas constant, 8.31 J K^{-1} mol^{-1}, since 1 kPa·dm$^3 = 1$ J).

Step 1 – solute potential of the solution.

$$\psi_s = -iCRT = -(1)(0.3)(8.31)(300) = -747.9 \text{ kPa} \approx -748 \text{ kPa}.$$

Step 2 – total water potential of the solution. The solution sits in an open beaker (unconfined,

so no pressure builds up): $\psi_p = 0$.

$$\psi_{\text{solution}} = \psi_s + \psi_p = -748 + 0 = -748 \text{ kPa}.$$

Step 3 – predict water movement. A plant cell is placed in this solution. The cell's own water potential is $\psi_{\text{cell}} = -500$ kPa. Since

$$\psi_{\text{cell}}(-500 \text{ kPa}) > \psi_{\text{solution}}(-748 \text{ kPa}),$$

the cell has the *higher* (less negative) water potential, so water will move down the gradient, **out of the cell and into the solution**. The cell will lose water and may become flaccid or even plasmolyzed if it loses enough water.

VN **GIẢI THÍCH TIẾNG VIỆT**

Thế nước (ψ, đơn vị kPa) đo xu hướng di chuyển của nước, với nước nguyên chất ở áp suất khí quyển được quy ước $\psi = 0$. Nước LUÔN di chuyển từ nơi có ψ **cao hơn (ít âm hơn)** đến nơi có ψ **thấp hơn (âm hơn)**. ψ gồm hai thành phần: $\psi = \psi_s + \psi_p$, trong đó ψ_s (thế thẩm thấu/thế chất tan) luôn ≤ 0 và càng âm khi nồng độ chất tan càng cao; ψ_p (thế áp suất) thường dương trong tế bào thực vật có vách (do áp suất trương – turgor pressure – của vách tế bào đẩy ngược lại), có thể bằng 0 (tế bào mềm/nhũn – flaccid) hoặc âm (như trong mạch xylem). Khi tế bào hút nước, nó trở nên **trương nước** (turgid); khi mất nước quá nhiều, nguyên sinh chất co lại tách khỏi vách tế bào, gọi là **co nguyên sinh** (plasmolysis). Công thức $\psi_s = -iCRT$ (với i = hệ số ion hoá, C = nồng độ mol, R = hằng số khí, T = nhiệt độ Kelvin) cho phép tính định lượng thế thẩm thấu của một dung dịch.

Ví dụ mẫu · Water potential of a turgid cell and predicting osmosis

A walled plant cell has a solute potential $\psi_s = -900$ kPa. At full turgor, its pressure potential is $\psi_p = +400$ kPa.

(a) Calculate the cell's total water potential.

$$\psi_{\text{cell}} = \psi_s + \psi_p = -900 + 400 = -500 \text{ kPa}.$$

(b) The cell is placed in an open beaker of solution with $\psi_{\text{solution}} = -300$ kPa (unconfined, so $\psi_p = 0$ for the solution). Predict the direction of net water movement and describe the immediate effect on the cell.

Comparing the two values, $\psi_{\text{solution}}(-300 \text{ kPa}) > \psi_{\text{cell}}(-500 \text{ kPa})$, so the solution has the higher (less negative) water potential. Water therefore moves **into the cell**, down the water-potential gradient. As the cell takes up more water, its protoplast presses harder against the rigid cell wall, so ψ_p rises further; this in turn raises ψ_{cell} (makes it less negative) until $\psi_{\text{cell}} = \psi_{\text{solution}} = -300$ kPa, at which point net water movement stops (a new equilibrium). Because the cell is already turgid, the wall's resistance prevents unlimited swelling or bursting – unlike an animal cell, which has no wall and would instead continue swelling and could lyse.

Determining water potential experimentally. A common practical method is to cut equal-sized samples of plant tissue (e.g., potato) and immerse them in a range of sucrose solutions of known concentration, recording the percentage change in mass after a fixed time. Plotting percentage change in mass against solution concentration produces a line that crosses zero (no net mass change) at the concentration whose water potential equals that of the tissue itself – at concentrations below this point the tissue gains mass (the solution's ψ is higher than the tissue's), and above it the tissue loses mass (the solution's ψ is lower than the tissue's).

VN **GIẢI THÍCH TIẾNG VIỆT**

Phương pháp thực nghiệm xác định thế nước mô thực vật: cắt các mẫu mô (ví dụ khoai tây) kích thước bằng nhau, ngâm vào dãy dung dịch sucrose có nồng độ đã biết, đo phần trăm thay đổi khối lượng sau một khoảng thời gian cố định. Vẽ đồ thị phần trăm thay đổi khối lượng theo nồng độ dung dịch; điểm mà đường đồ thị cắt trục hoành (khối lượng không đổi) chính là nồng độ có thế nước bằng với thế nước của mô – ở nồng độ thấp hơn điểm này mô tăng khối lượng (dung dịch có ψ cao hơn mô), ở nồng độ cao hơn mô giảm khối lượng (dung dịch có ψ thấp hơn mô).

Summary table – reading water-potential scenarios.

External solution vs. cell	Net water movement	Resulting cell state
Solution ψ higher (less negative) than cell ψ	Into the cell	Cell gains water → becomes more turgid
Solution ψ equal to cell ψ	No net movement	Cell remains flaccid (equilibrium)
Solution ψ lower (more negative) than cell ψ	Out of the cell	Cell loses water → flaccid, then plasmolyzed if severe

4.3 D3 Organisms: Reproduction, Inheritance and Homeostasis

4.3.1 D3.1 Reproduction

Asexual vs. sexual reproduction

Asexual reproduction involves a single parent producing offspring through mitosis (or an equivalent process), without the fusion of gametes. Offspring are **genetically identical** to the parent (clones), aside from any new mutations. It is fast, does not require a mate, and allows rapid population growth when conditions are favourable — but because it generates essentially no new genetic variation, a population reproducing only asexually can be uniformly vulnerable to a new disease or a changing environment.

Sexual reproduction involves two parents, each contributing a haploid gamete produced by **meiosis**; the gametes fuse at **fertilization** to form a genetically unique offspring. It is slower and costlier (time and energy spent finding a mate; only part of the population directly bears offspring), but the **genetic variation** it generates in every generation is the raw material for natural selection and improves a population's long-term capacity to adapt to changing conditions.

VN **GIẢI THÍCH TIẾNG VIỆT**

Sinh sản vô tính chỉ cần một cá thể bố/mẹ, dựa trên nguyên phân, tạo ra con giống hệt bố/mẹ về mặt di truyền (bản sao/clone) – nhanh nhưng không tạo biến dị mới, khiến quần thể dễ bị tổn thương đồng loạt trước bệnh dịch hay thay đổi môi trường. **Sinh sản hữu tính** cần hai cá

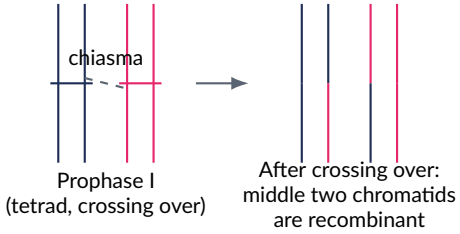
thể bố mẹ, dựa trên giảm phân tạo giao tử đơn bội rồi thụ tinh, tạo ra con có tổ hợp gen **mới, đa dạng** – chậm và tốn kém hơn nhưng biến dị di truyền tạo ra chính là nguyên liệu cho chọn lọc tự nhiên, giúp quần thể thích nghi tốt hơn về lâu dài.

Meiosis overview

Meiosis is a specialized form of nuclear division that reduces the chromosome number by half, converting a diploid ($2n$) cell into four haploid (n) cells (gametes), through **two** successive divisions following a single round of DNA replication.

- **Meiosis I** (reductional division): homologous chromosome pairs (each already duplicated into sister chromatids) line up together and then separate, halving the chromosome number. During prophase I, non-sister chromatids of homologous chromosomes undergo **crossing over**, physically exchanging segments of DNA and creating new allele combinations on individual chromosomes. During metaphase I, each homologous pair aligns and orients **independently** of every other pair (**independent assortment**), so which parental chromosome of each pair ends up in a given daughter cell is random.
- **Meiosis II** (equational division): resembles mitosis — sister chromatids of each (now unpaired) chromosome separate into different daughter cells. No further reduction in chromosome number occurs.

The result of meiosis is **four genetically unique haploid gametes**, each with half the chromosome number of the parent cell. **Fertilization** (fusion of a haploid sperm and a haploid egg) restores the full diploid chromosome number in the zygote, combining genetic material from two parents.



During prophase I of meiosis, homologous chromosomes (one from each parent; navy and pink) pair up, and non-sister chromatids can exchange segments at a chiasma (point of physical crossing over). The result is two recombinant chromatids (each now part navy, part pink – a new combination of parental alleles) and two non-recombinant chromatids (unchanged, single colour) – one further source of the genetic variation described in this subtopic.

(!) Lỗi thường gặp: Học sinh thường nhầm lẫn giữa **nguyên phân** và **giảm phân**. Nguyên phân: MỘT lần phân chia, từ 1 tế bào $2n \to 2$ tế bào con $2n$, giống hệt nhau và giống tế bào mẹ về mặt di truyền. Giảm phân: HAI lần phân chia liên tiếp (sau một lần nhân đôi ADN), từ 1 tế bào $2n \to 4$ tế bào con n (đơn bội), mỗi tế bào con **khác nhau** về mặt di truyền (do trao đổi chéo và phân li độc lập) và khác cả tế bào mẹ ban đầu. Lỗi thường gặp: viết nhầm nguyên phân là "$2n \to n$", hoặc quên rằng giảm phân gồm HAI lần phân chia tạo ra BỐN tế bào con (không phải một lần tạo hai tế bào như nguyên phân).

Ví dụ mẫu · Genetic variation from independent assortment

Human somatic cells contain 23 pairs of homologous chromosomes ($n = 23$).

(a) Considering independent assortment alone (ignoring crossing over), calculate the number

of genetically distinct chromosome combinations possible in a single gamete.
Each of the 23 homologous pairs assorts independently, with 2 possible chromosomes (maternal or paternal) contributed per pair:

$$2^{23} = 8{,}388{,}608 \approx 8.4 \text{ million distinct possible gametes.}$$

(b) Hence estimate the number of genetically distinct zygotes a particular couple could produce, considering independent assortment alone.
Each parent independently contributes one of their own 2^{23} possible gametes:

$$2^{23} \times 2^{23} = 2^{46} = 70{,}368{,}744{,}177{,}664 \approx 7.0 \times 10^{13} \text{ (over } 70 \text{ trillion)}.$$

This number, already immense, does not even include the additional variation generated by **crossing over** (which creates recombinant chromosomes not present in either parent's original chromosome set) or the essentially random pairing of a particular sperm with a particular egg at fertilization — both of which further multiply the genetic uniqueness of each offspring. This is why, other than identical twins, no two siblings are genetically identical.

Ví dụ mẫu · Comparing chromosome number through mitosis and meiosis

An organism has a diploid chromosome number $2n = 6$ ($n = 3$). Compare the chromosome number and DNA content (number of chromatids) at equivalent points of mitosis (Subtopic D2.1) and meiosis.

Stage	Chromosomes	DNA molecules (chromatids)
Before S phase (G_1)	6	6
After S phase – prophase/metaphase of mitosis, *or* prophase I/metaphase I of meiosis	6	12
Mitosis – each daughter cell after telophase	6	6
Meiosis – each cell after meiosis I (entering meiosis II)	3	6
Meiosis – each final gamete after meiosis II	3	3

Interpretation. Up to and including metaphase, mitosis and meiosis are indistinguishable in chromosome/DNA content – both simply reflect the single round of S-phase replication. The two processes diverge from anaphase I of meiosis onward: mitosis separates sister chromatids (restoring the original diploid number, 6, unreplicated, in each daughter cell), whereas meiosis I separates whole homologous chromosomes (halving the chromosome number to 3, while each chromosome still has 2 chromatids), and only meiosis II – which separates sister chromatids, exactly as mitosis does – finally produces haploid ($n = 3$) gametes with unreplicated chromosomes.

Human gametogenesis

Spermatogenesis occurs continuously in the testes from puberty onward: each diploid primary spermatocyte undergoes meiosis to produce **four** equal-sized, functional haploid sperm cells.

Oogenesis occurs in the ovaries: each diploid primary oocyte begins meiosis I (which is arrested for years, resuming around ovulation) to produce one large **secondary oocyte** and one much smaller **first polar body** — the division of cytoplasm is highly unequal. Meiosis II only completes if fertilization occurs, producing one mature **ovum** and a second polar body. Polar bodies are non-functional and eventually degenerate; this asymmetric division concentrates nutrients and cytoplasmic resources into the single functional egg cell, which must support the earliest stages of embryonic development.

VN **GIẢI THÍCH TIẾNG VIỆT**

Giảm phân gồm **hai** lần phân chia liên tiếp sau một lần nhân đôi ADN: giảm phân I (phân li của các cặp NST tương đồng, có trao đổi chéo ở kỳ đầu I và phân li độc lập ở kỳ giữa I) làm giảm một nửa số lượng NST; giảm phân II (tương tự nguyên phân, chromatid chị em tách nhau) không làm giảm thêm số lượng NST. Kết quả: từ 1 tế bào $2n$ tạo ra 4 tế bào con n, mỗi tế bào khác nhau về mặt di truyền. Thụ tinh (kết hợp giao tử đực và cái đơn bội) khôi phục lại bộ NST lưỡng bội $2n$ ở hợp tử. Ở người, **sinh tinh** (spermatogenesis) tạo ra 4 tinh trùng chức năng có kích thước bằng nhau; **sinh trứng** (oogenesis) chỉ tạo ra 1 trứng chức năng (cùng các thể cực nhỏ, thoái hoá) do phân chia tế bào chất không đều, giúp tập trung dưỡng chất cho trứng.

Hormonal control of the human menstrual cycle

Four hormones regulate the roughly 28-day human menstrual cycle:

- **FSH (follicle-stimulating hormone)**, from the anterior pituitary, stimulates the growth of ovarian follicles and their secretion of oestrogen.
- **LH (luteinizing hormone)**, from the anterior pituitary, triggers **ovulation** (release of a secondary oocyte) at a sharp mid-cycle surge, and afterward stimulates the ruptured follicle to develop into the **corpus luteum**.
- **Oestrogen**, from the developing follicle, stimulates growth and thickening (repair) of the uterine lining (endometrium). Sustained high oestrogen just before ovulation switches from negative to **positive feedback** on the hypothalamus/pituitary — an unusual exception to the normal negative-feedback pattern — directly triggering the LH surge.
- **Progesterone**, from the corpus luteum after ovulation, maintains and further develops the endometrium in preparation for a possible pregnancy, and (together with oestrogen) exerts **negative feedback** that suppresses further FSH/LH release, preventing new follicles from developing during this phase.

If fertilization and implantation do not occur, the corpus luteum degenerates, causing progesterone and oestrogen levels to fall sharply; the endometrium, no longer hormonally maintained, breaks down and is shed (menstruation), and the fall in progesterone/oestrogen releases the pituitary from inhibition, allowing FSH to rise again and a new cycle to begin.

VN **GIẢI THÍCH TIẾNG VIỆT**

Bốn hormone điều hoà chu kỳ kinh nguyệt: **FSH** (kích thích nang trứng phát triển và tiết oestrogen), **LH** (đỉnh LH gây rụng trứng, sau đó kích thích nang trứng đã vỡ biến thành thể vàng), **oestrogen** (làm dày niêm mạc tử cung; khi đạt đỉnh cao trước rụng trứng lại gây phản hồi **dương** hiếm gặp, kích hoạt đỉnh LH), và **progesterone** (do thể vàng tiết ra, duy trì niêm mạc tử cung, đồng thời ức chế ngược FSH/LH). Nếu không thụ tinh, thể vàng thoái hoá, progesterone và oestrogen giảm mạnh, niêm mạc tử cung bong ra (hành kinh), đồng thời tuyến yên được giải phóng khỏi ức chế nên FSH tăng trở lại, bắt đầu chu kỳ mới.

4.3.2 D3.2 Inheritance

Mendelian vocabulary

Gene: a section of DNA that codes for a specific characteristic, existing at a specific location (**locus**) on a chromosome. **Allele**: one of two or more alternative versions of a gene. **Genotype**: the specific combination of alleles an individual carries for a gene. **Phenotype**: the observable characteristic that results from an individual's genotype (and, often, its environment). **Dominant** allele: an allele whose phenotypic effect is expressed whenever it is present (even with only one copy). **Recessive** allele: an allele whose phenotypic effect is only expressed when *no* dominant allele is present (i.e., in the homozygous recessive state). **Homozygous**: carrying two identical alleles for a gene (AA or aa). **Heterozygous**: carrying two different alleles for a gene (Aa).

Monohybrid and dihybrid crosses; test crosses

A **monohybrid cross** tracks the inheritance of a single gene. Crossing two heterozygotes ($Aa \times Aa$) for a completely dominant/recessive trait produces offspring in a classic $3:1$ phenotypic ratio ($1\,AA:2\,Aa:1\,aa$ genotypically), predictable using a 2×2 **Punnett square**.

A **dihybrid cross** tracks two genes simultaneously. If the two genes assort independently (different chromosomes, or far apart on the same chromosome), crossing two double heterozygotes ($AaBb \times AaBb$) produces the classic $9:3:3:1$ phenotypic ratio, predictable using a 4×4 Punnett square (16 equally likely offspring genotype combinations).

A **test cross** is used to determine the unknown genotype of an individual showing a dominant phenotype (which could be homozygous or heterozygous): the individual is crossed with a known homozygous recessive individual. If *all* offspring show the dominant phenotype, the unknown parent was homozygous dominant; if offspring show an approximately $1:1$ ratio of dominant to recessive phenotypes, the unknown parent was heterozygous.

Ví dụ mẫu · Using a test cross to determine an unknown genotype

A tall pea plant of unknown genotype (either TT or Tt; tall T is dominant to dwarf t) is crossed with a homozygous recessive dwarf plant (tt). Among 50 offspring, 24 are tall and 26 are short.

Hypothesis A ($TT \times tt$):

	T	T
t	Tt	Tt
t	Tt	Tt

Predicts 100% tall offspring (50 tall : 0 short) — clearly inconsistent with the observed 26 short offspring.

Hypothesis B ($Tt \times tt$):

	T	t
t	Tt	tt
t	Tt	tt

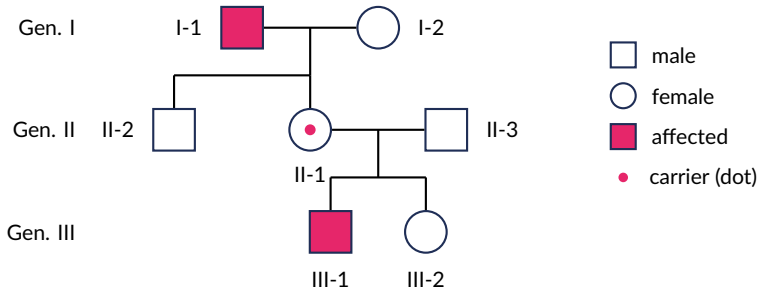
Predicts a $1:1$ ratio, i.e., 25 tall : 25 short of 50 — closely matching the observed $24:26$. A quick chi-square check confirms the fit: $\chi^2 = \frac{(24-25)^2}{25} + \frac{(26-25)^2}{25} = 0.04 + 0.04 = 0.08$, far below the critical value of 3.84 (df$= 1$), so the small deviation is easily explained by chance.

Conclusion: the unknown parent's genotype is Tt (heterozygous).

Pedigree analysis

A **pedigree chart** records the inheritance of a trait through a family, using squares for males, circles for females, filled symbols for affected individuals, horizontal lines connecting mates, and vertical/branching lines connecting parents to offspring. Comparing the pattern of affected/unaffected individuals across generations allows the mode of inheritance to be deduced:

Pattern	Key diagnostic features
Autosomal recessive	Affected individuals often have two *unaffected* (carrier) parents; can "skip" generations; roughly equal numbers of affected males and females.
Autosomal dominant	Every affected individual normally has at least one affected parent (barring a new mutation); does not skip generations; roughly equal numbers of affected males and females.
X-linked recessive	Much more common in males (who need only one copy of the recessive allele on their single X); an affected father cannot pass the trait to any son (sons receive his Y, not his X), but *every* daughter of an affected father becomes at least a carrier; can skip a generation via unaffected carrier daughters, then reappear in their sons.



A three-generation pedigree consistent with X-linked recessive inheritance: an affected father (I-1) has only unaffected children, but his daughter (II-1) is an obligate carrier (dot); her son (III-1), with an unrelated, unaffected husband (II-3), is affected — the trait has "skipped" generation II entirely.

Ví dụ mẫu · Deducing a mode of inheritance from a pedigree

Using the pedigree above, explain why the trait is much more likely to be **X-linked recessive** than **autosomal recessive**.

Key observation: the affected grandfather (I-1) has an affected grandson (III-1) through his *daughter* (II-1, unaffected), while none of I-1's own children are affected, and II-1's husband (II-3) is unrelated and unaffected.

Reasoning. If the gene were X-linked recessive, I-1 (X^aY, affected) passes his single X^a allele to *every* daughter (making II-1 an obligate carrier, X^AX^a) but to *no* son (sons receive his Y chromosome instead) — exactly matching the pattern that only daughters of I-1 carry the allele silently, and it resurfaces only when a carrier daughter's son inherits her X^a (a $\frac{1}{2}$ chance for each son, consistent with III-1 being affected). If the gene were instead autosomal recessive, this specific pattern would require both I-1 and I-2 to be carriers *and* would require the unrelated spouse II-3 to also happen to be a carrier purely by chance for III-1 to be affected — a far less parsimonious explanation than the direct, deterministic X-linked logic. **Conclusion: X-linked recessive inheritance.**

Ví dụ mẫu · An X-linked recessive monohybrid cross: colour blindness

In humans, red-green colour blindness is caused by an X-linked recessive allele (X^b); the dominant allele (X^B) gives normal colour vision. A colour-blind man (X^bY) has children with a woman of normal vision who is a carrier (X^BX^b). Determine the expected proportion of colour-blind offspring among (a) daughters, (b) sons, and (c) all offspring combined.

	X^B	X^b
X^b	X^BX^b	X^bX^b
Y	X^BY	X^bY

The four equally likely offspring genotypes are X^BX^b (carrier daughter, normal vision), X^bX^b (colour-blind daughter), X^BY (normal son), and X^bY (colour-blind son), each with probability $\frac{1}{4}$.

(a) Among daughters (the two daughter genotypes, X^BX^b and X^bX^b, each $\frac{1}{2}$ of daughters): $\frac{1}{2} = 50\%$ of daughters are colour-blind.

(b) Among sons (X^BY and X^bY, each $\frac{1}{2}$ of sons): $\frac{1}{2} = 50\%$ of sons are colour-blind.

(c) Overall: colour-blind offspring $= X^bX^b + X^bY = \frac{1}{4} + \frac{1}{4} = \frac{1}{2} = 50\%$ of all offspring, regardless of sex.

Note: this cross is a useful reminder that although X-linked recessive conditions are usually described as "more common in males" at the *population* level (because males need only one copy to be affected), a specific cross such as this one – an affected father with a carrier mother – can produce colour-blind daughters just as frequently as colour-blind sons.

Codominance and multiple alleles

In **codominance**, both alleles in a heterozygote are *fully* and simultaneously expressed in the phenotype (neither masks the other) — distinct from incomplete dominance, where a heterozygote shows a blended, intermediate phenotype. A gene can also have **multiple alleles** segregating in a population (even though any one diploid individual carries only two). The classic example combining both ideas is the human **ABO blood group**, controlled by three alleles at one locus: I^A and I^B are codominant with each other (both are expressed if present together), and both are dominant to i.

Genotype(s)	Blood type (phenotype)	Note
I^AI^A or I^Ai	A	
I^BI^B or I^Bi	B	
I^AI^B	AB	both antigens expressed – codominance
ii	O	recessive to both I^A and I^B

Epistasis: gene interaction

(HL only) Epistasis occurs when the alleles of one gene mask or modify the phenotypic expression of a different gene at a separate locus (as distinct from dominance, which describes the interaction between two alleles of the *same* gene). A classic example is coat colour in Labrador retrievers, controlled by two interacting genes: the **B gene** (B = black pigment, dominant; b = brown/chocolate pigment) determines *which* pigment is produced, while the separate **E gene** (E = pigment deposited in the coat, dominant; e = no pigment deposited at all) determines *whether* that pigment is deposited in the fur. A dog that is homozygous recessive at the E gene (ee) produces no coat pigment regardless of its genotype at the B gene, and appears **yellow** – the E gene is **epistatic** to the B gene. Crossing two double heterozygotes ($BbEe \times BbEe$)

therefore produces a modified dihybrid ratio of 9 black : 3 brown : 4 yellow (rather than the standard $9:3:3:1$), because the 3 *B_ee* and 1 *bbee* classes are combined into a single yellow phenotypic class.

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(Nội dung sau đây chỉ dành cho chương trình HL.) **Tương tác gen át chế** (epistasis) xảy ra khi alen của MỘT gen che lấp/làm thay đổi sự biểu hiện kiểu hình của một gen KHÁC (khác locus) – khác với tính trội/lặn vốn chỉ mô tả quan hệ giữa hai alen của CÙNG một gen. Ví dụ kinh điển: màu lông chó Labrador do hai gen quyết định – gen B quyết định loại sắc tố (đen trội/nâu lặn), gen E quyết định sắc tố CÓ được lắng đọng vào lông hay không (ee = không lắng đọng sắc tố, lông có màu **vàng** bất kể kiểu gen ở gen B). Gen E được gọi là át chế gen B. Lai hai cá thể dị hợp kép ($BbEe \times BbEe$) cho tỉ lệ kiểu hình 9 đen : 3 nâu : 4 vàng (thay vì $9:3:3:1$ thông thường), do hai lớp *B_ee* và *bbee* gộp chung thành một kiểu hình vàng duy nhất.

The chi-square (χ^2) goodness-of-fit test

When observed offspring counts from a genetic cross do not exactly match the expected Mendelian ratio, a **chi-square goodness-of-fit test** determines whether the deviation is small enough to be explained by ordinary chance sampling, or large enough to be statistically significant (suggesting the proposed ratio/hypothesis is wrong).

Chi-square formula and decision rule.

$$\chi^2 = \sum \frac{(O-E)^2}{E},$$

where O = observed count in a category and E = expected count in that category (based on the hypothesized ratio). **Degrees of freedom**: df = (number of phenotype/genotype categories) $-\,1$.

df	1	2	3
Critical value ($p = 0.05$)	3.84	5.99	7.82

Decision rule: if the calculated χ^2 is **greater than** the critical value, **reject** the null hypothesis H_0 (the observed data deviate significantly from the expected ratio, more than chance alone would explain). If the calculated χ^2 is **less than or equal to** the critical value, **fail to reject** H_0 (the data are consistent with the expected ratio; any deviation is attributable to normal sampling variation).

Ví dụ mẫu · Chi-square test on a dihybrid cross

Mendel self-crossed pea plants heterozygous for two genes (round/wrinkled seed shape, R/r; yellow/green seed colour, Y/y), expecting the classic dihybrid $9:3:3:1$ ratio. Out of 556 offspring, the actual counts observed were: round yellow $= 315$, round green $= 108$, wrinkled yellow $= 101$, wrinkled green $= 32$. Test whether this data set is consistent with the expected $9:3:3:1$ ratio.

Step 1 – expected counts (out of 556, in a $9:3:3:1$ ratio):

$$E_{\text{RY}} = \tfrac{9}{16}(556) = 312.75, \quad E_{\text{RG}} = E_{\text{WY}} = \tfrac{3}{16}(556) = 104.25, \quad E_{\text{WG}} = \tfrac{1}{16}(556) = 34.75.$$

Step 2 – chi-square statistic:

$$\chi^2 = \frac{(315-312.75)^2}{312.75} + \frac{(108-104.25)^2}{104.25} + \frac{(101-104.25)^2}{104.25} + \frac{(32-34.75)^2}{34.75}$$

$$= 0.0162 + 0.1349 + 0.1013 + 0.2176 = 0.47 \text{ (to 2 d.p.)}.$$

Step 3 – degrees of freedom and decision. There are 4 phenotype categories, so $df = 4-1 = 3$; the critical value at $p = 0.05$ is 7.82. Since

$$\chi^2_{\text{calc}} = 0.47 \ll 7.82 = \chi^2_{\text{critical}},$$

we **fail to reject** the null hypothesis. Mendel's observed data are consistent with the expected $9:3:3:1$ dihybrid ratio — the small deviations are readily explained by ordinary sampling variation.

(!) Lỗi thường gặp: Hai lỗi phổ biến nhất khi làm bài χ^2: **(1)** tính SAI bậc tự do – df luôn bằng (số LOẠI kiểu hình/kiểu gen đang so sánh) trừ 1, KHÔNG phải tổng số cá thể trừ 1, và cũng không phải số gen trừ 1. Lai một tính (2 loại kiểu hình) $\rightarrow df = 1$ (giá trị tới hạn 3.84); lai hai tính kiểu $9:3:3:1$ (4 loại kiểu hình) $\rightarrow df = 3$ (giá trị tới hạn 7.82). **(2)** hiểu SAI chiều so sánh – χ^2 tính được LỚN HƠN giá trị tới hạn nghĩa là độ lệch có ý nghĩa thống kê $\rightarrow$ **BÁC BỎ** H_0 (số liệu KHÔNG khớp tỉ lệ kỳ vọng); χ^2 tính được NHỎ HƠN hoặc bằng giá trị tới hạn nghĩa là độ lệch chỉ do ngẫu nhiên $\rightarrow$ **KHÔNG bác bỏ** H_0 (số liệu phù hợp với tỉ lệ kỳ vọng). Nhiều học sinh nhớ ngược chiều so sánh này.

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Từ vựng Mendel cơ bản: **alen** (một phiên bản của gen), **kiểu gen** (tổ hợp alen), **kiểu hình** (biểu hiện quan sát được), **trội/lặn**, **đồng hợp/dị hợp**. Lai một tính dị hợp $\times$ dị hợp cho tỉ lệ $3:1$; lai hai tính dị hợp $\times$ dị hợp (hai gen phân li độc lập) cho tỉ lệ $9:3:3:1$. **Phép lai phân tích** (test cross) dùng để xác định kiểu gen chưa biết của cá thể mang kiểu hình trội, bằng cách lai với cá thể đồng hợp lặn. Phả hệ giúp suy luận kiểu di truyền: lặn trên NST thường thường "bỏ qua" thế hệ (bố mẹ không biểu hiện nhưng đều là người mang gen); di truyền liên kết X lặn phổ biến hơn nhiều ở nam giới, và người bố mắc bệnh không bao giờ truyền cho con trai (chỉ truyền NST Y) nhưng TẤT CẢ con gái của người bố đó đều mang alen lặn (ít nhất là dị hợp). **Đồng trội** (cả hai alen cùng biểu hiện, ví dụ nhóm máu AB) khác với trội không hoàn toàn (kiểu hình trung gian). Kiểm định χ^2 dùng để đánh giá xem số liệu lai thực tế có phù hợp với tỉ lệ Mendel kỳ vọng hay không, dựa vào bậc tự do và giá trị tới hạn.

4.3.3 D3.3 Homeostasis

The negative feedback loop

Homeostasis is the maintenance of a relatively stable internal environment despite external changes, achieved mainly through **negative feedback**: a **receptor** detects a deviation of some variable from its normal **set point** and signals a **coordinator** (control centre), which processes the information and activates one or more **effectors** to bring the variable back toward the set point. As the variable returns to normal, the original stimulus is reduced, and the corrective response is switched off — a self-limiting loop. (Positive feedback, by contrast, *amplifies* a change rather than reversing it, and is used more sparingly in the body — e.g., the LH surge in D3.1 above.)

Thermoregulation

The **hypothalamus** is the body's main thermoregulatory coordinator, receiving input from thermoreceptors in the skin and from receptors monitoring blood temperature directly.

- **Response to overheating**: **vasodilation** of blood vessels near the skin surface increases blood flow to the skin, increasing heat loss by radiation; **sweating** increases evaporative cooling as sweat evaporates from the skin surface, removing heat energy.
- **Response to cold**: **vasoconstriction** of skin blood vessels reduces blood flow to the skin, minimizing heat loss and redirecting blood toward the warmer core; **shivering** (rapid, involuntary skeletal-muscle contraction) generates additional heat as a metabolic byproduct.

Blood glucose regulation

The **islets of Langerhans** in the pancreas contain two key cell types with antagonistic (opposing) hormonal effects on blood glucose:

- **Beta cells** secrete **insulin** when blood glucose rises (e.g., after a meal). Insulin promotes glucose uptake into liver and muscle cells and its conversion to glycogen for storage (**glycogenesis**), lowering blood glucose.
- **Alpha cells** secrete **glucagon** when blood glucose falls (e.g., during fasting). Glucagon promotes the breakdown of stored liver glycogen back into glucose (**glycogenolysis**) and its release into the blood, raising blood glucose.

Together, insulin and glucagon act as a continuous negative feedback system, keeping blood glucose within a narrow homeostatic range.

Diabetes mellitus. **Type 1 diabetes** results from autoimmune destruction of the pancreatic beta cells, so little or no insulin is produced; it usually develops early in life and requires lifelong insulin replacement (injection or pump). **Type 2 diabetes** results from target cells becoming increasingly resistant/less responsive to insulin (insulin resistance), often associated with obesity and inactivity; it typically develops later in life and is initially managed through diet, exercise, and oral medication, sometimes progressing to also require insulin.

Ví dụ mẫu · Interpreting a blood glucose response curve

The table shows blood glucose concentration (mg/dL) at intervals after eating a carbohydrate-rich meal, for a healthy individual and for an individual with untreated Type 1 diabetes.

Time after meal (min)	0	30	60	90	120	180
Healthy individual	90	140	125	100	85	90
Untreated Type 1 diabetic	90	160	195	220	235	238

(a) Describe and explain the healthy individual's curve. Blood glucose rises sharply after the meal as carbohydrates are digested and absorbed, then falls back toward the baseline (≈ 90 mg/dL) by 180 minutes. This fall occurs because rising blood glucose stimulates the pancreatic beta cells to secrete insulin, which promotes glucose uptake into liver and muscle cells (and glycogen synthesis), lowering blood glucose back to its set point – a negative feedback response.

(b) Explain why the diabetic individual's curve looks so different. In untreated Type 1 diabetes, the beta cells have been destroyed and little or no insulin is secreted, so the normal negative feedback response to rising blood glucose is absent. Glucose continues to accumulate in the

blood after the meal instead of being taken up by cells, producing a much higher and still-rising blood glucose concentration even at 180 minutes, rather than returning to baseline.

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Mô hình phản hồi ngược âm chung: **thụ thể** (receptor) phát hiện sự lệch khỏi điểm chuẩn (set point) → **trung khu điều phối** (coordinator, ví dụ vùng dưới đồi) xử lý thông tin → **cơ quan đáp ứng** (effector) tạo phản ứng đưa biến số trở lại điểm chuẩn. **Điều nhiệt**: vùng dưới đồi là trung khu; khi nóng, cơ thể giãn mạch da (vasodilation) và đổ mồ hôi; khi lạnh, co mạch da (vasoconstriction) và run cơ (shivering) sinh nhiệt. **Điều hoà đường huyết**: tế bào beta tuỵ tiết **insulin** khi đường huyết cao (thúc đẩy tế bào hấp thu glucose, tổng hợp glycogen – glycogenesis), tế bào alpha tuỵ tiết **glucagon** khi đường huyết thấp (thúc đẩy phân giải glycogen thành glucose – glycogenolysis). **Đái tháo đường type 1** do hệ miễn dịch phá huỷ tế bào beta (thiếu insulin, cần tiêm insulin suốt đời); **type 2** do tế bào đích giảm đáp ứng với insulin (kháng insulin, thường liên quan béo phì/lối sống).

4.4 D4 Ecosystems: Natural Selection, Stability and Climate

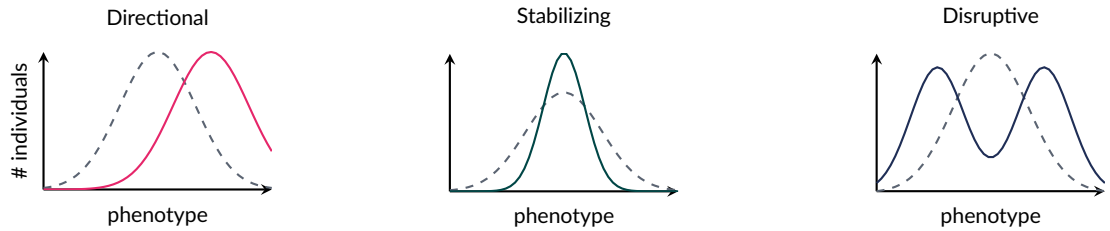
4.4.1 D4.1 Natural Selection

Mechanism of natural selection, recap

Natural selection requires **heritable variation** within a population; when a **selection pressure** (e.g., predation, disease, competition, a changing environment) causes individuals with certain heritable traits to survive and reproduce more successfully than others, those traits become more common in the next generation. Repeated over many generations, this produces a **change in allele frequencies** in the population – the modern, precise definition of evolution.

Patterns of selection

Directional selection favours one phenotypic extreme, shifting the population mean toward it (e.g., dark-coloured peppered moths becoming more common as pollution darkened tree bark). **Stabilizing selection** favours the intermediate phenotype and selects against both extremes, reducing variance around an unchanged mean (e.g., human birth weight near the population average has the lowest mortality). **Disruptive selection** favours *both* extremes over the intermediate phenotype, increasing variance and potentially producing two distinct phenotype peaks (e.g., seed-cracking finches with either very small or very large bills outcompeting birds with intermediate bill size).



Effect of three patterns of natural selection on a normally-distributed phenotype (grey dashed curve = distribution before selection; solid coloured curve = after several generations of selection). **Directional** selection shifts the mean toward one extreme. **Stabilizing** selection favours the intermediate phenotype, narrowing variance around an unchanged mean. **Disruptive** selection favours both extremes over the intermediate, producing two phenotype peaks.

The Hardy–Weinberg principle

The **Hardy–Weinberg model** describes a theoretical population whose allele and genotype frequencies do *not* change from one generation to the next – i.e., a population that is **not evolving** at the locus considered. It requires **all five** of the following assumptions to hold:

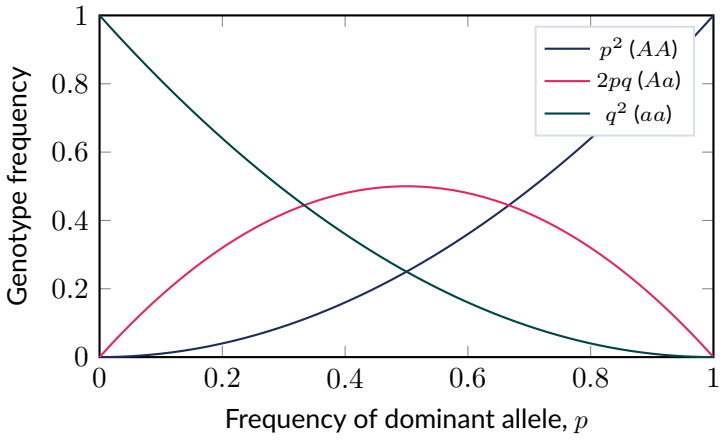
1. No mutation (allele sequences do not change).
2. No gene flow (no individuals, and their alleles, enter or leave the population).
3. Infinitely large population (no genetic drift / no random sampling error).
4. Random mating (no mate choice based on genotype).
5. No natural selection (all genotypes have equal survival and reproductive success).

Real populations are compared against Hardy–Weinberg expectations as a **null model**: if a population's observed genotype frequencies deviate substantially from Hardy–Weinberg proportions, this is evidence that the population is evolving – i.e., that natural selection, or another evolutionary force (mutation, gene flow, genetic drift, or non-random mating), is acting on that locus.

Hardy–Weinberg equations. For a two-allele locus with $p =$ frequency of the dominant allele and $q =$ frequency of the recessive allele:

$$p + q = 1, \qquad p^2 + 2pq + q^2 = 1,$$

where $p^2 =$ frequency of the homozygous dominant genotype, $2pq =$ frequency of the heterozygous genotype, and $q^2 =$ frequency of the homozygous recessive genotype (which equals the frequency of the recessive *phenotype*, since only aa individuals display it under complete dominance).



Hardy–Weinberg genotype frequencies as a function of the dominant allele frequency p (with $q = 1 - p$). The heterozygote curve $2pq$ peaks at $p = q = 0.5$; the two homozygote curves dominate near the extremes. Note that a dominant allele can still be the *rarer* of the two alleles – dominance and allele frequency are independent properties.

Ví dụ mẫu · Hardy–Weinberg allele and genotype frequency calculation

In a population of $5{,}000$ people, a recessive metabolic disorder occurs in 1% of individuals. Assuming Hardy–Weinberg equilibrium, find p, q, the genotype frequencies, and the expected number of people with each genotype.

Step 1 – identify q^2. Only homozygous recessive individuals show the disorder:

$$q^2 = 0.01.$$

Step 2 – solve for q, then p.

$$q = \sqrt{0.01} = 0.10, \qquad p = 1 - q = 1 - 0.10 = 0.90.$$

Step 3 – genotype frequencies.

$$p^2 = (0.90)^2 = 0.81, \qquad 2pq = 2(0.90)(0.10) = 0.18, \qquad q^2 = (0.10)^2 = 0.01.$$

Check: $0.81 + 0.18 + 0.01 = 1.00$. ✓

Step 4 – expected numbers in a population of $5{,}000$.

Homozygous dominant: $0.81 \times 5000 = 4050$, Heterozygous carriers: $0.18 \times 5000 = 900$,

Homozygous recessive (affected): $0.01 \times 5000 = 50$.

Check: $4050 + 900 + 50 = 5000$. ✓ Notably, 900 people (18% of the population) are unaffected heterozygous carriers of the disorder allele – far more than the 50 people who actually show the disorder.

(!) Lỗi thường gặp: Một ngộ nhận phổ biến: cho rằng alen **trội** chắc chắn **phổ biến hơn** trong quần thể, còn alen **lặn** chắc chắn **hiếm hơn**. ĐÂY LÀ SAI. Tính trội/lặn chỉ mô tả cách một alen biểu hiện ra kiểu hình khi có mặt alen kia (quan hệ "che lấp"), hoàn toàn ĐỘC LẬP với việc alen đó phổ biến hay hiếm trong quần thể – tần số alen do các yếu tố tiến hoá (đột biến, di nhập gen, biến động di truyền, chọn lọc tự nhiên) quyết định qua thời gian, không liên quan gì đến trội/lặn. Ví dụ kinh điển: alen gây bệnh Huntington ở người là alen TRỘI nhưng lại RẤT HIẾM trong quần thể. Trong các bài Hardy–Weinberg, hoàn toàn có thể gặp trường hợp q (tần số alen lặn) LỚN HƠN p (tần số alen trội).

Ví dụ mẫu · Detecting selection from a change in allele frequency across generations

In a population of $1{,}000$ beetles, a recessive allele a causes a metabolic disorder. In generation 1, the allele frequency is measured directly: $q_1 = 0.20$. Ten years later (generation 2), a new sample finds that only 1% of the population now shows the recessive (aa) phenotype.

Step 1 – genotype frequencies in generation 1 (assuming Hardy–Weinberg equilibrium held at that time): $p_1 = 1 - 0.20 = 0.80$, so

$$p_1^2 = 0.64\,(AA), \qquad 2p_1q_1 = 2(0.80)(0.20) = 0.32\,(Aa), \qquad q_1^2 = (0.20)^2 = 0.04\,(aa,\ 4\%\ \text{affected}).$$

Step 2 – allele frequency in generation 2. Only 1% show the recessive phenotype:

$$q_2^2 = 0.01 \ \Rightarrow\ q_2 = \sqrt{0.01} = 0.10, \qquad p_2 = 1 - 0.10 = 0.90.$$

Step 3 – calculate the change in allele frequency.

$$\Delta q = q_2 - q_1 = 0.10 - 0.20 = -0.10,$$

i.e., the recessive allele frequency has **halved** in a single generation.

Step 4 – interpret. Assuming no mutation, migration, or genetic drift (the population is reasonably large), such a large, directional shift in allele frequency within a single generation is far more than random sampling would typically produce, and strongly suggests that **natural selection** is acting against the recessive phenotype (e.g., individuals with the metabolic disorder may survive or reproduce less successfully). The "no selection" assumption of Hardy–Weinberg equilibrium is being violated, and the population is evolving at this locus.

VN **GIẢI THÍCH TIẾNG VIỆT**

Định luật Hardy–Weinberg mô tả một quần thể lý tưởng KHÔNG tiến hoá, cần thoả cả 5 điều kiện: không đột biến, không di nhập gen, quần thể vô hạn lớn (không có biến động di truyền ngẫu nhiên), giao phối ngẫu nhiên, và không có chọn lọc tự nhiên. Hai phương trình cốt lõi: $p + q = 1$ và $p^2 + 2pq + q^2 = 1$. Quy trình giải: (1) xác định q^2 từ tần số kiểu hình lặn quan sát; (2) lấy căn bậc hai ra q; (3) tính $p = 1 - q$; (4) tính p^2, $2pq$, q^2 và nhân với kích thước quần thể nếu cần số lượng cá thể. Khi tần số kiểu gen QUAN SÁT lệch đáng kể so với tần số KỲ VỌNG theo Hardy–Weinberg, đó là bằng chứng cho thấy quần thể đang chịu tác động của chọn lọc tự nhiên hoặc một nhân tố tiến hoá khác.

4.4.2 D4.2 Stability and Change

Resilience and resistance

Resistance is an ecosystem's ability to *withstand* a disturbance without changing significantly in the first place. **Resilience** is an ecosystem's ability to *recover* its original structure and function *after* being disturbed/changed. An ecosystem can be high in one property but low in the other – e.g., a system that resists small, frequent disturbances well may nonetheless recover slowly from a rare, severe one, or vice versa.

Ecological succession

Succession is the gradual, directional change in the species composition of a community over time.

- **Primary succession** begins on a newly exposed substrate that has *no* pre-existing soil or organisms (e.g., bare rock exposed by a retreating glacier, or a new volcanic lava flow). **Pioneer species** (such as lichens and mosses), tolerant of harsh conditions, colonize first and gradually break down rock and accumulate organic matter, forming a thin soil that allows less hardy, more complex species to colonize in turn.
- **Secondary succession** follows a disturbance (fire, storm, agricultural abandonment) to an area where soil (and often a seed bank) already exists. Because soil and some organisms typically survive the disturbance, secondary succession usually proceeds much *faster* than primary succession.

In both types, species diversity and community complexity (e.g., number of trophic levels, complexity of feeding relationships) typically increase over successional time, tending toward a comparatively stable **climax community** – though modern ecology recognizes that many "climax" communities are themselves dynamic and shaped by ongoing small-scale disturbance, rather than a truly permanent fixed endpoint.

Disturbance, biodiversity, and stability

Greater biodiversity and more complex, interconnected food webs generally tend to increase an ecosystem's **resilience**, because a greater variety of species provides more alternative pathways for energy and nutrient flow and more **functional redundancy** (multiple species capable of performing a similar ecological role, so the loss of any one species is less likely to collapse the whole system). The relationship between disturbance and biodiversity is nonetheless context-dependent: very frequent or severe disturbance tends to reduce diversity (few species can tolerate it), while a complete absence of disturbance can also reduce diversity (competitively dominant species may exclude others over time) – moderate, intermediate levels of disturbance sometimes support the highest diversity by preventing any single species from dominating indefinitely.

VN **GIẢI THÍCH TIẾNG VIỆT**

Độ chống chịu (resistance) là khả năng hệ sinh thái KHÔNG thay đổi nhiều khi gặp nhiễu loạn; **độ đàn hồi/phục hồi** (resilience) là khả năng hệ sinh thái QUAY TRỞ LẠI trạng thái ban đầu SAU khi bị nhiễu loạn – đây là hai khái niệm khác nhau. **Diễn thế nguyên sinh** (primary succession) bắt đầu từ nền chưa từng có sự sống (đá trần, dung nham mới) với loài tiên phong (địa y, rêu) hình thành đất theo thời gian; **diễn thế thứ sinh** (secondary succession) xảy ra sau nhiễu loạn tại nơi đã có sẵn đất/ngân hàng hạt giống, nên diễn ra nhanh hơn nhiều. Độ đa dạng sinh học và độ phức tạp của quần xã thường tăng dần qua các giai đoạn diễn thế, hướng tới một **quần xã đỉnh cực** (climax community) tương đối ổn định. Đa dạng sinh học cao và lưới thức ăn phức tạp thường làm tăng độ đàn hồi của hệ sinh thái nhờ có nhiều loài dự phòng chức năng cho nhau.

4.4.3 D4.3 Climate Change

The greenhouse effect

Incoming short-wavelength solar radiation (visible and ultraviolet light) passes through the atmosphere largely unimpeded and is absorbed by Earth's surface, which warms and re-emits energy as longer-wavelength **infrared radiation**. Certain atmospheric gases – **greenhouse gases** – absorb this outgoing infrared radiation and re-emit it in all directions, including back down toward the surface, trapping heat within the lower atmosphere. This natural **greenhouse effect** is essential for maintaining Earth's habitable surface temperature; the concern with anthropogenic climate change is that rapidly rising greenhouse gas concentrations are **enhancing** this natural effect, trapping more heat than before and warming the planet.

Major greenhouse gases.

Gas	Notes on sources / contribution
CO_2 (carbon dioxide)	The largest anthropogenic contributor by mass and atmospheric persistence; sources: fossil fuel combustion, deforestation/land-use change, cement production.
CH_4 (methane)	Sources: livestock digestion (enteric fermentation), rice paddies, landfills, natural gas leakage. Far more potent per molecule than CO_2, but breaks down in the atmosphere much faster.
Water vapour (H_2O)	The largest greenhouse gas by natural concentration/effect, but acts mainly as a **feedback** rather than a direct driver: a warmer atmosphere holds more water vapour, which traps more heat, warming the atmosphere further (a positive feedback loop amplifying warming from other gases).
N_2O (nitrous oxide)	Sources: nitrogen-based agricultural fertilizer use, combustion. Long-lived and potent per molecule.

Evidence for anthropogenic climate change

Three independent lines of evidence converge to show that recent climate change is driven by human activity: **(1) Direct atmospheric CO_2 records** (continuous monitoring since 1958, the "Keeling Curve") show atmospheric CO_2 rising steadily, closely tracking the rate of global fossil fuel combustion. **(2) Ice-core data** (gas bubbles trapped in ancient polar ice, extending the record back roughly $800{,}000$ years) show that current CO_2 concentrations far exceed the entire natural range of at least the last $800{,}000$ years. **(3) Instrumental global temperature records** (since roughly 1880) show a clear warming trend that closely tracks the rise in greenhouse gas concentrations, with warming accelerating markedly since the mid-20th century.

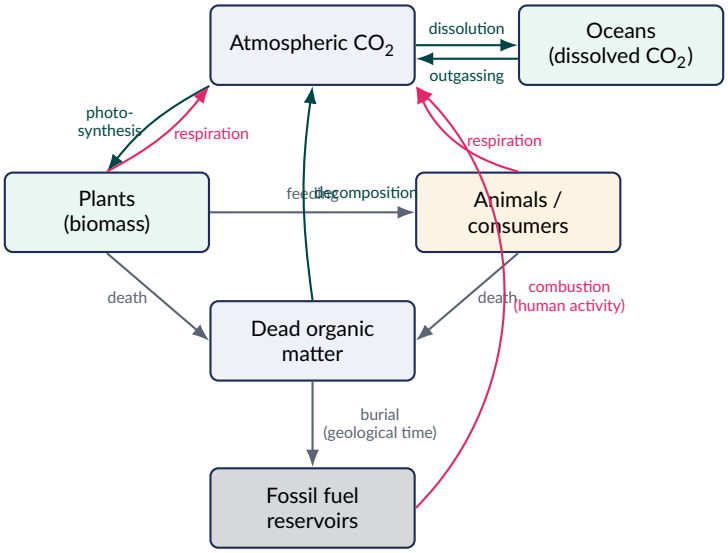
Consequences for ecosystems

Range shifts: many species are shifting their geographic distribution poleward or to higher elevations as they track the climatic conditions to which they are adapted. **Phenology changes**: the timing of seasonal biological events (flowering, breeding, migration) is shifting earlier in many species, which can create a **mismatch** between interacting species (e.g., a pollinator emerging after its preferred flower has already bloomed). **Coral bleaching**: thermal stress causes corals to expel their symbiotic photosynthetic algae (zooxanthellae), which provide the coral's colour and most of its energy; prolonged bleaching can lead to coral death. **Ocean acidification**: rising atmospheric CO_2 dissolves into the oceans, forming carbonic acid and lowering seawater pH; this reduces the availability of carbonate ions needed by corals, molluscs, and some plankton to build calcium carbonate shells and skeletons.

The carbon cycle as the mechanistic link

The **carbon cycle** describes the continuous movement of carbon between the atmosphere, living organisms, and long-term reservoirs, via four key fluxes: **photosynthesis** (removes atmospheric CO_2, fixes carbon into organic molecules in plants/algae), **respiration** (returns CO_2 to the atmosphere as organisms break down organic molecules for energy), **decomposition** (decomposers break down dead organic matter, releasing CO_2, generally more slowly than respiration by living organisms), and **combustion** (rapidly oxidizes organic matter or fossil fuels, releasing CO_2 almost instantly). Major carbon **sinks/reservoirs** include the **oceans** (which hold far more carbon, mostly as dissolved inorganic carbon, than the atmosphere), **forests and soils** (carbon stored in living biomass and organic matter), and **fossil fuel deposits** (carbon

removed from active circulation and sequestered underground over millions of years of geological burial). The mechanistic link between human activity and rising atmospheric CO_2 is a fundamental **imbalance of rates**: fossil fuel combustion releases ancient, long-sequestered carbon into the atmosphere within seconds, vastly faster than the slow geological processes that originally stored it, and faster than natural sinks can currently reabsorb it.



The carbon cycle. Photosynthesis and dissolution remove CO_2 from the atmosphere; respiration, decomposition, and outgassing return it. **Combustion** of fossil fuels (highlighted) releases carbon that natural burial had sequestered underground over geological time, at a rate far exceeding natural removal – the core mechanistic driver of rising atmospheric CO_2.

VN **GIẢI THÍCH TIẾNG VIỆT**

Hiệu ứng nhà kính: bức xạ sóng ngắn từ Mặt Trời xuyên qua khí quyển, được bề mặt Trái Đất hấp thụ rồi phát xạ lại dưới dạng bức xạ hồng ngoại (sóng dài); các **khí nhà kính** (CO_2, CH_4, hơi nước, N_2O) hấp thụ và phát xạ lại bức xạ hồng ngoại này theo mọi hướng, giữ nhiệt lại trong khí quyển thấp. Bằng chứng biến đổi khí hậu do con người: số liệu đo trực tiếp nồng độ CO_2 khí quyển tăng liên tục kể từ 1958 (đường cong Keeling), dữ liệu lõi băng cho thấy nồng độ CO_2 hiện tại vượt xa biên độ tự nhiên trong khoảng $800{,}000$ năm qua, và số liệu nhiệt độ toàn cầu cho thấy xu hướng ấm lên rõ rệt, tăng tốc từ giữa thế kỷ 20. Hậu quả với hệ sinh thái: dịch chuyển vùng phân bố loài, thay đổi thời điểm các sự kiện theo mùa (ra hoa, sinh sản, di cư), tẩy trắng san hô, và acid hoá đại dương (CO_2 hoà tan tạo acid carbonic, giảm pH nước biển). **Chu trình carbon** là mối liên hệ cơ chế trực tiếp: đốt nhiên liệu hoá thạch giải phóng carbon đã bị chôn vùi hàng triệu năm với tốc độ nhanh hơn rất nhiều so với tốc độ các bể chứa tự nhiên (đại dương, rừng) có thể hấp thụ lại.

4.5 Theme D Practice Bank

Bài tập luyện tập

During DNA replication, which enzyme synthesizes a short RNA sequence that provides DNA polymerase with the free $3'$-OH group it needs to begin adding nucleotides?

(A) Helicase
(B) Ligase
(C) Primase
(D) DNA polymerase

Lời giải chi tiết

DNA polymerase cannot initiate a new strand from scratch; it can only extend an existing $3'$-OH end. Primase lays down a short RNA primer to provide that starting point. **(C)**.

Bài tập luyện tập

At a single replication fork, one new strand is synthesized continuously while the other is synthesized as a series of short fragments joined together afterward. This difference occurs because:

(A) The two template strands are antiparallel, and DNA polymerase can only synthesize in the $5' \to 3'$ direction

(B) One strand is transcribed while the other is replicated

(C) Helicase only unwinds one of the two strands

(D) DNA ligase only recognizes one of the two template strands

Lời giải chi tiết

Because the template strands run in opposite directions and DNA polymerase always synthesizes $5' \to 3'$, the strand whose template is oriented so synthesis runs *toward* the fork (leading strand) can be made continuously, while the other (lagging strand) must be made in short fragments running away from the fork. **(A)**.

Bài tập luyện tập

The coding (non-template) strand of a short gene reads $5'$-ATG CAC TGG TAA-$3'$. (a) Write the sequence of the template strand. (b) Write the mRNA sequence transcribed from this gene. (c) Explain the relationship between the coding-strand sequence and the mRNA sequence.

Lời giải chi tiết

(a) The template strand is complementary and antiparallel to the coding strand: $3'$-TAC GTG ACC ATT-$5'$.
(b) mRNA is synthesized from the template strand and is therefore identical in sequence to the coding strand, except U replaces T: $5'$-AUG CAC UGG UAA-$3'$.
(c) The coding strand and the mRNA have the same sequence (reading in the same $5' \to 3'$ direction) because both are independently complementary to the template strand; however, mRNA is not directly copied from the coding strand – RNA polymerase physically reads only the template strand.

Bài tập luyện tập

If a mutation disables DNA polymerase's proofreading function (but not its ability to add nucleotides), what is the most likely consequence for the genome over subsequent replication cycles?

(A) Replication will stop completely

(B) The mutation rate in newly replicated DNA will increase

(C) Only the leading strand will be affected

(D) The genetic code itself will change

Lời giải chi tiết

Proofreading is what corrects most misincorporated bases during replication. Without it, more incorrect bases will persist uncorrected, raising the overall mutation rate. **(B)**.

Bài tập luyện tập

Explain one structural difference between prokaryotic and eukaryotic cells that allows ribosomes to begin translating a prokaryotic mRNA molecule before its transcription is even complete, whereas this cannot happen in eukaryotes.

Lời giải chi tiết

Prokaryotes lack a nucleus, so transcription and translation both occur in the cytoplasm and can be physically coupled: ribosomes can attach to and begin translating the $5'$ end of an mRNA while RNA polymerase is still transcribing further downstream. Eukaryotic transcription occurs inside the nucleus, and the pre-mRNA must first be processed (splicing, capping, addition of a poly-A tail) and exported through nuclear pores into the cytoplasm before any ribosome can access it, so translation cannot begin until transcription and processing are complete.

Bài tập luyện tập

A coding sequence normally reads (mRNA) `AUG–GAA–UGU–UAG` (Met–Glu–Cys–Stop). Using the codon table from this chapter, classify each altered sequence: (a) `AUG–GAG–UGU–UAG`; (b) `AUG–GCA–UGU–UAG`; (c) `AUG–UAA–UGU–UAG`.

Lời giải chi tiết

(a) GAA→GAG: both code for glutamic acid (Glu) ⇒ **silent mutation** (protein unchanged).
(b) GAA→GCA: Glu→Ala, a different amino acid ⇒ **missense mutation**.
(c) GAA→UAA: Glu→Stop ⇒ **nonsense mutation** – translation terminates immediately after the start codon, producing only a single-amino-acid fragment (Met) instead of the full protein.

Bài tập luyện tập

(a) Briefly explain how the guide RNA and Cas9 protein work together to edit a specific DNA sequence in the CRISPR-Cas9 system. (b) State one ethical concern associated with editing human germline cells (embryos) rather than somatic cells.

Lời giải chi tiết

(a) The guide RNA has a sequence complementary to the target DNA sequence; it binds Cas9 and directs the Cas9–gRNA complex to that specific sequence by base pairing. Cas9 then cuts both DNA strands at that site, and the cell's repair machinery (potentially guided by a supplied repair template) disables or corrects the target gene.
(b) Germline edits would be inherited by all future offspring of the edited individual, raising concerns such as: future generations cannot consent to the edit; unintended off-target mutations could be passed on indefinitely; and unequal access to the technology could create new forms of social inequality. (Any one well-explained concern is acceptable.)

Bài tập luyện tập

A cell that has sustained DNA damage is normally halted at a cell-cycle checkpoint before proceeding further. Which checkpoint most directly prevents a cell with damaged DNA from beginning DNA replication?

(A) G_2/M checkpoint
(B) Spindle-assembly (metaphase) checkpoint
(C) G_1/S checkpoint
(D) Cytokinesis checkpoint

Lời giải chi tiết

The G_1/S checkpoint occurs before S phase (DNA replication), and checks for conditions including DNA integrity before allowing the cell to proceed to replicate its genome. **(C)**.

Bài tập luyện tập

A student examines a root-tip squash and counts 1000 cells in total, classified by stage:

Stage	Interphase	Prophase	Metaphase	Anaphase	Telophase
Cell count	760	90	30	25	95

If the total cell cycle length is 20 hours, calculate: (a) the mitotic index; (b) the total time spent in mitosis; (c) the time spent specifically in prophase.

Lời giải chi tiết

(a) Mitotic index $= \dfrac{90+30+25+95}{1000} = \dfrac{240}{1000} = 0.24 = 24\%$.
(b) Time in mitosis $= 0.24 \times 20$ h $= 4.8$ h $= 288$ minutes.
(c) Prophase fraction of mitotic cells $= 90/240 = 0.375 = 37.5\%$; time in prophase $= 0.375 \times 4.8$ h $= 1.8$ h $= 108$ minutes.

Bài tập luyện tập

Sister chromatids are joined together at a specialized, constricted chromosomal region called the:

(A) Centriole
(B) Kinetochore
(C) Centromere
(D) Chromatid junction

Lời giải chi tiết

The centromere is the constricted region joining sister chromatids; spindle fibres attach at kinetochore protein complexes assembled on the centromere, but the constriction itself is the centromere. **(C)**.

Bài tập luyện tập

Distinguish between a benign and a malignant tumour, and explain why loss of function of a tumour-suppressor gene such as $p53$ can contribute to tumour formation.

Lời giải chi tiết

A benign tumour grows locally and does not invade surrounding tissue or spread elsewhere. A malignant tumour invades neighbouring tissue and can metastasize (spread via the blood or lymphatic system to other parts of the body), which is what makes cancer potentially life-threatening. Tumour-suppressor genes such as $p53$ normally halt the cell cycle or trigger apoptosis (programmed cell death) in cells with damaged DNA. If $p53$ itself loses function through mutation, damaged cells are no longer arrested or eliminated and can continue dividing, accumulating further mutations and potentially forming a tumour.

Bài tập luyện tập

(HL) In the *lac* operon of *E. coli*, when lactose is absent from the environment, which of the following occurs?

(A) The repressor protein binds the operator, blocking transcription of the lactose-digesting genes

(B) RNA polymerase transcribes the structural genes continuously

(C) The operator sequence is deleted from the genome

(D) Transcription factors bind enhancer sequences to activate the operon

Lời giải chi tiết

Without lactose (or a lactose derivative) to bind and inactivate it, the repressor protein remains bound to the operator, physically blocking RNA polymerase from transcribing the lactose-digesting genes – the operon is repressed. **(A)**.

Bài tập luyện tập

(HL) Identical twins share 100% identical DNA sequence at birth, yet as adults can show measurable differences in which genes are actively expressed in their cells. Explain how this is possible, referring to epigenetics.

Lời giải chi tiết

Although the twins' DNA sequences remain identical, they experience different environmental exposures over their lifetimes (diet, stress, toxin exposure, etc.), which can alter epigenetic marks such as DNA methylation patterns and histone modifications at specific genes. These marks change chromatin accessibility and gene expression without altering the underlying DNA sequence, so over time the twins can accumulate different, individually acquired gene-expression patterns despite sharing the same genome.

Bài tập luyện tập

Cell P has a water potential of -200 kPa. Cell Q, in direct contact with Cell P, has a water potential of -350 kPa. State and explain the direction of net water movement between the two cells.

Lời giải chi tiết

Net movement is from Cell P to Cell Q. Water always moves from a region of higher (less negative) water potential to a region of lower (more negative) water potential; Cell P's water

potential (-200 kPa) is higher than Cell Q's (-350 kPa), so water moves down this gradient from P to Q.

Bài tập luyện tập

A population of aphids reproduces asexually via parthenogenesis for several generations before switching to sexual reproduction. Compared with the sexually produced generation, the asexually produced generations are expected to show:

(A) Greater genetic variation among individuals

(B) Less genetic variation among individuals, since offspring are genetically identical to the parent

(C) Exactly the same genetic variation, since both processes use meiosis

(D) A chromosome number reduced by half

Lời giải chi tiết

Asexual reproduction (by mitosis) produces offspring that are clones of the parent, so a population produced this way has much less genetic variation than one produced sexually, which combines alleles from two parents via meiosis and fertilization. **(B)**.

Bài tập luyện tập

State and briefly explain two distinct events during meiosis that each generate genetic variation among the resulting gametes.

Lời giải chi tiết

Crossing over: during prophase I, non-sister chromatids of homologous chromosomes exchange segments of DNA, creating new combinations of alleles on individual chromosomes that were not present in either original parental chromosome.
Independent assortment: during metaphase I, each pair of homologous chromosomes orients randomly and independently of every other pair, so the particular combination of maternal and paternal chromosomes distributed to a given gamete is random and differs each time meiosis occurs.

Bài tập luyện tập

The table below shows relative hormone levels across the human menstrual cycle.

Day	FSH	LH	Oestrogen	Progesterone
1	Rising	Low	Low	Low
7	Moderate, falling	Low	Rising	Low
14	Low	**Peak (surge)**	**Peak**	Low, starting to rise
21	Low	Low	Moderate	**Peak**
28	Low, rising	Low	Falling	Falling sharply

(a) Identify the day on which ovulation most likely occurs, and name the hormone that directly triggers it. (b) Explain why oestrogen reaches a peak just before day 14. (c) Explain why progesterone falls sharply by day 28 if fertilization has not occurred, and state the consequence of this fall.

Lời giải chi tiết

(a) Ovulation occurs around **day 14**, directly triggered by the **LH surge**.
(b) The maturing ovarian follicle secretes increasing amounts of oestrogen throughout the follicular phase. This sustained high oestrogen level switches from negative to positive feedback on the hypothalamus/pituitary, which is what triggers the LH surge that causes ovulation.
(c) After ovulation, the ruptured follicle becomes the corpus luteum, which secretes progesterone to maintain the endometrium. Without fertilization/implantation there is no signal to sustain the corpus luteum, so it degenerates and progesterone (and oestrogen) fall sharply. This hormone withdrawal causes the endometrium to break down and be shed (menstruation), and releases the pituitary from negative feedback, allowing FSH to rise again and start a new cycle.

Bài tập luyện tập

In pea plants, tall (T) is dominant to dwarf (t). Two heterozygous tall plants ($Tt \times Tt$) are crossed. What is the probability that a randomly chosen offspring is dwarf?

(A) 0
(B) $1/4$
(C) $1/2$
(D) $3/4$

Lời giải chi tiết

$Tt \times Tt$ gives genotype ratio $1\,TT : 2\,Tt : 1\,tt$. Only tt (dwarf) individuals show the recessive phenotype, so the probability is $1/4$. **(B)**.

Bài tập luyện tập

A pea plant heterozygous for both seed shape and seed colour ($RrYy$, round yellow) is crossed with a plant of unknown genotype for the same two genes. The offspring are: round yellow $= 90$, round green $= 91$, wrinkled yellow $= 0$, wrinkled green $= 0$ (total 181). Determine the unknown parent's genotype and phenotype.

Lời giải chi tiết

Shape gene: no wrinkled offspring at all (0%), even though the known parent is Rr (can contribute r). If the unknown parent were Rr, roughly 25% of offspring would be wrinkled (rr) – not observed. The unknown parent must be homozygous RR, so every offspring receives at least one R and is round.
Colour gene: yellow:green offspring $\approx 90 : 91 \approx 1 : 1$. Since the known parent is Yy (contributes Y or y equally), a $1 : 1$ ratio only arises if the unknown parent contributes only y, i.e., the unknown parent is homozygous yy.
Conclusion: the unknown parent's genotype is $RRyy$ (phenotype: round, green).

Bài tập luyện tập

A father with blood type B and a mother with blood type A have a child with blood type O. Which best describes the parents' genotypes?

(A) Father I^BI^B, mother I^AI^A
(B) Father I^Bi, mother I^Ai
(C) Father ii, mother ii
(D) Father I^BI^B, mother I^Ai

Lời giải chi tiết

For the child to be genotype ii (blood type O), it must inherit one i allele from each parent. This is only possible if both parents carry a recessive i allele – i.e., are heterozygous I^Bi (type B) and I^Ai (type A). If either parent were homozygous (I^BI^B or I^AI^A), they could not pass on an i allele, and an O-type child would be impossible. **(B)**.

Bài tập luyện tập

In a family pedigree, two phenotypically unaffected parents have a daughter who is affected by a recessive disorder. Explain why this observation alone is sufficient to rule out X-linked recessive inheritance for this disorder, and state the mode of inheritance that must apply instead.

Lời giải chi tiết

Under X-linked recessive inheritance, an affected female must be homozygous (X^aX^a), inheriting an X^a allele from *both* parents, including her father. But a father who donates an X^a allele to a daughter must himself be X^aY – i.e., affected. Since the father here is stated to be unaffected, he cannot supply an X^a allele, so an affected, X-linked-recessive daughter from two unaffected parents is impossible. The disorder must instead be **autosomal recessive**, where both unaffected parents are heterozygous carriers ($Aa \times Aa$), each contributing one recessive allele to produce an affected aa child of either sex.

Bài tập luyện tập

In a genetics experiment, 200 offspring from a monohybrid cross expected to show a $3:1$ ratio of tall to dwarf pea plants are counted: 130 tall and 70 dwarf. Using a chi-square goodness-of-fit test (critical value at $p = 0.05$, $df = 1$ is 3.84), determine whether these results are consistent with the expected $3:1$ ratio.

Lời giải chi tiết

Expected counts (out of 200, in a $3:1$ ratio): 150 tall, 50 dwarf.

$$\chi^2 = \frac{(130-150)^2}{150} + \frac{(70-50)^2}{50} = \frac{400}{150} + \frac{400}{50} = 2.67 + 8.00 = 10.67.$$

There are 2 phenotype categories, so $df = 1$; critical value $= 3.84$. Since $\chi^2_{\text{calc}} = 10.67 > 3.84$, we **reject** the null hypothesis: the observed data deviate significantly from the expected $3:1$ ratio (something other than simple Mendelian segregation, or a bias in the data, appears to be occurring).

Bài tập luyện tập

Using the terms receptor, coordinator, and effector, describe the sequence of events that occurs when the body's core temperature drops below its normal set point.

Lời giải chi tiết

Thermoreceptors (**receptor**) in the skin and hypothalamus detect the fall in temperature and relay this information to the hypothalamus (**coordinator**), which compares the detected temperature to the internal set point and, on detecting a deviation, signals **effectors**: skin arteri-

oles undergo vasoconstriction, reducing blood flow to the skin and so reducing heat loss by radiation, while skeletal muscles begin shivering, generating heat as a byproduct of rapid involuntary contraction. These responses raise body temperature back toward the set point; once restored, the original stimulus (low temperature) is removed and the corrective response switches off – a self-limiting negative feedback loop.

Bài tập luyện tập

Within a beetle population, individuals with either very light or very dark shell colouration are more likely to be eaten by birds than individuals with intermediate, mottled colouration. Over several generations, the range of shell colours in the population narrows around the intermediate phenotype. This is an example of:

(A) Directional selection
(B) Disruptive selection
(C) Stabilizing selection
(D) Genetic drift

Lời giải chi tiết

Both phenotypic extremes are selected against and the intermediate phenotype is favoured, narrowing variance around an unchanged mean – the definition of stabilizing selection. **(C)**.

Bài tập luyện tập

In a population of $2{,}000$ people, a recessive metabolic disorder occurs in 4% of individuals. Assuming Hardy–Weinberg equilibrium, calculate the allele frequencies and the expected number of individuals with each genotype.

Lời giải chi tiết

$q^2 = 0.04 \Rightarrow q = \sqrt{0.04} = 0.20$; $p = 1 - 0.20 = 0.80$.

$$p^2 = (0.80)^2 = 0.64, \qquad 2pq = 2(0.80)(0.20) = 0.32, \qquad q^2 = 0.04.$$

Expected numbers (of $2{,}000$): homozygous dominant $= 0.64 \times 2000 = 1280$; heterozygous carriers $= 0.32 \times 2000 = 640$; homozygous recessive (affected) $= 0.04 \times 2000 = 80$. Check: $1280 + 640 + 80 = 2000$. ✓

Bài tập luyện tập

A population of endangered rhinoceroses is reduced from several thousand individuals to only 15 survivors after a period of intense poaching. Which Hardy–Weinberg assumption is most directly violated by this event, making the population more susceptible to further evolutionary change?

(A) No mutation
(B) No natural selection
(C) Infinitely large population size (no genetic drift)
(D) Random mating

Lời giải chi tiết

A drastic reduction to a very small population size introduces strong genetic drift – random, chance fluctuation in allele frequencies – directly violating the "infinitely large population" assumption. **(C)**.

Bài tập luyện tập

A volcanic island's bare lava field is surveyed for the number of species present at intervals after an eruption:

Years since eruption	0	10	50	100	200	500
Number of species	0	3	15	40	85	120

Describe the trend shown, name the type of succession illustrated, and explain the ecological mechanism that allows species richness to increase over this time.

Lời giải chi tiết

Species richness starts at zero on the bare substrate and increases continuously over 500 years, with the rate of increase appearing to slow somewhat as it approaches 500 years. Because the community begins on bare volcanic rock with no pre-existing soil or organisms, this is **primary succession**. Pioneer species (e.g., lichens and mosses) are able to colonize bare rock, gradually weathering it and accumulating organic matter to form a thin soil. This more hospitable, nutrient-enriched substrate then allows less hardy, more complex species (grasses, shrubs, eventually trees) to colonize in turn, and increasing habitat complexity supports growing numbers of animal species – each successional stage facilitates colonization by the next, driving species richness upward.

Bài tập luyện tập

A forest ecosystem experiences a severe drought but shows little change in the relative abundance of its component species throughout the drought. This ecosystem is best described as showing high:

(A) Resilience
(B) Succession
(C) Resistance
(D) Primary productivity

Lời giải chi tiết

The ecosystem is withstanding the disturbance without significant change – the definition of resistance, as distinct from resilience (the ability to recover *after* being changed). **(C)**.

Bài tập luyện tập

Approximate annual mean atmospheric CO_2 concentration, based on direct atmospheric monitoring:

Year	1960	1980	2000	2020
CO_2 (ppm)	317	339	369	414

(a) Calculate the average rate of increase in CO_2 concentration, in ppm per decade, between 1960 and 2020. (b) Calculate the rate of increase between 2000 and 2020 alone, and comment

on what this shows about the overall trend. (c) Identify the main human activity responsible for this long-term rise, and name the process by which it releases carbon that had been stored for millions of years.

Lời giải chi tiết

(a) Total change $= 414 - 317 = 97$ ppm over 60 years $= 6$ decades: $97/6 \approx 16.2$ ppm per decade.
(b) $2000 \to 2020$: $414 - 369 = 45$ ppm over 2 decades $= 22.5$ ppm per decade – noticeably higher than the 60-year average of 16.2 ppm/decade, showing that the rate of atmospheric CO_2 increase has been **accelerating** in recent decades.
(c) The combustion of fossil fuels (coal, oil, natural gas) for energy is the principal driver. The process is **combustion**, which rapidly releases carbon that had been sequestered in fossil fuel reservoirs over millions of years, far faster than natural sinks can reabsorb it.

Bài tập luyện tập

Using the concept of the carbon cycle, explain why burning fossil fuels causes a net increase in atmospheric CO_2 concentration, whereas an actively growing forest does not (over the timescale of its own growth).

Lời giải chi tiết

A growing forest is not adding new carbon to the actively cycling atmosphere-biosphere-ocean system: photosynthesis removes CO_2 from the atmosphere and converts it into organic carbon stored in biomass, while respiration and eventual decomposition of that same biomass will, over time, return a comparable amount of CO_2 to the atmosphere – so, over the timescale of the forest's growth and turnover, its net effect on atmospheric CO_2 is close to neutral (and can even be a net carbon sink while actively accumulating biomass). Fossil fuels, by contrast, contain carbon that was removed from active circulation and sequestered underground many millions of years ago through a slow geological process. Burning fossil fuels releases this ancient, long-stored carbon back into the atmosphere within seconds – far faster than natural sinks (oceans, forests, soil) can absorb it – representing a genuinely new net input of carbon into the actively cycling system, rather than a recycling of carbon that was already actively cycling.

Bài tập luyện tập

Most normal human somatic cells cannot divide indefinitely, whereas cells expressing telomerase (germ-line cells, stem cells, and many cancer cells) can. Which statement best explains why?

(A) Somatic cells lack DNA polymerase entirely

(B) Telomerase adds repetitive sequence to the ends of chromosomes, compensating for sequence lost through the end-replication problem

(C) Somatic cells replicate their DNA conservatively rather than semi-conservatively

(D) Telomerase repairs point mutations throughout the genome

Lời giải chi tiết

DNA polymerase cannot fully replicate the extreme end of a linear chromosome's lagging-strand template (the end-replication problem), so telomeres shorten with each division in most somatic cells. Telomerase, which carries its own internal RNA template, can extend chromosome ends and restore telomere length, allowing telomerase-expressing cell lineages to keep dividing. **(B)**.

Bài tập luyện tập

In the Meselson–Stahl experiment, starting from fully heavy (^{15}N) DNA transferred into ^{14}N medium, the following data were recorded:

Generation	% heavy	% hybrid	% light
0	100	0	0
1	0	100	0
2	0	50	50
3	0	25	75

(a) Predict the percentages of hybrid and light DNA at generation 4. (b) Explain why the percentage of *fully heavy* DNA is 0% at every generation from generation 1 onward.

Lời giải chi tiết

(a) The number of hybrid duplexes is always exactly 2 (the two original heavy strands, each permanently paired with a new light strand), while the total number of duplexes doubles each generation (2^n). At generation 4: total $= 2^4 = 16$; hybrid $= 2$, so $2/16 = 12.5\%$ hybrid and $14/16 = 87.5\%$ light.
(b) A fully heavy duplex would require *both* strands to be original (old) strands. But semi-conservative replication always splits each duplex into two templates, each of which pairs with a brand-new (light) strand – so no duplex with two original heavy strands can ever be re-formed after the first round of replication. This is exactly why the conservative model (which predicts a persistent heavy band) was ruled out.

Bài tập luyện tập

A tRNA molecule has the anticodon $3'$-UAC-$5'$. (a) Determine the mRNA codon (state its $5' \to 3'$ sequence) that base-pairs with this anticodon. (b) Using the standard genetic code, identify the amino acid (or start/stop signal) this codon specifies. (c) State the DNA template-strand triplet (in the $3' \to 5'$ direction) that was originally transcribed to produce this codon.

Lời giải chi tiết

(a) Base pairing is antiparallel: aligning the anticodon $3'$-U A C-$5'$ against the codon lets each position pair correctly only if the codon reads $5'$-A U G-$3'$ (U pairs with A, A pairs with U, C pairs with G, with the two strands running in opposite directions).
(b) `AUG` codes for **methionine** and also serves as the **start** codon.
(c) mRNA is synthesized complementary and antiparallel to the DNA template strand. For mRNA $5'$-AUG-$3'$, the template strand must read $3'$-TAC-$5'$ (T pairs with A, A pairs with U, C pairs with G).

Bài tập luyện tập

The original mRNA reads `AUG–GAA–CCU–UAA` (Met–Glu–Pro–Stop). A single nucleotide (the first base, G, of the second codon) is deleted. (a) Write out the new nucleotide sequence and regroup it into codons from the start codon onward. (b) Identify the new amino acid sequence using the standard genetic code. (c) Classify the type of mutation, and explain why this type of mutation typically has more severe effects than a single point substitution.

Lời giải chi tiết

(a) Original (12 nt): AUG GAA CCU UAA. Deleting the G at the start of codon 2 leaves (11 nt): AUGAACCUUAA, which regroups as `AUG–AAC–CUU–AA` (only 2 nucleotides remain in the final, incomplete group).
(b) AUG = Met, AAC = Asn, CUU = Leu; the protein so far reads Met–Asn–Leu–… (translation would continue into whatever sequence follows, since no stop codon has yet appeared in the new frame).
(c) This is a **frameshift (deletion) mutation**: removing a number of nucleotides not divisible by three shifts the reading frame for every codon downstream of the deletion, so essentially every amino acid from that point onward differs from the original, and the original stop codon (UAA) is no longer read in frame. Frameshift mutations tend to be more severe than point substitutions because a substitution changes at most one amino acid, whereas a frameshift corrupts the entire downstream sequence and frequently eliminates the normal stop codon.

Bài tập luyện tập

Besides correcting disease-causing mutations in humans, CRISPR-Cas9 is also used to edit crop-plant genomes. State one potential agricultural benefit of this technology, and one general ethical or practical concern associated with releasing gene-edited crops.

Lời giải chi tiết

Benefit (example): editing genes to confer resistance to a specific plant disease, drought tolerance, or improved nutritional content, potentially increasing yield or food security with fewer pesticide or water inputs.
Concern (example): unintended off-target edits could have unknown ecological effects if the edited plant cross-breeds with wild relatives, or the cost/control of the technology could create unequal access for smaller farmers. (Any one well-explained benefit and concern is acceptable.)

Bài tập luyện tập

Non-disjunction is the failure of homologous chromosomes (in meiosis I) or sister chromatids (in meiosis II) to separate correctly. If non-disjunction of chromosome 21 occurs during meiosis I in a human egg cell, and that egg is subsequently fertilized by a chromosomally normal sperm, what will be the chromosome 21 status of the resulting zygote, and what condition does this produce?

(A) Monosomy 21; not a viable condition
(B) Trisomy 21 (three copies of chromosome 21); Down syndrome
(C) Normal disomy; no effect
(D) Tetrasomy 21; always lethal immediately

Lời giải chi tiết

If the homologous pair of chromosome 21 fails to separate in meiosis I, one resulting egg cell receives both copies of chromosome 21, while the other receives neither. If the egg carrying both copies is fertilized by a normal sperm (contributing one chromosome 21), the zygote will have three copies of chromosome 21 – **trisomy 21**, the genetic basis of **Down syndrome**. **(B)**.

Bài tập luyện tập

(HL) Histone acetylation typically has which effect on gene expression, and why?

(A) It increases expression, because acetyl groups neutralize the histones' positive charge, loosening DNA–histone packing and making the gene more accessible to transcription machinery

(B) It decreases expression, because it tightens chromatin packing

(C) It has no effect on expression, only on DNA replication

(D) It permanently removes the gene from the genome

Lời giải chi tiết

Acetylation of histone tails neutralizes their positive charge, reducing the strong electrostatic attraction between histones and the negatively charged DNA backbone. This loosens chromatin structure, making genes in that region more accessible to transcription factors and RNA polymerase, and generally increases transcription. **(A)**.

Bài tập luyện tập

(HL) Explain, in terms of transcription factors, why a liver cell and a neuron – which contain exactly the same DNA sequence – express substantially different sets of genes.

Lời giải chi tiết

Both cell types inherited an identical genome, but during development each cell type comes to express a different specific combination of transcription factors (activators and repressors). Because a given gene's promoter and enhancer sequences respond to the particular combination of transcription factors present in a cell, the same gene can be switched on in one cell type (where the necessary activating transcription factors are present) and kept off in another (where they are absent, or where repressing transcription factors dominate). This combinatorial control, often reinforced by epigenetic marks that help maintain the pattern through subsequent cell divisions, allows cells with an identical genome to differentiate into functionally distinct types such as liver cells and neurons.

Bài tập luyện tập

Equal-sized potato tissue cylinders are immersed in sucrose solutions of different concentration for 24 hours, and the percentage change in mass is recorded:

Sucrose conc. (mol dm^{-3})	0.0	0.2	0.4	0.6	0.8	1.0
% change in mass	$+12$	$+6$	$+1$	-5	-11	-17

(a) Estimate the sucrose concentration at which there is no net water movement, and explain what this concentration represents in terms of water potential. (b) Explain, in terms of water

potential, why the cylinders gained mass in the more dilute solutions and lost mass in the more concentrated ones. (c) At 1.0 mol dm^{-3}, would you expect the potato cells to be turgid, flaccid, or plasmolyzed? Explain.

Lời giải chi tiết

(a) Between 0.4 mol dm^{-3} ($+1\%$) and 0.6 mol dm^{-3} (-5%), the mass change crosses zero. Interpolating: $0.4 + 0.2 \times \frac{1}{1+5} = 0.4 + 0.033 \approx 0.43$ mol dm^{-3}. At this concentration, the external solution's water potential equals the average water potential of the potato tissue cells – no net water movement.
(b) In more dilute solutions, the external solution has a higher (less negative) water potential than the potato cells, so water moves *into* the cells by osmosis, increasing mass. In more concentrated solutions, the external solution has a lower (more negative) water potential than the cells, so water moves *out of* the cells, decreasing mass.
(c) At 1.0 mol dm^{-3} (strongly hypertonic relative to the tissue, with a large 17% mass loss), the potato cells would be expected to be **plasmolyzed** – having lost a large proportion of their internal water, the protoplast shrinks and pulls away from the cell wall.

Bài tập luyện tập

Which statement correctly distinguishes human spermatogenesis from oogenesis?

(A) Spermatogenesis produces four functional gametes per meiotic division, while oogenesis produces only one functional gamete plus non-functional polar bodies, due to highly unequal cytoplasmic division

(B) Oogenesis produces four functional gametes, spermatogenesis only one

(C) Both processes produce four functional, equal-sized gametes

(D) Spermatogenesis occurs entirely before puberty, while oogenesis occurs throughout adult life

Lời giải chi tiết

Spermatogenesis divides the cytoplasm equally, producing four functional sperm cells per primary spermatocyte. Oogenesis divides the cytoplasm highly unequally, concentrating resources into a single large, functional egg cell while the rest of the genetic material is discarded into small, non-functional polar bodies. **(A)**.

Bài tập luyện tập

In snapdragons, flower colour shows incomplete dominance: red (C^RC^R) $\times$ white (C^WC^W) produces pink (C^RC^W) offspring. Two pink-flowered snapdragons are crossed, producing 84 offspring: 22 red, 41 pink, 21 white. (a) State the expected phenotypic ratio for this cross. (b) Calculate the expected numbers out of 84. (c) Using a chi-square test (critical value at $p = 0.05$, $df = 2$, is 5.99), determine whether the observed data are consistent with the expected ratio.

Lời giải chi tiết

(a) $C^RC^W \times C^RC^W$ gives genotypes $1\,C^RC^R : 2\,C^RC^W : 1\,C^WC^W$, i.e., phenotypes in a 1 red : 2 pink : 1 white ratio.
(b) Expected out of 84: red $= \frac{1}{4}(84) = 21$; pink $= \frac{1}{2}(84) = 42$; white $= \frac{1}{4}(84) = 21$.

(c)

$$\chi^2 = \frac{(22-21)^2}{21} + \frac{(41-42)^2}{42} + \frac{(21-21)^2}{21} = 0.048 + 0.024 + 0 = 0.07 \text{ (to 2 d.p.)}.$$

There are 3 phenotype categories, so $df = 2$; critical value $= 5.99$. Since $\chi^2_{\text{calc}} = 0.07 \ll 5.99$, we **fail to reject** the null hypothesis: the data are consistent with the expected $1:2:1$ ratio.

Bài tập luyện tập

Haemophilia is caused by an X-linked recessive allele (X^h). A woman who is a carrier for haemophilia (X^HX^h, unaffected) has children with a man who does not have haemophilia (X^HY). (a) Construct a Punnett square for this cross. (b) State the probability that a son of this couple will have haemophilia. (c) State the probability that a daughter of this couple will have haemophilia. (d) State the probability that a daughter will be a carrier.

Lời giải chi tiết

Gametes: mother contributes X^H or X^h (each $\frac{1}{2}$); father contributes X^H or Y (each $\frac{1}{2}$). Offspring genotypes, each with probability $\frac{1}{4}$: X^HX^H (normal daughter), X^HX^h (carrier daughter), X^HY (normal son), X^hY (affected son).
(b) Among sons (X^HY and X^hY, each $\frac{1}{2}$ of sons): probability of haemophilia $= \frac{1}{2} = 50\%$.
(c) No daughter genotype is X^hX^h, since the father (unaffected, X^HY) cannot contribute an X^h allele – probability $= 0\%$.
(d) Among daughters (X^HX^H and X^HX^h, each $\frac{1}{2}$ of daughters): probability of being a carrier $= \frac{1}{2} = 50\%$.

Bài tập luyện tập

Blood glucose concentration (mg/dL) was measured after an oral glucose tolerance test for a healthy individual and for an individual with untreated Type 2 diabetes:

Time after drink (min)	0	30	60	90	120	180
Healthy individual	90	140	125	100	85	90
Untreated Type 2 diabetic	95	175	205	210	195	175

(a) Describe the difference between the two curves. (b) Explain, in terms of insulin receptor sensitivity, why blood glucose remains persistently elevated in the Type 2 diabetic individual even though insulin is still being produced. (c) State one lifestyle-related risk factor associated with the development of Type 2 diabetes.

Lời giải chi tiết

(a) Both individuals show glucose rising after the drink, but the Type 2 diabetic individual's peak is much higher (≈ 210 vs. 140 mg/dL) and remains substantially elevated even at 180 minutes (175 mg/dL, far above the fasting baseline), rather than returning close to baseline as in the healthy individual.
(b) In Type 2 diabetes, beta cells generally still produce insulin (unlike Type 1, where beta cells are destroyed), but target cells (liver, muscle, fat) have become less responsive to it – a condition called **insulin resistance**. Glucose uptake into cells and glycogen synthesis are impaired even in the presence of insulin, so blood glucose remains elevated for much longer

after a meal.
(c) Risk factors linked to Type 2 diabetes include obesity/excess body fat and physical inactivity, both associated with reduced insulin sensitivity in target tissues. (Any one reasonable, well-explained factor is acceptable.)

Bài tập luyện tập

In a population of Galápagos ground finches, the average beak depth was 9.4 mm before a severe drought that greatly reduced the availability of small, soft seeds (leaving mainly large, hard seeds). In the generation following the drought, average beak depth was 10.1 mm. (a) Identify the type of natural selection illustrated by this shift. (b) Explain the mechanism producing this shift, referring to selection pressure and heritable variation. (c) Predict what would happen to mean beak depth if several wet years followed, restoring abundant small soft seeds, and justify your prediction.

Lời giải chi tiết

(a) **Directional selection** – the population mean has shifted toward one phenotypic extreme (deeper beaks).
(b) During the drought, small soft seeds became scarce, leaving mainly large, hard seeds that require deeper, stronger beaks to crack efficiently. Finches with shallower beaks survived and reproduced less successfully, while deeper-beaked finches (a heritable trait) survived and reproduced more successfully, passing the trait to more offspring. Repeated selection increased the frequency of alleles for deeper beaks, raising the population mean.
(c) If wet conditions returned and small, soft seeds became abundant again, the selection pressure favouring deep beaks would be relaxed (or reversed), and mean beak depth would likely decrease back toward, or below, its original value – consistent with long-term field studies showing beak depth fluctuating with alternating drought and wet years. This shows that selection pressures depend on, and can reverse with, environmental conditions.

Bài tập luyện tập

The percentage of dark-coloured (melanic) peppered moths in a population near an industrial city was recorded over more than a century:

Year	1850	1900	1950	1970	2000
% dark moths	2	90	95	80	10

(a) Describe the trend shown. (b) Explain the increase from 1850 to 1950 in terms of natural selection and predation by birds. (c) Explain the reversal after 1950–1970, and identify the type of selection illustrated by the fact that the direction of selection reversed as the environment changed back.

Lời giải chi tiết

(a) The percentage of dark moths rises sharply from 1850 (2%) to a peak around 1950–1970 (95%, 80%), then falls substantially by 2000 (10%).
(b) Before industrialization, tree trunks were pale (covered in lichen), so light-coloured moths were camouflaged while dark moths were conspicuous and heavily predated by birds. As industrial pollution killed lichen and coated trunks with soot, light moths became conspicuous and were preferentially eaten, while dark moths were now camouflaged and survived/repro-

duced more successfully – directional selection rapidly increased the dark allele's frequency. (c) After pollution controls reduced soot and allowed lichen to recover, trunks became paler again, reversing the camouflage advantage: light moths again became better camouflaged, so directional selection now favoured the light allele, and the percentage of dark moths fell. The overall pattern – selection favouring one phenotype, then reversing to favour the other as the environment changed – illustrates that **directional selection** tracks the current selection pressure rather than acting in a single fixed direction indefinitely.

Bài tập luyện tập

Unlike ABO blood groups, the human MN blood group is controlled by two **codominant** alleles (L^M and L^N), so all three genotypes (L^ML^M, L^ML^N, L^NL^N) can be distinguished directly by blood typing (blood groups M, MN, and N respectively). In a sample of 200 people: 72 are type M, 96 are type MN, and 32 are type N. (a) Calculate the frequency of the L^M and L^N alleles directly by counting alleles. (b) Check whether these frequencies are consistent with Hardy–Weinberg equilibrium by calculating expected genotype numbers and comparing with the observed data.

Lời giải chi tiết

(a) Total individuals $= 200$, total alleles $= 400$. L^M alleles: from 72 type-M individuals ($72 \times 2 = 144$) plus from 96 type-MN individuals ($96 \times 1 = 96$), total $= 240$, so frequency $p = 240/400 = 0.6$. L^N alleles: from 96 type-MN (96) plus 32 type-N ($32 \times 2 = 64$), total $= 160$, so frequency $q = 160/400 = 0.4$. Check: $p + q = 1.0$. ✓
(b) Expected genotype frequencies: $p^2 = (0.6)^2 = 0.36$, $2pq = 2(0.6)(0.4) = 0.48$, $q^2 = (0.4)^2 = 0.16$. Expected counts (of 200): M $= 0.36 \times 200 = 72$; MN $= 0.48 \times 200 = 96$; N $= 0.16 \times 200 = 32$ – these match the observed counts exactly, so this population is consistent with Hardy–Weinberg equilibrium at this locus (no evidence of selection, non-random mating, or other evolutionary force acting on the MN gene here).

Bài tập luyện tập

Two forest plots are surveyed for percentage canopy cover before, and at intervals after, a wildfire:

Time since fire (years)	Pre-fire	0	5	10	20	40
Forest A (old-growth)	85	20	35	55	75	84
Forest B (previously logged)	60	5	10	20	35	50

(a) Which forest showed higher resistance to the fire disturbance, and how can you tell from the data? (b) Compare the resilience of the two forests based on their recovery trajectories. (c) After 40 years, has either forest fully recovered to its pre-fire state? Explain using the data.

Lời giải chi tiết

(a) Comparing the *proportional* drop in canopy cover: Forest A fell from 85% to 20%, a loss of $\frac{65}{85} \approx 76.5\%$; Forest B fell from 60% to 5%, a loss of $\frac{55}{60} \approx 91.7\%$. Forest A lost a smaller proportion of its canopy, so Forest A shows higher **resistance** (it withstood the disturbance with comparatively less change).
(b) Over the following 40 years, Forest A recovers from 20% to 84% (nearly all the way back to its original 85%), while Forest B recovers from 5% only to 50% (still well below its original 60%).

Forest A therefore also shows higher **resilience** – both a faster and a more complete recovery. (c) Forest A (84% vs. an original 85%) has essentially fully recovered. Forest B (50% vs. an original 60%) has not – it remains about 10 percentage points (roughly one-sixth of its original cover) below its pre-fire state after 40 years.

Bài tập luyện tập

Estimated global mean surface temperature anomaly (relative to a 1951–1980 baseline), by decade:

Decade	1960s	1980s	2000s	2020s
Temperature anomaly (°C)	-0.05	$+0.18$	$+0.55$	$+1.02$

(a) Calculate the overall rate of warming (°C per decade) between the 1960s and the 2020s. (b) Calculate the rate of warming between the 2000s and the 2020s alone, and compare it with the overall long-term rate. (c) Explain, using the enhanced greenhouse effect, why rising atmospheric CO_2 concentration is considered the primary driver of this warming trend.

Lời giải chi tiết

(a) Total change $= 1.02 - (-0.05) = 1.07$°C over 60 years $= 6$ decades: $1.07/6 \approx 0.18$°C per decade.
(b) 2000s $\rightarrow$ 2020s: change $= 1.02 - 0.55 = 0.47$°C over 2 decades $= 0.235$°C per decade – noticeably faster than the 60-year average of 0.18°C/decade, indicating that the rate of warming has been **accelerating** in recent decades.
(c) Rising atmospheric CO_2 (and other greenhouse gases) absorb and re-emit outgoing infrared radiation from Earth's surface, trapping additional heat in the lower atmosphere beyond the natural greenhouse effect – the **enhanced greenhouse effect**. Because directly measured CO_2 concentration and global temperature have risen together over the same period, and because the physical mechanism by which greenhouse gases trap heat is well understood and quantifiable, rising CO_2 is considered the primary driver of the observed warming, rather than a coincidental correlation.

Bài tập luyện tập

A newly synthesized polypeptide destined to become a secreted digestive enzyme has an N-terminal signal sequence that is later enzymatically removed, and several sugar groups are subsequently attached to specific amino acids on the mature protein. (a) Name this general category of change to a protein after translation. (b) Suggest one reason such modifications might be necessary before the protein becomes fully functional.

Lời giải chi tiết

(a) **Post-translational modification**.
(b) Cleavage of the signal sequence and addition of chemical groups (here, glycosylation) can be necessary for correct protein folding, stability, intracellular targeting/sorting (e.g., directing the protein into the secretory pathway so it is correctly packaged and released from the cell), and/or the protein's ultimate biological activity – an unmodified polypeptide may fold incorrectly, be sent to the wrong location, or be non-functional. (Any one well-explained reason is acceptable.)

Bài tập luyện tập

(HL) In Labrador retrievers, coat colour is controlled by two genes: the B gene (B = black pigment, dominant; b = brown pigment) and the E gene (E = pigment deposited in the coat, dominant; e = no pigment deposited, coat appears yellow regardless of the B gene genotype). The E gene is epistatic to the B gene. Two double heterozygous black dogs ($BbEe \times BbEe$) are crossed. (a) Determine the expected phenotypic ratio of black : brown : yellow puppies. (b) Out of 144 puppies (from many such crosses), calculate the expected number of each coat colour.

Lời giải chi tiết

(a) A standard dihybrid cross gives genotype classes in a 9 *B_E_* : 3 *bbE_* : 3 *B_ee* : 1 *bbee* ratio (of 16). Because ee always produces yellow regardless of the B genotype, the 3 *B_ee* and 1 *bbee* classes combine into a single yellow class: 9 black (*B_E_*) : 3 brown (*bbE_*) : 4 yellow ($3+1$).
(b) Out of 144 puppies ($144/16 = 9$ per ratio unit): black $= 9 \times 9 = 81$; brown $= 3 \times 9 = 27$; yellow $= 4 \times 9 = 36$. Check: $81 + 27 + 36 = 144$. ✓

Ôn tập nhanh

- **Theme A (Đa dạng và thống nhất):** mọi sinh vật có cấu trúc tế bào, dùng chung mã di truyền và các phân tử sinh học cơ bản (nước, carbohydrate, lipid, protein, nucleic acid) – bằng chứng cho tổ tiên chung; sinh vật được phân loại theo hệ thống thứ bậc và cây phát sinh chủng loại.
- **Theme A:** nước có các tính chất đặc biệt (liên kết hydro, tính phân cực, nhiệt dung riêng cao, tính kết dính/bám dính) quyết định vai trò trung tâm của nó trong sự sống.
- **Theme B (Hình thái và chức năng):** cấu trúc màng tế bào (mô hình khảm động) và các cơ chế vận chuyển qua màng (khuếch tán, thẩm thấu, vận chuyển chủ động) liên hệ trực tiếp với khái niệm thế nước ở D2.3.
- **Theme B:** enzyme làm giảm năng lượng hoạt hoá; hoạt tính enzyme phụ thuộc nhiệt độ, pH và nồng độ cơ chất – luôn mô tả đúng dạng đồ thị đặc trưng.
- **Theme B:** hô hấp tế bào và quang hợp là hai quá trình chuyển hoá năng lượng đối lập nhưng liên kết chặt chẽ qua chu trình carbon (liên hệ D4.3).
- **Theme C (Tương tác và phụ thuộc lẫn nhau):** sinh vật tương tác qua quan hệ dinh dưỡng (chuỗi/lưới thức ăn, tháp sinh khối và năng lượng) và các mối quan hệ khác loài (cạnh tranh, con mồi–vật ăn thịt, cộng sinh).
- **Theme C:** dòng năng lượng qua hệ sinh thái là MỘT CHIỀU (không tuần hoàn), trong khi vật chất (carbon, nitrogen) được TUẦN HOÀN – đây là nền tảng để hiểu diễn thế và ổn định hệ sinh thái ở D4.2.
- **Theme D1:** nhân đôi ADN là bán bảo toàn; nhớ đúng chiều tổng hợp $5' \to 3'$ và vai trò riêng biệt của bốn enzyme (helicase, primase, DNA polymerase, ligase).
- **Theme D1:** phiên mã đọc mạch khuôn theo chiều $3' \to 5'$, tổng hợp mRNA theo chiều $5' \to 3'$; mã di truyền có tính bộ ba, suy biến (degenerate) và phổ quát (universal).
- **Theme D2:** phân biệt rõ nguyên phân ($2n \to 2n$, một lần phân chia, hai tế bào con giống hệt nhau) và giảm phân ($2n \to n$, hai lần phân chia, bốn tế bào con khác nhau nhờ trao đổi chéo và phân li độc lập).
- **Theme D2:** thế nước luôn di chuyển từ nơi ψ cao (ít âm) sang nơi ψ thấp (âm hơn); $\psi = \psi_s + \psi_p$.
- **Theme D3:** khi giải bài Hardy–Weinberg, luôn lấy CĂN BẬC HAI của tần số kiểu hình lặn (q^2) để ra q, rồi mới suy $p = 1 - q$ – tuyệt đối không nhầm q^2 với q.
- **Theme D3:** kiểm định χ^2 – bậc tự do luôn bằng (số loại kiểu hình/kiểu gen -1); χ^2 tính được LỚN HƠN giá trị tới hạn thì BÁC BỎ H_0 (số liệu không khớp tỉ lệ kỳ vọng), NHỎ HƠN thì KHÔNG bác bỏ.
- **Toàn bộ 4 Theme:** luôn liên hệ theo mạch tư duy xuyên suốt của IB Biology – phân tử (Theme D1) → tế bào (Theme D2 / Theme B) → cơ thể sinh vật (Theme D3) → quần thể và hệ sinh thái (Theme D4 / Theme C).

Đồng hành cùng 8020 English

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Bảng vàng học viên

AP Calculus BC — 5/5
SAT 1590 / 1570 / 1550
AP Microeconomics — 5/5
IELTS 8.0–9.0
IB Economics — 90/100
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