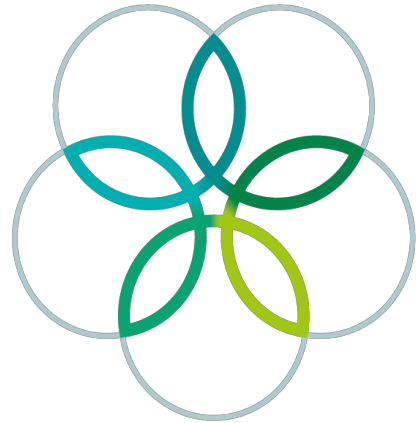
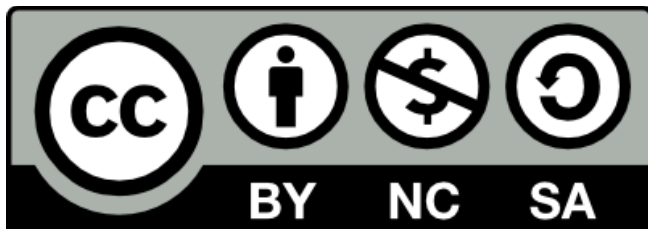


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Theory 1



34th International
Biology Olympiad
United Arab Emirates 2023

Q1-1

English (Official)

Theory 1

34th International Biology Olympiad

3-10 July 2023, United Arab Emirates University

Duration: 3 hours

General Instructions:

QUESTION 4 AND 9 HAVE BEEN DELETED. PLEASE DO NOT ATTEMPT TO ANSWER IT.

No answers on the exam paper will be graded.

You must use a dot to separate decimal places not a comma.

You will use a dedicated browser application to enter your responses. This application includes two different types of screens, namely question screen and "Translation" screen.

You do not need to submit the exam: it will be submitted automatically, once the exam is over. There will be a timer showing the time remaining until the end of the exam.

YOU MUST PRESS "Save" after completing EACH question or else your answers will not be registered.

You MUST NOT quit the Safe Exam Browser.

Questions which are fully or at least partially answered and saved are highlighted in green in the side panel. You can flag questions, and these will be highlighted in orange in the side panel. The current question is highlighted in blue.

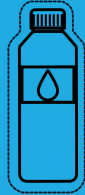
To see an electronic copy of the questions, press "Translation". You can select any language version by using the dropdown menu.

You can search specific text using Ctrl-F, but you must first click on the window.

If you minimise the electronic copy of the questions, you can quickly return to it by clicking the icon on the bottom left of the screen.

If you face any technical issues with your computer, raise your card.

Use the following cards to ask for water/washroom/help.

Drinking water	Washroom	Other queries
		



TTT Phe (F)	TCT Ser (S)	TAT Tyr (Y)	TGT Cys (C)
TTC Phe (F)	TCC Ser (S)	TAC Tyr (Y)	TGC Cys (C)
TTA Leu (L)	TCA Ser (S)	TAA STOP	TGA STOP
TTG Leu (L)	TCG Ser (S)	TAG STOP	TGG Trp (W)
CTT Leu (L)	CCT Pro (P)	CAT His (H)	CGT Arg (R)
CTC Leu (L)	CCC Pro (P)	CAC His (H)	CGC Arg (R)
CTA Leu (L)	CCA Pro (P)	CAA Gln (Q)	CGA Arg (R)
CTG Leu (L)	CCG Pro (P)	CAG Gln (Q)	CGG Arg (R)
ATT Ile (I)	ACT Thr (T)	AAT Asn (N)	AGT Ser (S)
ATC Ile (I)	ACC Thr (T)	AAC Asn (N)	AGC Ser (S)
ATA Ile (I)	ACA Thr (T)	AAA Lys (K)	AGA Arg (R)
ATG Met (M)	ACG Thr (T)	AAG Lys (K)	AGG Arg (R)
GTT Val (V)	GCT Ala (A)	GAT Asp (D)	GGT Gly (G)
GTC Val (V)	GCC Ala (A)	GAC Asp (D)	GGC Gly (G)
GTA Val (V)	GCA Ala (A)	GAA Glu (E)	GGA Gly (G)
GTG Val (V)	GCG Ala (A)	GAG Glu (E)	GGG Gly (G)

This is a standard codon table which may be useful for some questions.

Theory 1



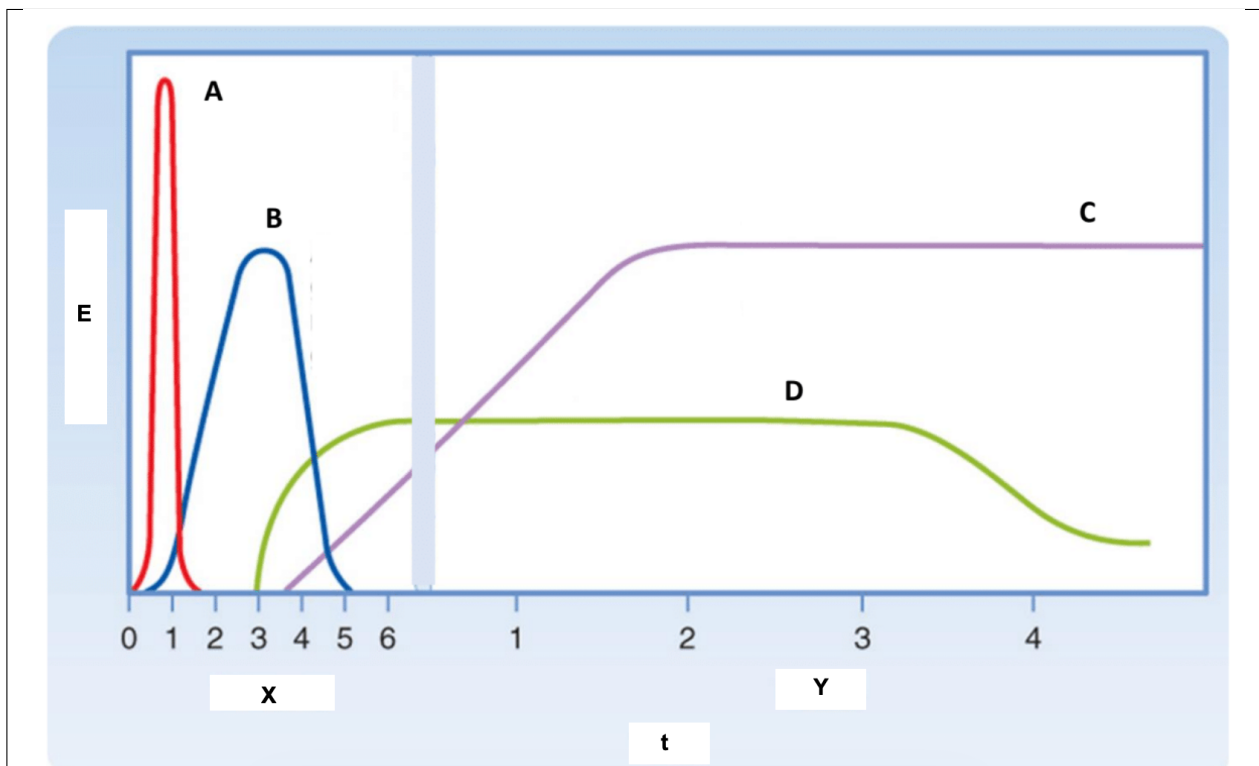
34th International
Biology Olympiad
United Arab Emirates 2023

Q1-3

English (Official)

Q.1

Skeletal muscle can be active over short or long times. There are several energy sources, each affecting the strength and endurance of muscles.



E	Energy
t	Time
X	Minutes
Y	Hours

Match the corresponding curves (A-D), showing the contribution of each energy source to power generation, with a corresponding energy source (1-4).

	Energy source
1	aerobic oxidation: muscle glycogen, plasma glucose or liver glycogen
2	aerobic oxidation: adipose tissue triglycerides and plasma fatty acids
3	ATP + creatine phosphate
4	anaerobic oxidation: muscle glycogen

Theory 1



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Q1-4

English (Official)

Q.1

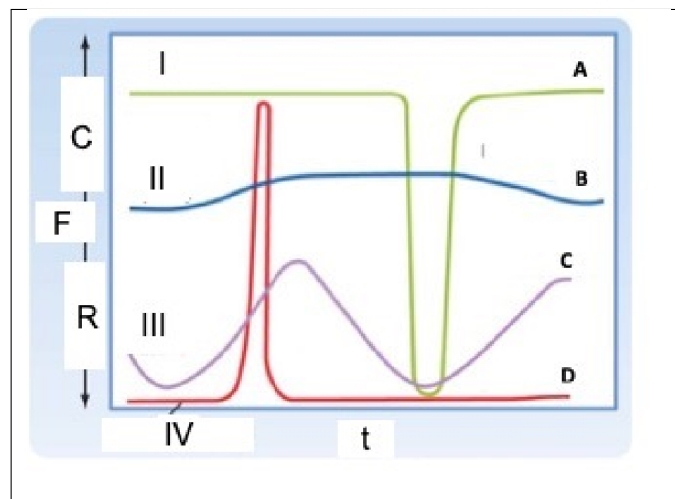
4.0pt

Energy source	Curves (A-D)
1	
2	
3	
4	



Q.2

The smooth muscle in various organs behaves differently, and has specialised contraction/relaxation dynamics.



C (Y-axis)	Contraction
F	Force
R	Relaxation
t	Time
I	Normally contracted
II	Normally partially contracted (tone)
III	Phasically active
IV	Normally relaxed

Theory 1



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Q1-6

English (Official)

Match the four curves (A-D), given below with the four corresponding organs (1-4).

	Organ
1	sphincters
2	oesophagus, urinary bladder
3	blood vessels, airways
4	stomach, intestines

Q.2.1

4.0pt

Organ	Curves (A-D)
1	
2	
3	
4	



Q.3

Flow cytometry is a method for analyzing multiple cells in suspension.

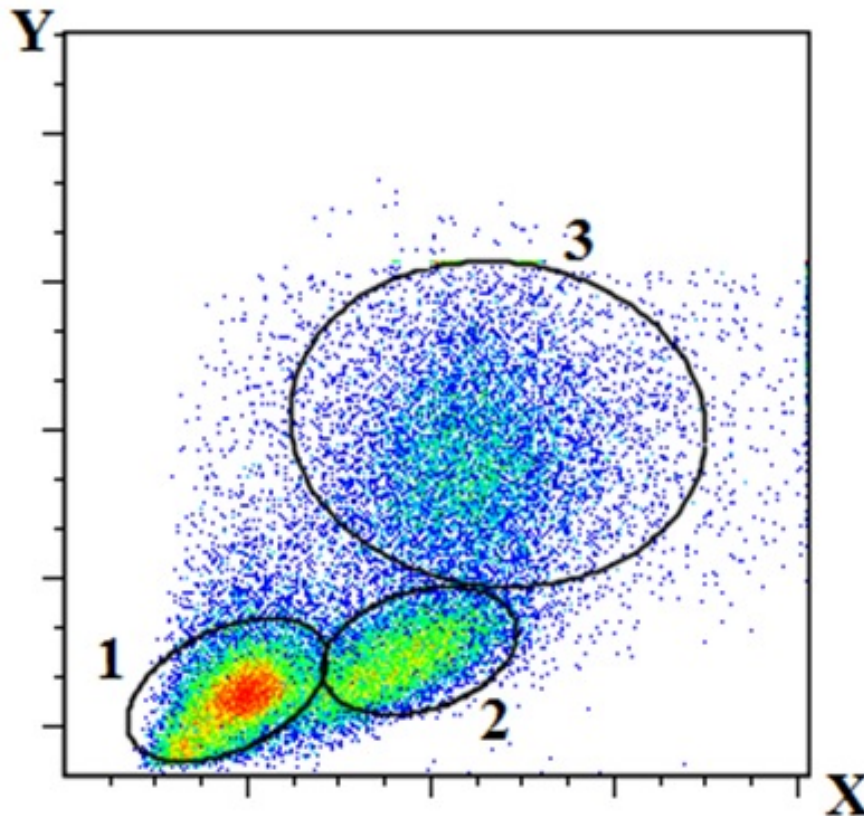
Cells pass through a microfluidic system, where they are irradiated by lasers. Laser light photons are partially scattered by cells and partially absorbed by fluorophores (fluorescent molecules). Excited fluorophores then emit secondary photons at longer wave lengths.

Fluorophores are typically small organic molecules with conjugated double bonds.

- Low angle scattering is measured by a forward scattering (FSC) detector.
- High angle scattering is measured by a side scattering (SSC) detector.
- Fluorescence is measured by wavelength-specific detectors.

FSC positively correlates with cell size, while SSC positively correlates with cell-surface 'texture' and 'granularity', including protrusions, pockets and underlying vesicles.

The results of measurement are typically represented on dot-plot diagrams. Each dot represents a single-cell, with the density of dots in an area indicated by color (Red is high density, dark blue is low density).



The figure above shows flow cytometry analysis of mouse blood. Blood was pretreated with red blood cell lysis buffer.

Axis **X** shows FSC

Axis **Y** shows SSC.

An FSC-threshold was used to exclude the particles with very low FSC from the plot (e.g. debris).

Indicate True and False statements:

Q.3.1 Lymphocytes are shown in Area 1.

1.0pt

Q.3.2 Residual red blood cells are shown in Area 2.

1.0pt

Q.3.3 Neutrophils and other granulocytes are shown in Area 3.

1.0pt

Q.3.4 In general, unstained blood cells show **no** fluorescence.

1.0pt



Q.4

THIS QUESTION HAS BEEN DELETED. PLEASE DO NOT ATTEMPT TO ANSWER IT.

The rate of development of insect pupae depends on the temperature.

Within a certain temperature range, the duration of pupal development depends on temperature according to the hyperbolic law:

$$y = \frac{a}{x+b} + c$$

Where, y – duration of pupal development (days);

x – ambient temperature ($^{\circ}\text{C}$);

a , b , c – empirical coefficients.

Two species of butterflies are bred in an insectarium: species S1 and species S2.

The pupae of S1 develop for 18 days at 20°C , but 12 days at 30°C . The pupae of S2 develop for 18.5 days at 20°C , but 11.5 days at 30°C .

In both cases, the coefficient b is equal to 0.

Answer the following questions:

Q.4.1 How many days do the pupae of S1 develop for at 18°C ?

3.0pt

Q.4.2 At what temperature will it take 10 days for S2 species pupae to develop? Give your answer to the first decimal place.

3.0pt

Q.4.3 At what temperature will the development of pupae of both species take the same time?

3.0pt

Theory 1



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Q1-10

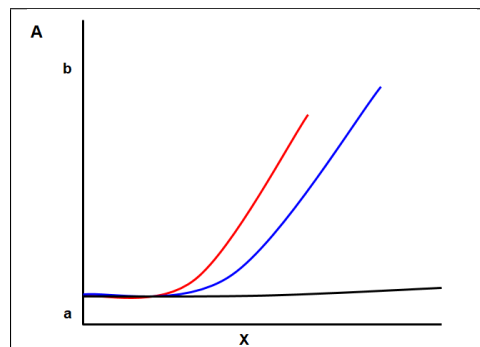
English (Official)

Q.5

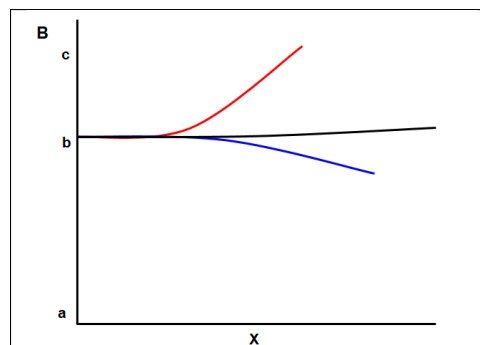
Part A

In an experiment, soldiers were ordered to march through a hot desert until exhaustion (they were then retrieved and given a reward).

- One group (red) had no food or water.
- The second (blue) group had access to limitless water.
- The third group (black) had access to both limitless water and limitless savoury (salty, low energy) food.



A	Core body temperature
X	Length of march
a	Normal
b	Hot



Theory 1

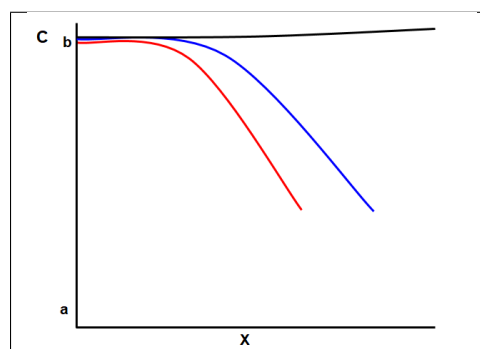


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Q1-11

English (Official)

B	Blood osmolarity
X	Length of March
a	Low
b	Medium
c	High



C	Cardiac output
x	Length of March
a	Low
b	Normal

Starling's law of the heart shows that cardiac output is always proportional to mean systemic filling pressure (the pressure of blood in the great veins). This is because the heart cannot suck blood through vessels (they collapse), it can only pressurise the blood which the great veins deliver to it.

Camels are adapted to withstand larger swings in osmolarity and core temperature than other mammals. Camels and humans both have the very rare ability to sweat. Sweat is mostly water, with a small amount of salt. (Note; camel humps are almost entirely fat, located to reduce surface area exposed to midday sun, similar to humans' unusually upright posture).

True or False?

Q.5.1 The change in blood osmolarity in the blue group is adaptive and helps them to last longer. 1.0pt

Q.5.2 The blue group drinks more water than the black group. 1.0pt

Q.5.3 Circulatory failure is the proximate cause of exhaustion in these conditions. 1.0pt



Q.5.4 Of the three groups, camels would follow a trajectory most similar to the blue group (but extended). Assume they do **not** eat or drink. 1.0pt

Q.5.5 A group given unlimited dry food, but not water, would last longer than the red group. 1.0pt

Part B

Antidiuretic hormone (ADH, also known as vasopressin) is usually released from the pituitary gland in proportion to blood osmolarity.

ADH acts on very-high affinity receptors in the kidney to increase urine concentration.

ADH also acts on low-affinity receptors across blood vessels, increasing their tone (squeezing on blood).

Some patients have tumours which secrete ADH (syndromes of inappropriate ADH secretion).

True or False?

Q.5.6 These patients have more concentrated urine than normal. 1.0pt

Q.5.7 These patients have higher blood osmolarity than normal. 1.0pt

Q.5.8 In the absence of compensation, these patients have higher blood volume than normal. 1.0pt

Q.5.9 These patients have higher cardiac output than normal. 1.0pt

Q.5.10 These patients have similar fluid-handling problems to patients with uncontrolled diabetes. 1.0pt



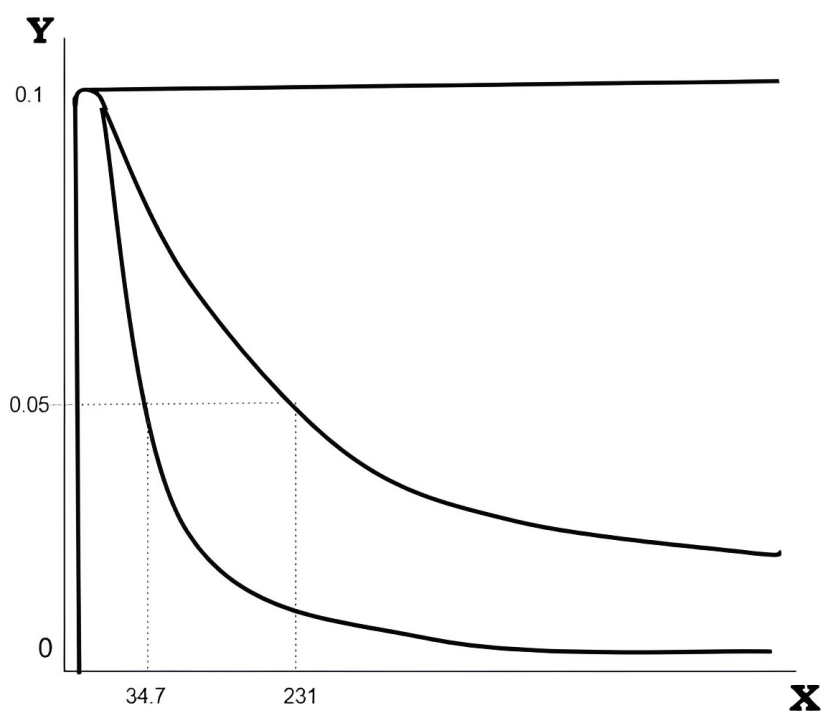
Q.6

Inulin is an inert 4 kDa polymer. Dextran is an inert 500 kDa polymer. Both are handled by the kidney as you would expect for non-actively transported molecules of their size.

Para-amino Hippurate (PAH) is unusual because it is completely removed from plasma as it moves past a nephron (i.e., it is actively transported into the urine).

All molecules were tagged with different color fluorescent dyes and injected by intravenous injection into pigs. The injection was a one-off and contained 0.75 miliMoles of each molecule.

Plasma concentration of each molecule overtime was then measured with a fiberoptic fluorescence imager inserted into a blood vessel.



Y	Concentration (mM)
X	Time (min)

Theory 1



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Q1-14

English (Official)

The equation for exponential decay is

$$A = A_0 e^{-kT}$$

Which can be rearranged as

$$-kT = \ln(A/A_0)$$

Where

A = the amount remaining

A_0 = the initial amount

k is the chance that each molecule is lost per unit time

T = time

Note: $\ln(2) \sim 0.693$

- | | | |
|--------------|--|-------|
| Q.6.1 | • Calculate the plasma volume of the pig. Give your answer in liters to one decimal place. | 3.0pt |
|--------------|--|-------|

For subsequent parts, take the plasma volume of the pig to be 10 liters

- | | | |
|--------------|---|-------|
| Q.6.2 | Calculate the renal plasma flow of the pig (how much plasma flow the kidneys receive).
Give your answer in ml/min to the nearest ml. Type a number without a unit. | 3.0pt |
|--------------|---|-------|

- | | | |
|--------------|--|-------|
| Q.6.3 | Calculate the glomerular filtration rate of the pig (how much plasma the bow-man's capsule excretes).
Give your answer in ml/min to the nearest ml. Type a number without a unit. | 3.0pt |
|--------------|--|-------|

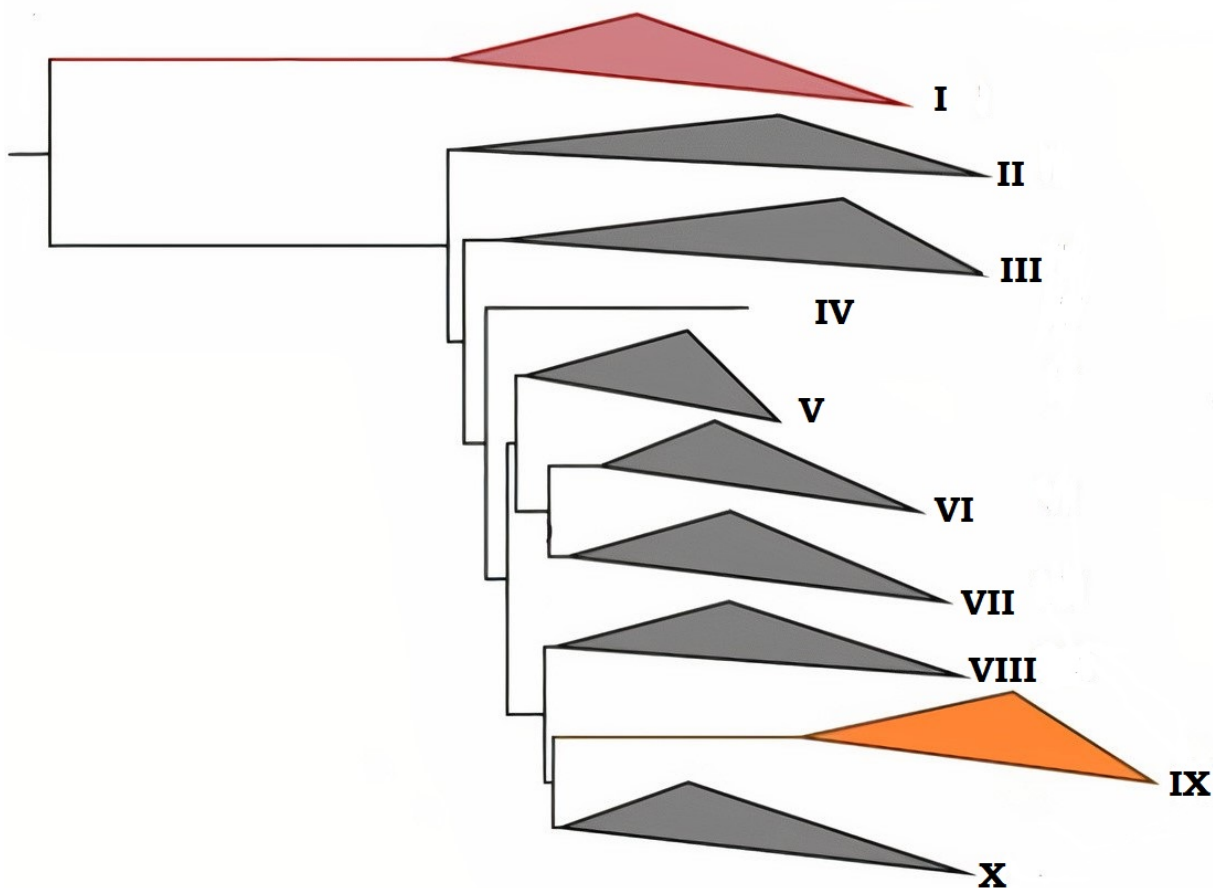


Q.7

Recent studies of Archaea using metagenomics and improved phylogenetic methods allowed us to:

- Confirm that Eukaryotes originated as a result of a symbiosis between an Archaeal host ("**Host**") and a Bacterial endosymbiont ("**Symbiont**").
- Search for an Archaeal group which is evolutionary closest to the "Host".

The tree below shows phylogenetic relationship between Bacteria, Eukaryotes and various Archaeal groups based on sequences of ribosomal proteins homologous among all those taxa. Triangles at the tips reflect the fact that each group includes multiple branches.



Theory 1



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Q1-16

English (Official)

I	Bacteria
II	Nanoarchaeota
III	Ianarchaeota/Micraarchaeota
IV	Altiarchaeota
V	Methanobacteriota
VI	Thermoplasmatota
VII	Halobacteriota
VIII	Thermoproteota
IX	Eukarya
X	Asgardarchaeota

Q.7.1 Based on the tree, which Archaeal group is the most promising research target in order to study the properties of the "Host"? 1.0pt

- A. Asgardarchaeota
- B. Thermoproteota
- C. Halobacteriota
- D. Thermoplasmatota
- E. Nanoarchaeota

Imagine a new group of Archaea was discovered.

Which of the following features in this group would provide evidence for it being evolutionarily closer to the "Host", compared to Archaeal groups that lack those features?

Indicate such features as "True" and the remaining as "False".

Q.7.2.1 A complex dynamic cytoskeleton consisting of actin-like filaments. 1.0pt

Q.7.2.2 Protrusions of the cellular membrane. 1.0pt

Q.7.2.3 A cellular membrane made of isoprenoid alkyl chains linked by ether bonds to glycerol-1-phosphate. 1.0pt

Q.7.2.4 Flagellin-based flagella. 1.0pt



Q.8

Gram-staining has long been used to classify bacteria.

Bacteria stain positively by the Gram method if they have a thick-enough layer of exposed peptidoglycan on the surface of their cells.

However, Gram-positive and Gram-negative bacteria are not monophyletic groups and can include species with rather different cell morphologies.

Some microbiologists have proposed to classify bacteria into *monoderms*, which have only the cytoplasmic membrane, and *diderms*, which additionally have an outer membrane. However, the evolution of the outer membrane is still a matter of research.

One recent study has investigated the *Firmicutes* phylum. The result of this study is summarized in Figure 1.

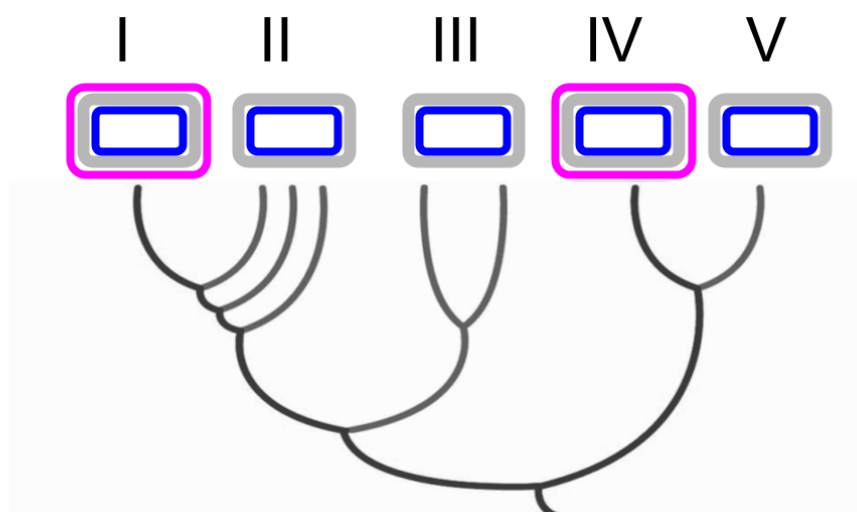


Figure 1

I	Negativicutes
II	Clostridiales and Thermoanaerobacterales
III	Bacillales and Lactobacillales
IV	Halanaerobiales
V	Natranaerobiales

Figure 1. Phylogenetic relationship between various Firmicutes groups. The silhouettes above the tree describe the cell morphology of those groups: blue is the cytoplasmic membrane, grey is peptidoglycan and purple is the outer membrane.

The study also showed that genes associated with the outer membrane are shared between Negativicutes and Halanaerobiales due to vertical transmission, and not due to horizontal gene transfer.

Theory 1



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Q1-18

English (Official)

Q.8.1 For each of the bacteria type described below, indicate if it stains positive or negative by the Gram method: 3.0pt

		Gram-positive (A)	Gram-negative (B)
Q.8.1.1	A typical diderm		
Q.8.1.2	A typical monoderm		
Q.8.1.3	A monoderm with no peptidoglycan on the surface		

Q.8.2 Based on the results of the study, indicate below if the monoderms and diderms within Firmicutes are mono-, para- or polyphyletic: 2.0pt

		Monophyletic (A)	Paraphyletic (B)	Polyphyletic (C)
Q.8.2.1	Monoderms			
Q.8.2.2	Diderms			

True or false?

Q.8.3.1 Based on these results, the most recent common ancestor of Firmicutes likely had the outer membrane 1.0pt

Q.8.3.2 Based on these results and the maximum parsimony principle, it is likely that Bacillales and Lactobacillales lost the outer membrane independently of each other. 1.0pt

Q.8.3.3 These results disprove the hypothesis that the outer membrane evolved as a protection against penicillin-like antibiotics. 1.0pt



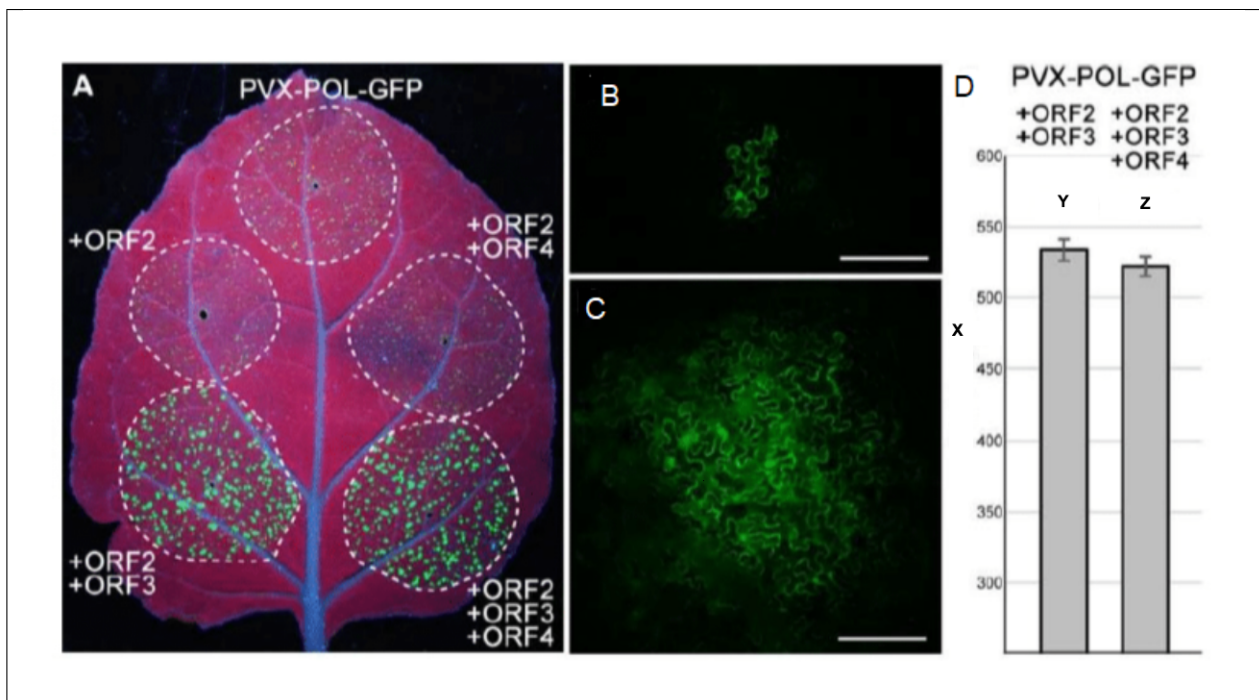
Q.9

THIS QUESTION HAS BEEN DELETED. PLEASE DO NOT ATTEMPT TO ANSWER IT.

Typically, plant viruses encode proteins which allow the virus to be transported between plant cells through plasmodesmata.

The RNA genome of the recently discovered Hibiscus green spot virus (HGSV) contains three open reading frames (ORF2, ORF3, ORF4), which may encode such transport proteins.

Each ORF was coexpressed, in different combinations, with the PVX-POL-GFP RNA-construct, which is easily detected as it expresses green fluorescent protein (GFP). The leaves of *Nicotiana benthamiana* (tobacco) were infiltrated with different constructs, and the movement of GFP into neighbouring cells was assessed.



A) Dashed lines encircle areas infiltrated with each construct.

B-C) Fluorescent microscopy of infiltrated areas (Scale bars = 200 μ m).

B) Image taken for PVX-POL-GFP.

C) Image taken for PVX-POL-GFP + ORF2 + ORF3

D) The mean area of fluorescent loci (X) observed in leaf areas in which PVX-POL-GFP was co-infiltrated with either ORF2 + ORF3 or ORF2 + ORF3 + ORF4. Error bars show 95 percent confidence intervals.

True or False?

Q.9.1 PVX-POL-GFP itself can independently move through plasmodesmata.

1.0pt

Theory 1



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Q1-20

English (Official)

Q.9.2	ORF4 is not necessary for the efficient transport of virus RNA into neighbouring cells.	1.0pt
--------------	--	-------

Q.9.3	This data is sufficient to conclude that ORF3 is necessary and sufficient for the transport of virus RNA through plasmodesmata.	1.0pt
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Q.9.4	This data is sufficient to conclude that both ORF2 and ORF3 in combination is necessary and sufficient for the transport of virus RNA through plasmodesmata.	1.0pt
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Q.9.5	ORF4, in combination with ORF2 and ORF3, drastically reduces transport of PVX-POL-GFP into neighbouring cells.	1.0pt
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Q.10

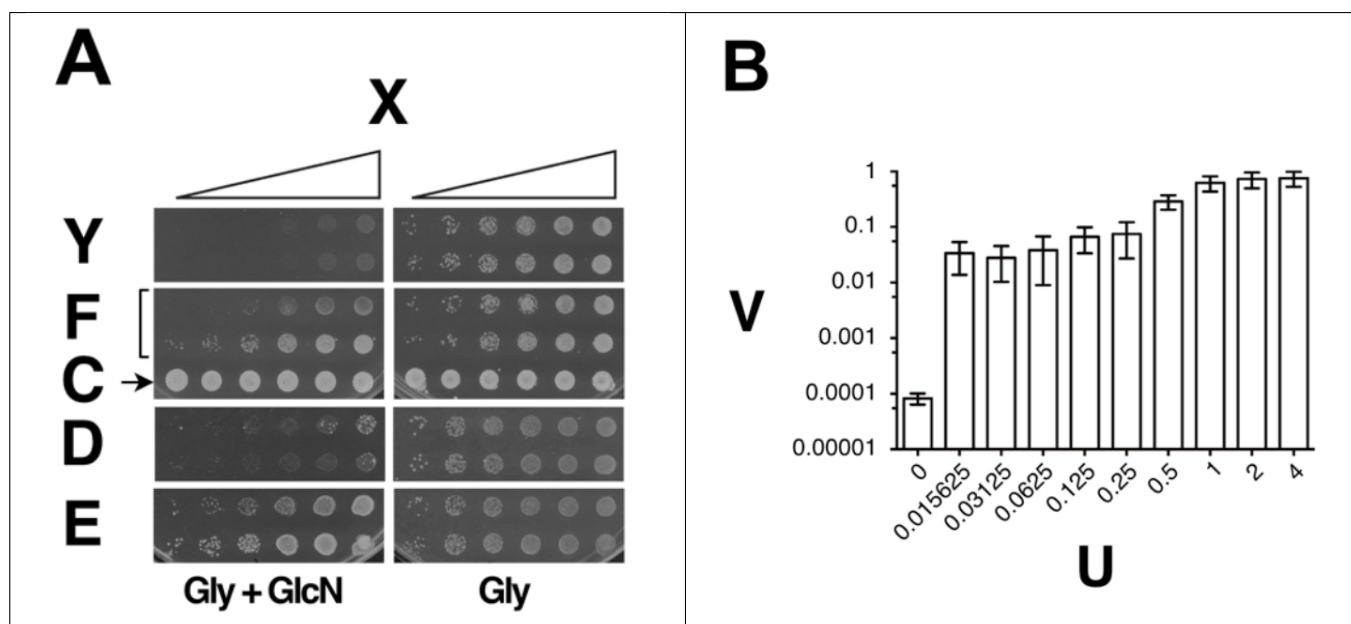
Yeast (*Saccharomyces cerevisiae*) prion protein Pma1 is found in two significantly different conformations.

In one of these conformations, the protein clumps resulting in loss of physiological function of the protein. This results in the '[GAR+]' phenotype. This phenotype is spread by cytoplasmic, non-Mendelian inheritance: sporadically daughter cells are formed which do not contain Pma1 protein clumps, so these have a [*gar*-] phenotype.

Catabolic repression describes the phenomenon of yeast using glucose as a sole source of carbon and energy, despite the presence of other organic compounds that yeast cells can use in metabolism. Only in the absence of glucose, will yeast cells use other sources of carbon and energy, e.g. glycerol.

In [GAR+] yeast, there is no catabolic repression.

Lactic acid secreted by *Staphylococcus gallinarum* bacteria, which live alongside *S. cerevisiae*, can induce a change in the yeast phenotype from [*gar*-] to [GAR+]. In an experiment, yeast was grown on solid agar-agar minimal medium containing glycerol (Gly) or glycerol plus glucosamine (Gly+GlcN). Glucosamine induces catabolic repression in yeast but is not metabolized by *S. cerevisiae*.



X	Serial dilution of <i>S. cerevisiae</i> suspension (diluted from right to left)
Y	<i>S. cerevisiae</i> only (In duplicates)
F	<i>S. cerevisiae</i> (In duplicates)
C	<i>S. gallinarum</i>
D	<i>S. cerevisiae</i> + filtered unused bacterial medium (In duplicates)
E	<i>S. cerevisiae</i> + filtered medium after <i>S. gallinarum</i> cultivation (In duplicates)
U	lactic acid concentration
V	fraction of [GAR+] colonies in yeast population ± standard deviation



True or False?

Q.10.1 A point mutation in the gene encoding the Pma1 protein, without any major conformational change, will result in the [GAR+] phenotype. 1.0pt

Q.10.2 The occurrence of [*gar*-] cells is higher in cultures lacking lactic acid, than cultures containing lactic acid. 1.0pt

Q.10.3 Cytofusion (the transfer of cytoplasm) from a [GAR+] cell to a [*gar*-] cell will change its phenotype to [GAR+]. 1.0pt

Q.10.4 The results show that the biggest change in yeast phenotype is caused by the products of the bacteria themselves, rather than components of the bacterial medium. 1.0pt

Q.10.5 Lactic acid secreted by *S. gallinarum* diffuses in the agar-agar solidified medium. 1.0pt



Q.11

Engineering proteins to have desired function and activity has been a long-standing goal of biotechnology.

In an experiment, researchers designed a minimal genome similar to that of a bacteriophage, which encodes two proteins. When expressed in the host *Escherichia coli*, multiple copies of these proteins assemble into an icosahedral package and sometimes encapsulate the genetic material within.

Three variations were designed;

I53-50, which is known to assemble into an icosahedral structure,

I53-50-v1 which was a mutated sequence of I53-50 thus named version 1,

and the I53-50-Btat which was generated by genetically inserting a naturally occurring nucleic acid binding peptide (Btat) to the interior-facing terminus of the capsid.

To test for viability of these engineered "viruses" two experiments were performed. In the first experiment the host bacteria were lysed and debris was removed, then put through affinity and size exclusion chromatography. The resulting material was treated with RNA-se and DNA-se enzymes and visualized on gel electrophoresis stained for protein, nucleic acid, and nucleic acid after addition of reverse transcriptase.

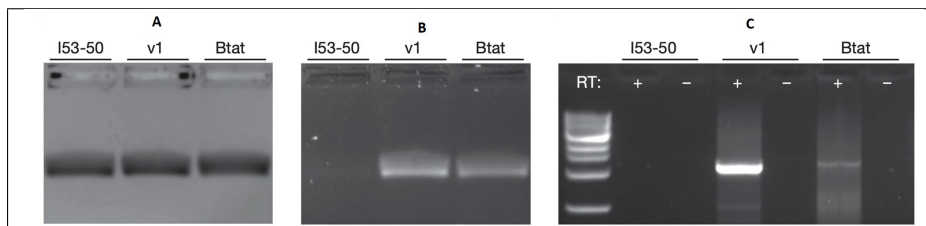


Figure 1. The first experiment. Nucleocapsids were purified and RNase and DNase enzymes were added, then A) protein content was examined. B) after denaturation of the protein and addition of DNase, nucleic acid content was examined. C) after denaturation of the proteins nucleic acid content was examined in the presence (shown by the plus sign above columns) and absence (shown by the minus sign above columns) of the reverse transcriptase (RT) enzyme. Note that highly diluted samples were used to perform RT-PCR.

A	Protein
B	Nucleic acid
C	RT-PCR

In order to improve this capsid, a second experiment was performed. Researchers analyzed the effect of single site mutations on the enrichment of the genome; which shows the degree of protection provided by the capsid. By the end of this experiment, overall beneficial mutations were selected to produce I53-50-v2, or the version 2 of this capsid.

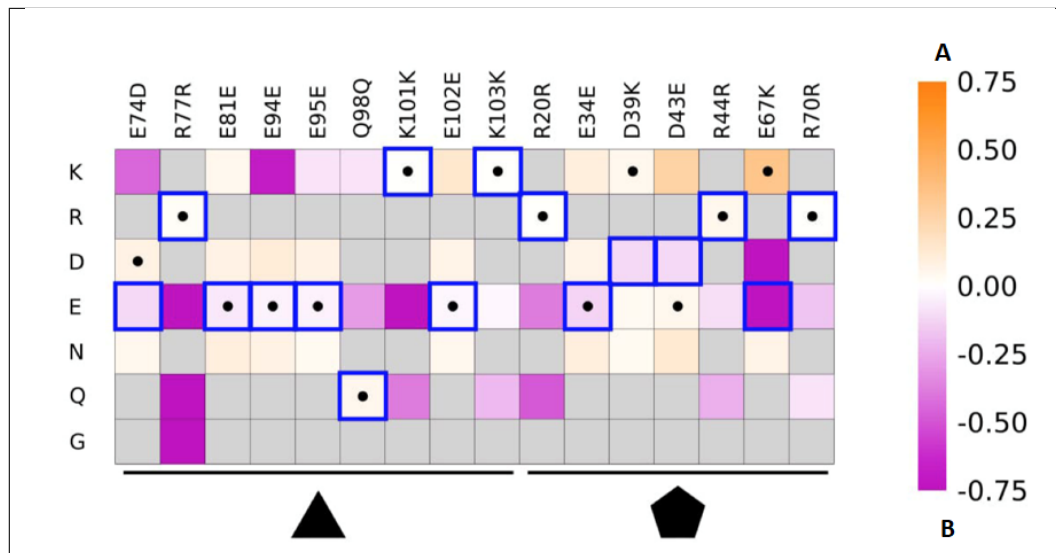


Figure 2. The second experiment was performed to improve the characteristics of the v1 nucleocapsids. The heat-map shows effects of various mutations on nucleic protection provided by the capsid. For the two proteins in the viral genome (denoted by the triangle and the pentagon), each column shows a site in the protein, and each row indicates what amino acid was substituted in that mutation. The effect of each of these mutations is represented as the color of that cell according to the color-bar. The text above each column, shows the chosen mutation at that site at the end of the experiment. For example K179N indicates the starting sequence had an Lysine at the 179th site and was replaced by a Asparagine in the evolved capsid protein. This is also shown by the Blue squares and black dots which indicate the I53-50-v1 starting sequence and I53-50-v2 selected sequence, respectively

A	Enriched
B	Depleted

True or False?

Q.11.1 The reason I53-50 did not package any nucleic acid is because it was unable to produce protein particles. 1.0pt

Q.11.2 The genetic material packaged in the v1 and Btat variants is RNA. 1.0pt

Q.11.3 The positive electrical charge inside the capsid could be the reason why the Btat variant can efficiently package the genome. 1.0pt

Q.11.4 Addition of positively charged amino-acids into the protein sequences is always beneficial to the protection of the encapsulated genetic material. 1.0pt



Q.12

Humans have about 20,000 protein-coding genes.

Assume the average (mean) human protein weighs 50 kDa.

The average amino acid weighs 110 Da.

Use this information to estimate the total length, in base-pairs, of coding sequence in the human genome.

Q.12.1 Give your answer to the nearest million base-pairs.
..... million base-pairs

3.0pt

In chimpanzees, < 1% of the genome is protein-coding. Centromeres are about 0.2-7 Mbp, depending on chromosome. Telomeres are about 5-15 Kbp at birth.

Q.12.2 What kind of sequences comprise the majority of the chimpanzee genome?

1.0pt

- A. Transposons, repeated elements, ancient viruses and other 'genetic parasites'.
- B. Promotor, enhancer and other adaptive gene regulatory sequences.
- C. Centromeric and telomeric sequences.
- D. siRNA, rRNA and other non-coding RNA sequences

An alien plant has 100 million base-pairs of protein-coding sequence in its genome.

The alien uses 20 different amino acids (like us) but has 3 different DNA base pairs (A/T, G/C and X/Y).

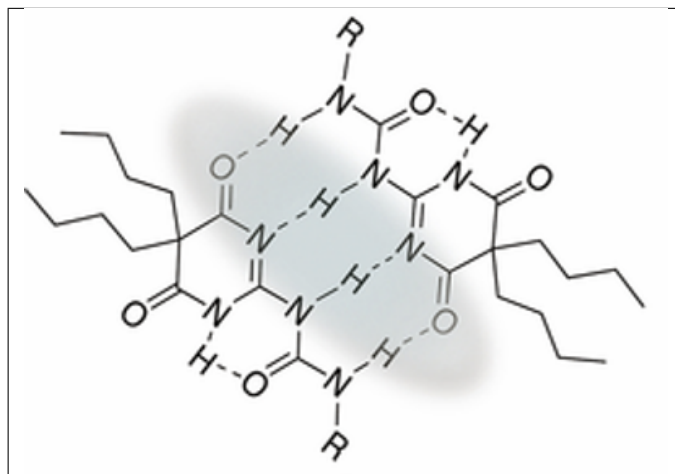
Q.12.3 Calculate the maximum total length of protein sequence (in amino acids) this alien could encode.

3.0pt

Assume there are no overlapping coding regions.

Give your answer to the nearest million amino acids. ----- million amino acids.

The chemical structure of an X/Y base pair is shown.



Q.12.4 Which DNA sequence has the highest melting temperature?

1.0pt

- A. ATTATAAAATAAT
- B. GCGCGCCCCGGCG
- C. GCGG
- D. ATGCGAYTCTX
- E. XYXYXYXYXYXY



Q.13

In bacteria, the molecular weight of the gene for 23S ribosomal RNA is 5.5×10^5 daltons.

In an experiment, the total DNA of the bacteria had an optical density (OD) of 8.0 arbitrary units.

The DNA encoding 23S rRNA had an optical density of 0.024 arbitrary units in the same sample volume.

The arbitrary extinction coefficient of both sequences is 1.0×10^9 .

The molecular weight of the bacterial genome is 1.1×10^9 daltons.

Q.13.1 How many copies of the gene for 23S rRNA does a single bacterial genome contain? 3.0pt

Write your answer rounded to the nearest whole number.



Q.14

Theoretically, in human cells, the rate of DNA polymerase during the replication is about 100 nucleotides per second. Assume that each copy of human genome contains 3×10^9 nucleotide and that both copies of the genome are identical.

Q.14.1 What is the minimum number of origins that such cells need to replicate their DNA every 12 hours (give your answer as integer (whole number))? 3.0pt

Q.14.2 On average, how many nucleotides are replicated from one origin within 12 hours? 3.0pt
Give your answer in millions of nucleotides to 2 decimal places
million nucleotides.



Q.15

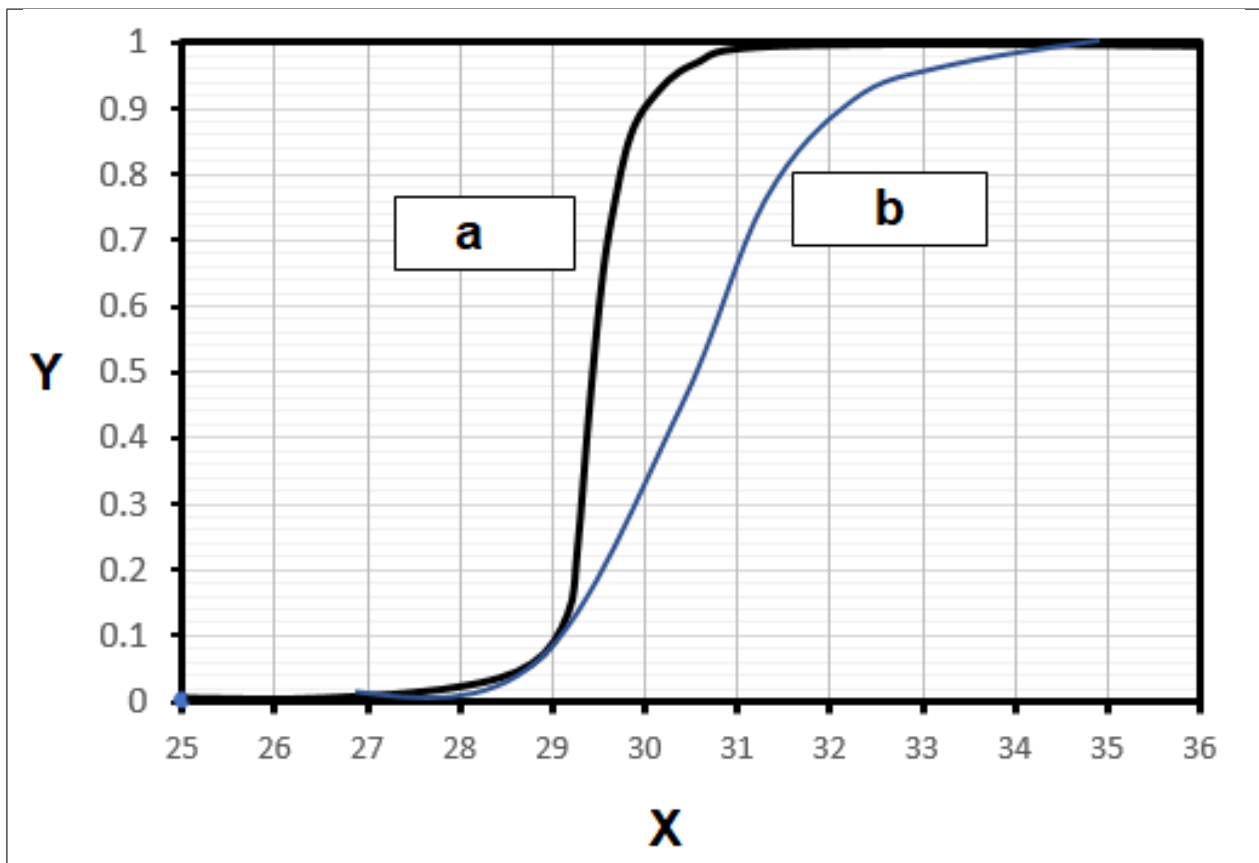
Hawksbill turtles breed on Saadiyat Island in Abu Dhabi.



Sex in sea turtles is controlled by the temperature of the developing eggs (temperature-dependent sex determination). Higher temperatures lead to more females, and lower temperatures, to more males.

As the global climate is rapidly heating, there is a risk that many populations of long-lived sea turtles could develop biased sex ratios.

On average, female sea turtles, which have a prolonged reproductive period extending to 60 to 70 years, mate once every three years, storing sperm within their bodies during this period, whilst the males try to mate every year. The figure below models the influence of temperature on the probability of eggs developing into females in two species of sea turtle.



Theory 1



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Q1-30

English (Official)

X	Temperature (°C)
Y	Probability of a female hatchling
a	Species 1
b	Species 2

Part A

Answer the following :

Q.15.1

3.0pt

If an individual of Species 1 has 150 eggs in a clutch, then, based on the model above, what would be the expected number of female hatchlings at 30°C?
Expected number of female hatchlings =

Part B

Q.15.2

True or false?

Q.15.2.1

Species 2 will be more vulnerable to skewed sex ratios as temperatures rise, compared to Species 1. 1.0pt

Q.15.2.2

Dark-coloured beaches are likely to produce more female hatchlings than pale-coloured beaches 1.0pt

Q.15.2.3

The production of more female hatchlings, due to climate change, is likely to enhance the natural rate of population growth of turtles in the next 10 years. 1.0pt

Q.15.2.4

Rising temperatures during climate change are more likely to skew the operational sex ratio of sea turtles, defined as the ratio of breeding females to breeding males in a population at any point of time, than the absolute sex ratio at hatching. 1.0pt

Q.15.2.5

Another important fear about the impact of climate change, is that increasing sand temperatures will lead to a significant increase in metabolic heating of the developing turtle eggs. 1.0pt

Theory 1



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Q1-31

English (Official)

Q.16

The basal metabolic rate of homoeothermic (warm-blooded) animals is described by Kleiber's law, which postulates that metabolic rate depends on animal mass according to a power law. The exponents vary between $2/3$ (for relatively small size animals) and $3/4$ (for relatively large animals).

Honey badgers are medium sized animals with a mass of about 6 kilograms. Assume the average daily consumed food energy honey badgers release is 2×10^6 J.

$$\text{Energy Consumption} = E = k * m^\alpha$$

Where α can be $\frac{2}{3}$ or $\frac{3}{4}$, m is mass, and k is constant coefficient.

Q.16.1 Calculate the daily food energy consumption of a lesser jerboa with mass 60 grams. (Give your answer as an integer (whole number) in kJ). 3.0pt

Q.16.2 Calculate the daily food energy consumption of a camel with mass 600 kilograms. (Give your answer in MJ to 1 decimal point). 3.0pt

Q.16.3 Calculate how many lesser jerboas could feed on the desert area sufficient for one camel feeding. Give your answer as an integer (whole number). 3.0pt

Theory 1



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Q1-32

English (Official)

Q.17

In ecology, the similarity of two communities can be measured by calculating the Sorensen-Dice coefficient (DSC) and Jaccard index (JI).

$$DSC = 2 \frac{A \cap B}{A + B}$$

$$JI = \frac{A \cap B}{A + B - (A \cap B)}$$

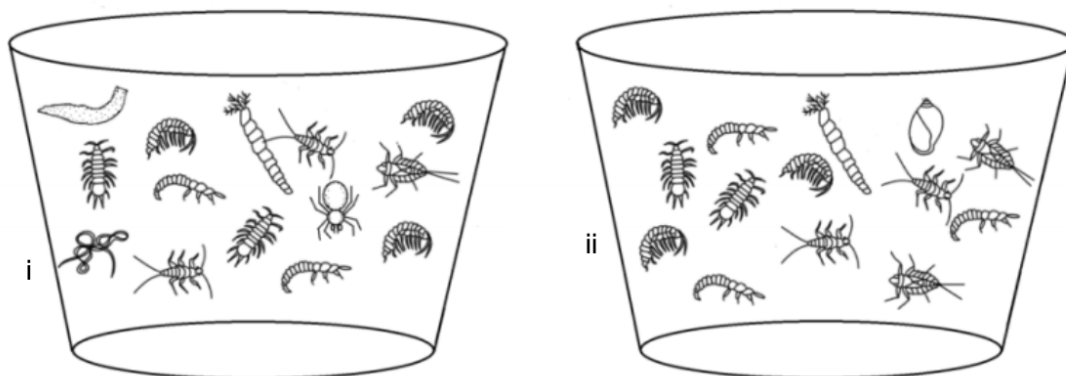
Where A and B are the number of species in the two communities and $A \cap B$ is the number of species common to both communities.

In the figure below, you can see two samples of invertebrates, collected from two small rivers, i and ii respectively. Similar looking animals belong to the same species. Calculate the Sorensen-Dice coefficient and Jaccard index for the rivers i and ii.

Q.17

6.0pt

Q.17.1 DSC	=
Q.17.2 JI	=



Theory 1



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Q1-33

English (Official)

True or False?

Q.17.3.1	For the same communities, DSC is always equal or higher than JI.	1.0pt
-----------------	--	-------

Q.17.3.2	Rivers iii and i have $DSC = 0.8$ and $JI = 0.67$; faunal similarity between rivers i and iii is thus higher than between rivers i and ii.	1.0pt
-----------------	---	-------

Q.17.3.3	The discriminative capacity of DSC is higher than that of JI for highly similar communities.	1.0pt
-----------------	--	-------

Theory 1



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Q1-34

English (Official)

Q.18

Ecosystems rarely remain in a steady state but fluctuate owing to various disturbances, including human activity.

The state of the ecosystem gradually changes with increasing disturbance intensity. However, beyond a certain level of disturbance, the ecosystem may suddenly change shift to another state. This level of disturbance intensity is called a “tipping point”.

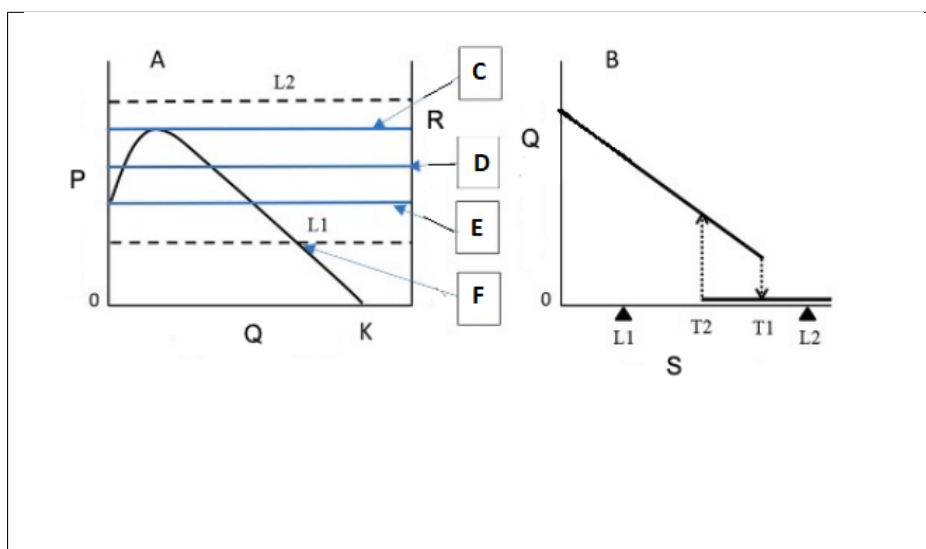
Furthermore, once the ecosystem changes to another state, it may not easily return to its original state, even if the disturbance is weakened. For example, the tipping point at which vegetation disappears differs from that at which it recovers.

In the figure below, this concept is illustrated based on the balance between the rate of increase in vegetation biomass, and the rate of vegetation consumption by livestock (a type of disturbance).

The solid line in Figure A is a plot of the change in vegetation growth rate per unit biomass as a function of vegetation biomass, where K indicates the carrying capacity of the biomass. Below a certain vegetation biomass, the vegetation growth rate decreases with decreasing vegetation biomass owing to soil degradation.

The dashed lines indicate the rate of biomass consumption by livestock. L1 and L2 represent consumption rates at low and high livestock densities, respectively.

In Figure B, the relationship between livestock density and steady-state vegetation biomass is shown, as presented in figure A. T1 is the tipping point of vegetation disappearance, and T2 is the tipping point of vegetation recovery.



P	Growth rate (Biomass)
Q	Vegetation Biomass
R	Consumption rate (Biomass)
S	Livestock density

Theory 1



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Q1-35

English (Official)

True or False?

Q.18.1 T1 decreases when plant productivity is low.

1.0pt

Q.18.2 T1 decreases when resource competition among plants is weak.

1.0pt

Q.18.3 T2 decreases when soil degradation is severe.

1.0pt

Q.18.4 T1 decreases when there are many unpalatable plants (plants livestock do not like to eat).

1.0pt

Q.18.5 In Figure A, T1 is represented by the line D.

1.0pt

Q.18.6 In Figure A, T2 is represented by the line E.

1.0pt

Q.18.7 In Figure A, point F is an **unstable** equilibrium.

1.0pt

Theory 1



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Q1-36

English (Official)

Q.19

Defending a territory requires time and energy. Any animal should only defend territories if the benefits of defence outweigh the costs.

Consider a bird species that feeds only on the nectar of flowers. The table below shows the foraging time required for the bird to meet its daily energy requirements when it obtains given amounts of nectar per flower.

The metabolic costs associated with various activities of the bird are as follows:

Foraging for nectar: 500 calories/h

Sitting on a perch: 200 calories/h

Territory defence: 1500 calories/h

Nectar per flower (microlitres)	Time to get energy (hours)
1	8
2	4
3	2.7

If a bird defends a territory, it excludes other nectar consumers and this increases the amount of nectar per flower from 2 microlitres to 3 microlitres. The bird thus spends less time foraging and more time sitting on a perch.

Answer the following questions:

Q.19.1 Calculate the energy saved by this bird, with reduced foraging time, as compared to an individual, which is not territorial.
..... calories. 3.0pt

Q.19.2 If the bird needs to spend 0.28 hours per day defending territory, instead of perching, what is the cost of defence faced by the bird, compared to a bird which is not territorial?
..... calories. 3.0pt

True or False?

Q.19.3.1 Under the conditions specified above, the bird is likely to show territorial defence. 1.0pt

Q.19.3.2 The birds will almost never be territorial if it reduces the amount of time spent perching. 1.0pt

Q.19.3.3 The birds will almost always be territorial if the cost of foraging per hour is higher than the cost of defence per hour. 1.0pt

Theory 1



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Q1-37

English (Official)

Q.19.3.4 The birds will not show territorial defence when the net costs, incurred by defence, are lower than those of not defending a territory.	1.0pt
--	--------------



Q.20

The pied flycatcher (*Ficedula hypoleuca*) and collared flycatcher (*F. albicollis*) are two closely related and morphologically very similar bird species.

Their cross-species hybrids are completely sterile.

Their geographical distributions partially overlap (Figure 1A).

A recent study recorded songs of 168 male flycatchers of both species from different geographic locations. Various acoustic parameters of individual songs were measured, and differences between songs were visualized using principal component analysis (PCA) (Figure 1B). PCA integrates different parameters of the song and transforms them into principal components (PC), which allows for the reduction of multidimensional data to a few dimensions (two in this case, PC1 and PC2). Similar songs will have similar values for a given principal component.

The recorded songs were also played to *F. hypoleuca* nestlings and the nestlings' begging calls in response to the songs were counted (Figures 2 and 3).

In this study, the rate at which nestlings responded to the played male songs from their population did not correlate with how similar the played songs were to the songs of their social fathers. Social fathers are the male whose calls nestlings hear most often.

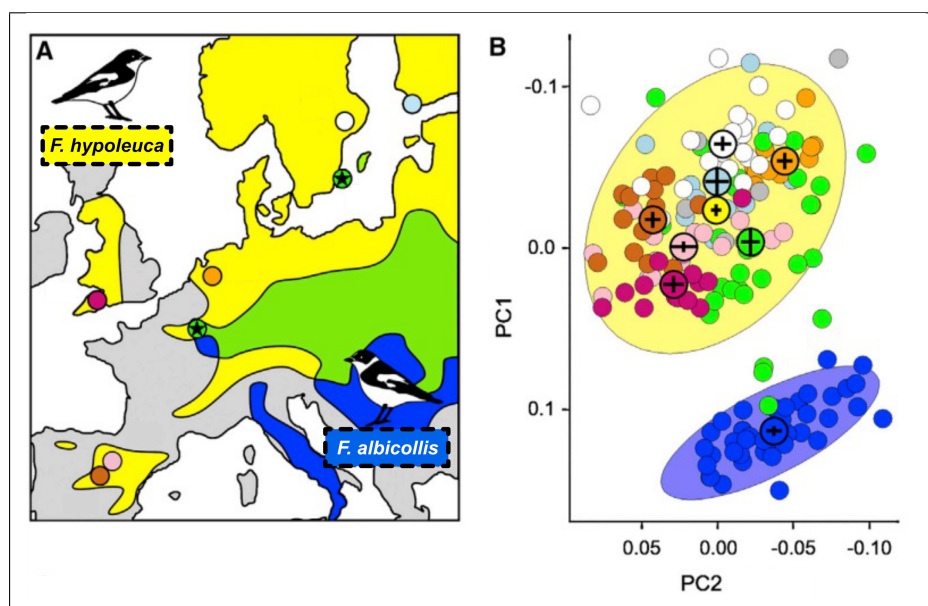


Figure 1A. Figure 1B.

Figure 1A. Geographic distribution of the *F. hypoleuca* (yellow) and *F. albicollis* (blue) and overlap (green). Colored dots show *F. hypoleuca* populations used in the study.

Figure 1B. Results of Principal Components Analysis. Each dot corresponds to a single individual's song. Blue and yellow ellipses include 95% of the data points of the corresponding species.

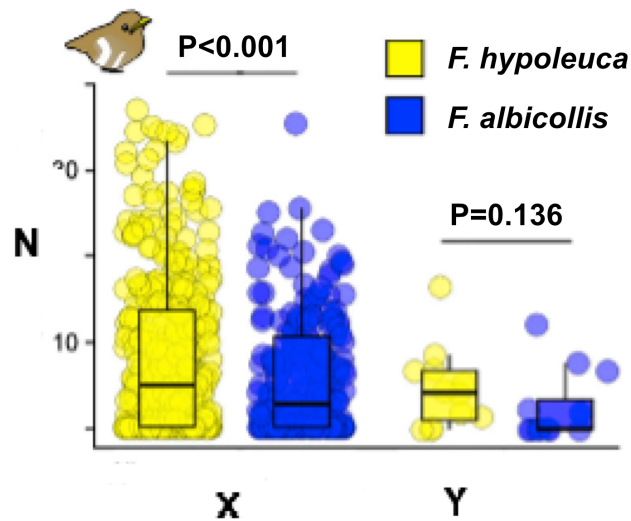


Figure 2

X	Allopatry (6 populations, 347 clutches)
Y	Sympatry (1 populations, 37 clutches)
N	Begging calls (mean within clutch)

Figure 2. Number of begging calls (N) by *F. hypoleuca* nestlings (mean per clutch) in response to a recorded song of *F. hypoleuca* (yellow) or *F. albicollis* (blue) males.

The left panel shows results for regions where only *F. hypoleuca* is found ("Allopatry") while the right panel represents a region where both species co-exist ("Sympatry").

P-values above the boxplots reflect significance of differences between groups.

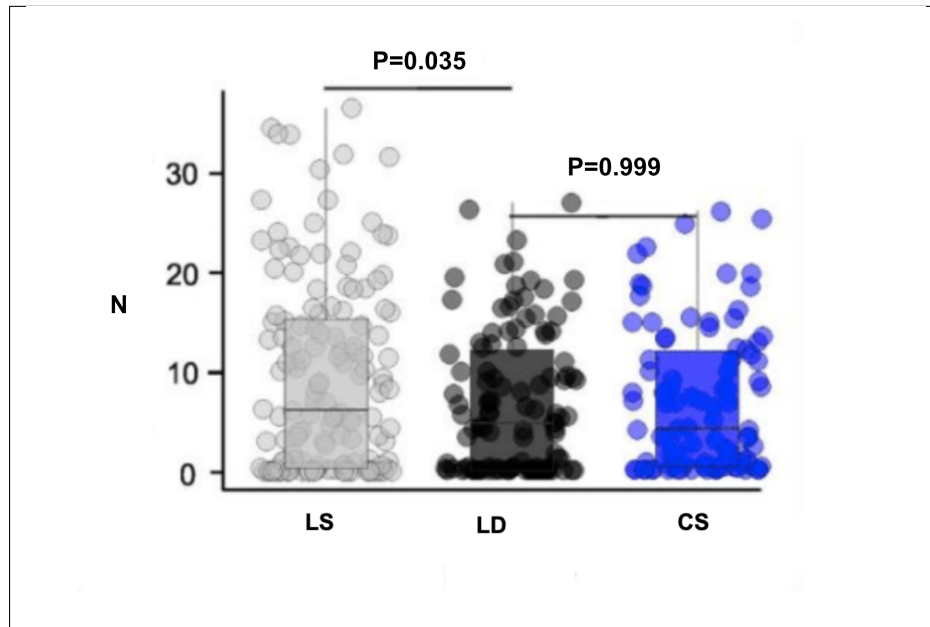


Figure 3

N	Begging calls (mean within clutch)
LS	Local-similar
LD	Local-dissimilar
CS	Collared-similar

Figure 3. Number of begging calls (N) by *F. hypoleuca* nestlings (mean per clutch) in response to recorded *F. hypoleuca* songs which are:

- similar to songs of the nestlings' local population (grey),
- dissimilar to songs of the nestlings' local population (black)
- similar to songs of *F. albicollis* (blue).

True or False?

Q.20.1 These results support the existence of local song dialects in *F. hypoleuca*. 1.0pt

Q.20.2 These results support the idea that song differences between *F. hypoleuca* and *F. albicollis* evolved primarily as an adaptation to avoid cross-species hybridization. 1.0pt

Q.20.3 This study provides evidence that *F. hypoleuca* nestlings learn their songs from their social fathers. 1.0pt



Q.20.4 It might be expected that genome-average genetic differences between *F. hy-* 1.0pt
poleuca populations will increase over time.



Q.21

Pioneering aquarium experiments showed that laboratory-reared, mature female Trinidadian guppy fish (*Poecilia reticulata*) could copy the mate-choice of other females.

Each experiment consisted of an observation period, when a 'focal female' could observe two males, each in a separate chamber at each end of her aquarium. One of the males could court another female (the 'model female'), who was adjacent to the male but separated by glass.

In a following preference test, the model female was removed, and the focal female was allowed to choose between the two males. The time that the focal female spent within the preference zones adjacent to the male chambers, indicated her mate preference.

In 17 out of 20 trials of this experiment (Experiment 1), the focal females preferred to associate with the male that they had previously observed interacting with the model female.

This provided evidence that newly acquired social cues could potentially influence mate selection.

However, four alternative hypotheses could also potentially explain these results. Four other sets of experiments, similar to Experiment 1, but with some modifications, were designed to test these hypotheses.

Match the four experimental designs, 1 to 4, given below with the four hypotheses, A to D, that were tested in these experiments.

	Hypothesis		Experimental Design
A	Schooling Hypothesis: Females prefer the side where they have seen the larger number of fish	1	After the observation period, both the females were removed and a 'naïve' female, never exposed to males, was introduced and allowed to choose between the same two males in the end chambers
B	No-Interaction Hypothesis: Females prefer the side where they have seen a male and a female together but without sexual interaction between the pair	2	Females were placed in the two end chambers of the test aquarium instead of males
C	Male-Activity Hypothesis: Females prefer a male that was more active in the recent past	3	Two tests, similar to Experiment 1 above, were carried out simultaneously in two test aquaria invisible to one another. The males from the two aquaria were exchanged immediately before the focal female was allowed to choose between them.
D	Female Sexual Priming Hypothesis: Females, who have seen a female-male encounter might choose males that behave as though they have just been involved in an interaction with a female	4	One-way mirrors were placed between the test aquarium and each of the end chambers. Lighting was such that the two males saw their own images but the model and the focal females saw through the mirrors as though they were clear glass



Q.21

4.0pt

Hypothesis	Experimental Design
A	
B	
C	
D	

Theory 1



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Q1-44

English (Official)

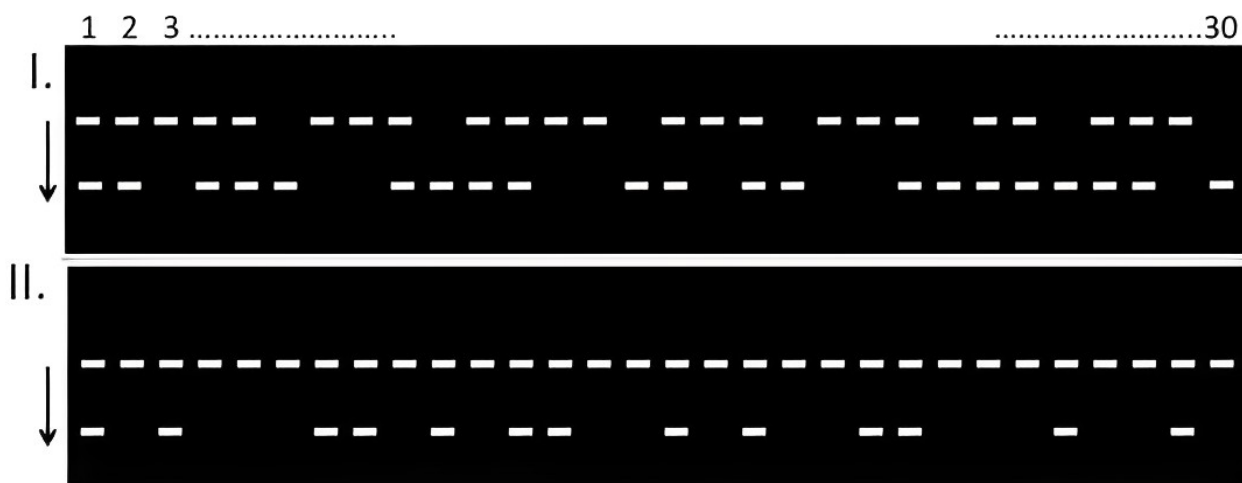
Q.22

Gregor Mendel described the inheritance of round and wrinkled pea seeds. He showed the round (R) phenotype was dominant over wrinkled (r).

After 135 years, the gene SBE1, and the insertion of a transposable element, which caused the wrinkled phenotype, were discovered. SBE1 codes for an enzyme involved in starch biosynthesis. Wrinkled seeds are characterized by higher levels of sucrose, and lower levels of starch, compared to round seeds.

In a PCR test, a pair of primers, targeting flanking sides of the site of insertion, are used to amplify the genomic DNA. The products are resolved by agarose gel electrophoresis.

A geneticist made two independent crosses (I and II) between peas with different genotypes. 30 progeny from each cross was analyzed by PCR. Each lane in the gel below represents analysis of one progeny.



The downward arrow denotes the direction of migration.

Q.22.1 Identify the parents for each of the cross by clicking the appropriate box in the table: 2.0pt

		Genotypes of parental cross ($P_1 \times P_2$)			
		Rr $\times$ RR (A)	rr $\times$ Rr (B)	Rr $\times$ Rr (C)	rr $\times$ RR (D)
Q.22.1.1	Cross I				
Q.22.1.2	Cross II				



Q.22.2 In cross I, what kind of seeds does individual 3 produce when self-pollinated? 1.0pt

- A. Round
- B. Wrinkled
- C. A mixture of round and wrinkled seeds
- D. All seeds are semi-wrinkled.

Q.22.3 True or false? 1.0pt

Heterozygous seeds have higher levels of SBE1 activity compared to insertion homozygotes.

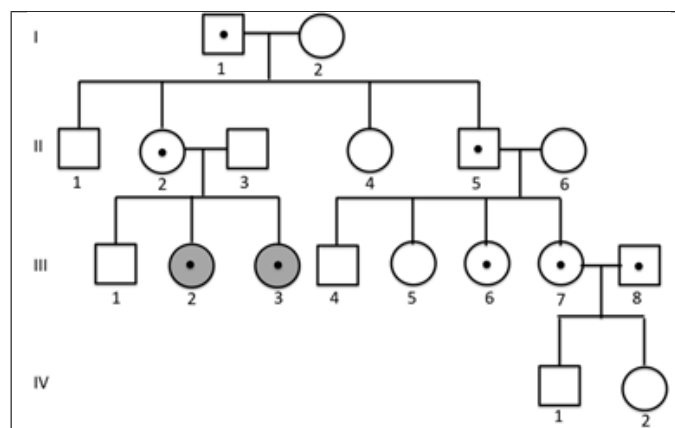


Q.23

The pedigree shows the inheritance pattern of gene X, whose mutation leads to a disorder in adults.

- The mutation leads to a loss-of-function allele.
- In addition, gene X undergoes genomic imprinting.
- In this case, the imprint prevents the allele from being expressed.

The expression of alleles that are subject to imprinting depend on whether they were inherited from the mother or the father. When the imprinting takes place during sperm formation, it is called as paternal imprinting. If it takes place during formation of egg, it is known as maternal imprinting. In each generation, the imprints are reset during gametogenesis.



Individuals who are carriers for the mutant allele are marked with a dot.

Individuals showing the disorder are shaded.

Individuals in generation IV have not reached adulthood and the presence of the mutant allele has not been analyzed.

True or false?

Q.23.1.1 Individual II-2 has inherited an imprinted allele. 1.0pt

Q.23.1.2 Gene 'X' is paternally imprinted. 1.0pt

For the following, give your answers as decimals to two decimal places.

Q.23.2 Calculate the probability that individual IV-1 will be homozygous for the mutant allele. 2.0pt

Theory 1



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Q1-47

English (Official)

Q.23.3 Calculate the probability that individual IV-1 will show the disorder.

2.0pt

Q.23.4 If the individuals III-7 and III-8 had a third child, calculate the probability that it would be a son showing the disorder.

2.0pt



Q.24

Identifying genetic relatedness between human individuals is useful for many applications.

A common approach to this is based on detecting identical-by-descent (IBD) segments shared by two individuals. IBD segments are chromosomal segments that the two individuals inherited from a common ancestor, and hence are identical in sequence except for any mutations that happened since that common ancestor. IBD segment ends correspond to sites where recombination happened.

At a given position in the genome two individuals can share 0, 1 or 2 IBD segments (IBD0, IBD1 and IBD2 states respectively). Looking at the fraction of the genome in IBD1 and IBD2 states, for a given pair of individuals, is a common practice to infer genealogical relationships between individuals.

In questions 24.1, 24.2 and 24.3 assume that parents of any individual are completely unrelated and don't share any IBD segments.

Indicate the expected fraction of the genome (in percentage, with 100 being the maximum) in IBD1 and IBD2 states between pairs of individuals with the family relationship listed below.

1. Monozygotic twins
2. Parent-offspring
3. Full-siblings
4. Half-siblings
5. Grandparent-grandchild

Q24.1 Fraction of the genome IBD1 state.

Q.24.1

2.0pt

Relationship	IBD1 fraction
1	
2	
3	
4	
5	

Q24.2 Fraction of the genome IBD2 state.

Q.24.2

2.0pt

Relationship	IBD2 fraction
1	
2	
3	
4	
5	



Q24.3 Choose the relationship types for which notable biological variation in IBD sharing is expected. **Indicate types which show variation as True, and others as False.**

Q.24.3

2.0pt

Relationship	True	False
1		
2		
3		
4		
5		

True or False?

Q.24.4.1 On average, IBD segments shared between a parent and an offspring are longer compared to those shared between full siblings. 1.0pt

Q.24.4.2 If we trace one's family tree deep into the past, in the 30th generation we will find 2^{30} people this individual shares IBD with. 1.0pt

Q.24.4.3 The fraction of IBD1 genome between two randomly picked individuals from a single population is higher in populations with smaller effective population size. 1.0pt



Q.25

The average pairwise difference between a pair of sequences in a population is called nucleotide diversity, which is a simple measure of the genetic diversity of a population.

Figure 1 describes 3 alleles (A, B, C) in terms of their frequency in a given population (column 2). Column 3 provides the nucleotide sequences: for alleles B and C only the sequence differences from allele A are provided while positions with the same nucleotide as in A are marked with an asteriks “*”.

A	0.5	GTATA GACTAGATCTACATGTAGCTGACTGCATATGCTGT
B	0.3	*****T*****A*****G*****A*****
C	0.2	*****C*****A*****

Figure 1

Nucleotide diversity can be calculated using the following formula:

$$pi = \sum_{i=1}^n \sum_{j=1}^n (f_i \times f_j \times d_{ij})$$

- Where pi is nucleotide diversity,
- n is the total number of alleles,
- f_i and f_j are frequencies of two alleles,
- d_{ij} is the difference between the two alleles. For example, sequences A and B differ by 4 bases out of 40, so the difference between them is 0.1.

Q.25.1 Calculate the nucleotide diversity in this population. Give the correct answer to 3 decimal places. 3.0pt

Q.25.2 Cheetahs were found to have significantly lower genome-wide genetic diversity than other mammals. Select the likeliest explanation for this observation: 1.0pt

A. Cheetahs adapted very rapidly to the environment.
 B. Cheetahs have an extremely high mutation rate.
 C. The population of cheetahs went through a bottleneck in the recent past.
 D. Natural selection is extremely efficient in removing mutations from Cheetahs' gene pool.

Figure 2 plots nucleotide diversity (y-axis), in 300 bp sliding windows along the sequence of gene Y (x-axis), for a modern cultivated crop plant (dashed line 2, and its wild ancestor (solid line 1). Below the plot the structure of the gene is shown: boxes indicate exons, with grey areas being protein-coding regions and white areas being untranslated regions. The thin bent line shows the intron; the 5' end is on the left.

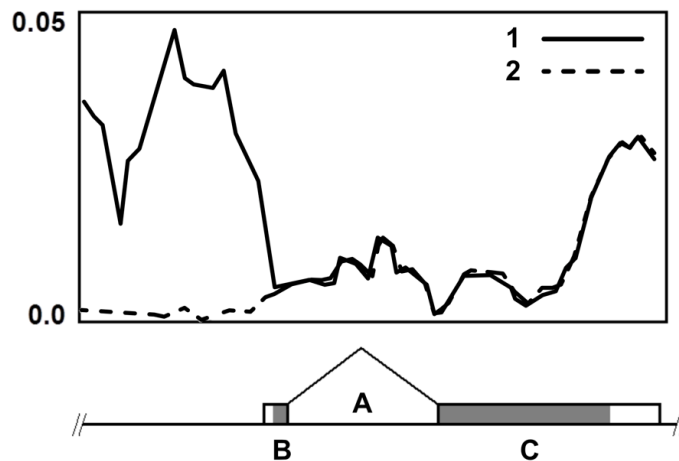


Figure 2

A	Intron
B	Exon 1
C	Exon 2

It has been concluded from the results in figure 2 that a mutation in this locus was positively selected during the domestication process.

- Q.25.3** What is the most likely effect of this mutation? 1.0pt
- A. It results in an amino acid substitution in the encoded protein.
 - B. It affects splicing of gene Y.
 - C. It affects expression of gene Y.
 - D. It results in a premature stop codon in gene Y.

True or false?

- Q.25.4.1** This data suggests purifying selection is acting more strongly on this locus in the wild ancestor than in the domesticated crop. 1.0pt

- Q.25.4.2** This data suggests, that in the wild ancestor, purifying selection is acting more strongly on the sequence upstream of exon 1 compared to the intron of gene Y. 1.0pt

- Q.25.4.3** No recombination occurred in the analysed region during the domestication process. 1.0pt

Theory 1



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Q1-52

English (Official)

Q.26

The question involves two transgenic plant lines, P1 and P2, that produce bisexual flowers.

P1 is transformed with *barnase* gene linked to a gene (*HR*) conferring resistance to a herbicide.

Expression of the Barnase protein in this plant inhibits pollen formation making the plant unable to produce fertile pollen. Male sterility and herbicide resistance are both dominant characters.

P2 is transformed with *barstar* gene, also linked to the *HR* gene. In the presence of Barstar protein the activity of Barnase protein is inhibited, restoring pollen formation. The activity of the Barstar protein is a dominant character.

In P1, the barnase gene lies in linkage group 2, whilst in P2, the barstar gene is in linkage group 3.

P1 is hemizygous for the *barnase* and *HR* genes. P2 is homozygous for both the *barstar* and *HR* genes.

A cross is made between P1 and P2. The F₁ progeny are self-pollinated and the F₂ progeny are analyzed.

Q.26.1 What percentage of F ₁ progeny will be unable to produce fertile pollen?	2.0pt
---	-------

Q.26.2 What percentage of F ₁ progeny will be herbicide resistant?	2.0pt
--	-------

Q.26.3 What percentage of F ₂ progeny will be unable to produce fertile pollen? Give your answer to the nearest whole number	3.0pt
---	-------

Q.26.4 What percentage of F ₂ progeny will be herbicide resistant? Give your answer to the nearest whole number	2.0pt
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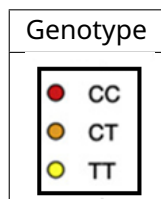
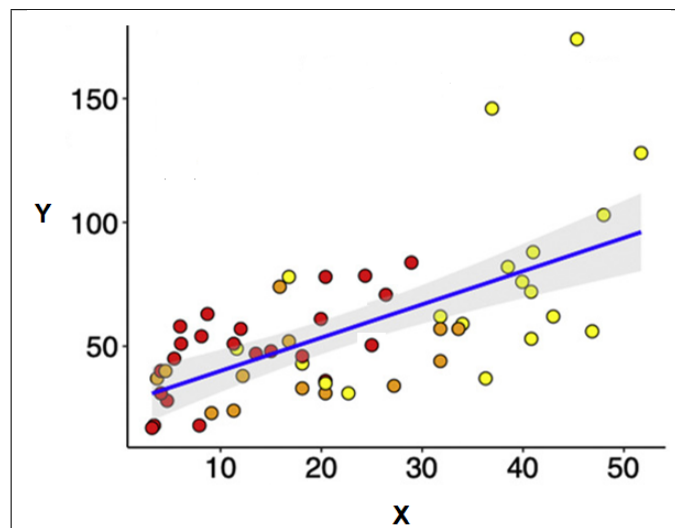


Q.27

Domestic dogs (*Canis lupus familiaris*) are a subspecies of grey wolves (*Canis lupus*). Dogs are unique amongst mammal species for their extremely large range of body sizes.

Scientists sequenced a region of DNA around the IGF1 (insulin-like growth factor 1) gene in thousands of dogs. They found a common SNP (single nucleotide polymorphism, also known as a SNV); a C vs T mutation.

The genotype of the IGF1 SNP was plotted against dog body mass, and against levels of IGF in serum (blood).



X	Body mass(Kg)
Y	IGF-1 Serum level (nmol/L)

Which of these hypotheses are supported by this data:

Q.27.1

True or false?

Q.27.1.1 The T allele is fully dominant to the C allele, which is fully recessive, in controlling dog size 1.0pt



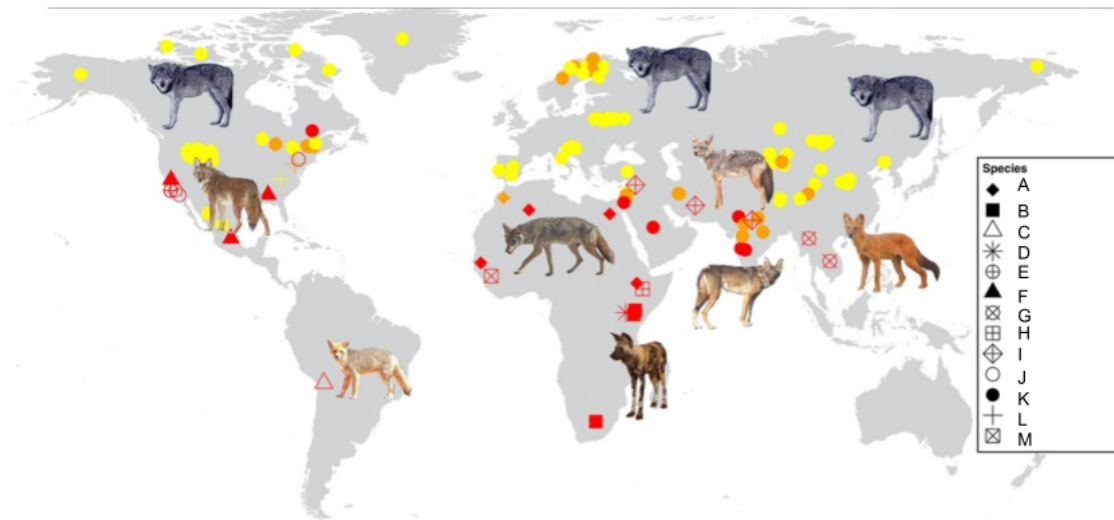
Q.27.1.2 IGF1 controls the majority of size variation of dogs

1.0pt

Q.27.1.3 The C/T SNP must only influence body size through changing levels of IGF1 in serum

1.0pt

Next, scientists sequenced the same SNP in individuals from species across the wider canid (dog) family.





A	Golden Wolf
B	Hunting Dog
C	Andean Fox
D	Black Jackal
E	Island Fox
F	Coyote
G	Dhole
H	Ethiopian Wolf
I	Golden Jackal
J	Grey Fox
K	Grey Wolf
L	Red Wolf
M	Striped Jackal

Which of these hypotheses are most likely based on this data:

Q.27.2

Choose the correct answer

- Q.27.2** A) The most recent common ancestors of domestic dogs were homozygous for the T allele. 1.0pt
- B) The most recent common ancestors of domestic dogs were heterozygous for the T/C alleles.
- C) The most recent common ancestors of domestic dogs were homozygous for the C allele.

Which of these hypotheses are most likely based on this data:

Q.27.3

Choose the correct answer

- Q.27.3** A) The C mutation in domestic dogs appeared recently, and separately to the C allele found in other canid species. 1.0pt
- B) The T mutation first appeared in wolves.
- C) The T allele is older than the C allele.



Q.28

'Embolism', in Xylem vessels, means the presence of air-filled tracheids and/or vessels. Embolisms can result in a substantial impairment of xylem transport and thus hydraulic failure.

Environmental causes of embolism include water stress and winter freezing; potential consequences include reduction of growth and dieback.

Choat et al. (2012) examined the vulnerability of forests to drought-induced hydraulic failure. They measured the minimum xylem pressure in plants under natural conditions (ψ_{min}), and the xylem pressure, ψ_{50} , at which 50% loss of conductivity occurs. They included both angiosperms and gymnosperms in different climate conditions: mean annual precipitation (MAP) ranged from 300 to 4,500 mm, and mean annual temperature from -4°C to 27°C (Figure a).

The difference between ψ_{min} and ψ_x (ψ_x at which X% loss of conductivity occurs) represents a 'safety margin', within which the plant operates in a given environment (Figure b).

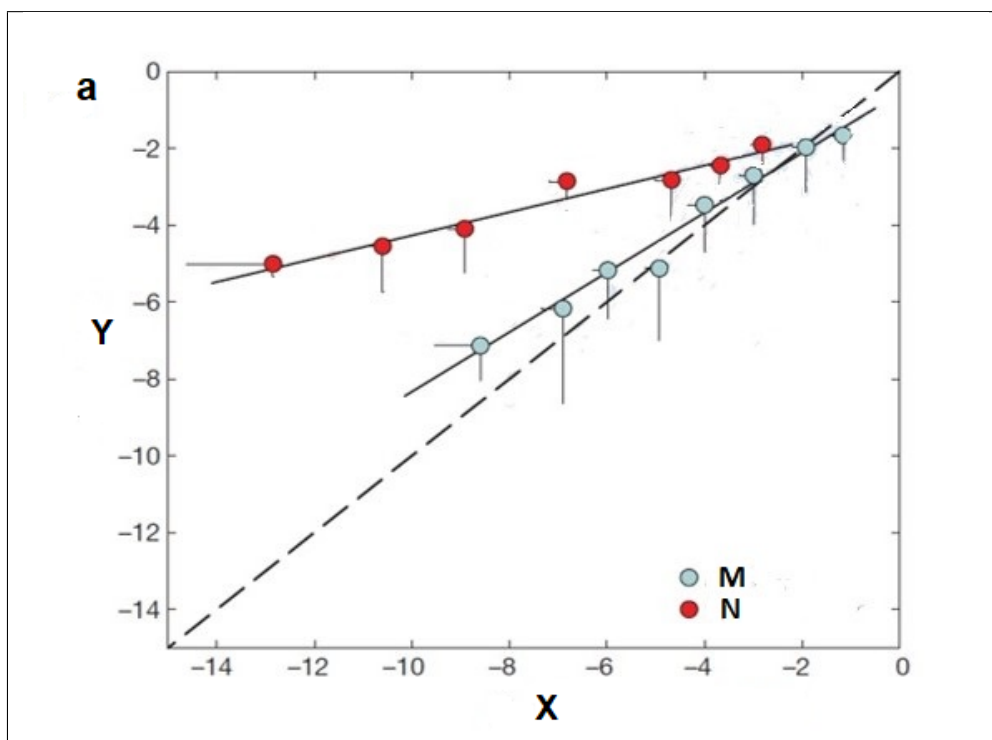


Figure a

X	ψ_{50} (MPa)
Y	ψ_{min} (MPa)
M	Angiosperms
N	Gymnosperms



Figure a. Minimum xylem pressure ($\psi_{\min}$) plotted against ψ_{50} for angiosperm and gymnosperm species.

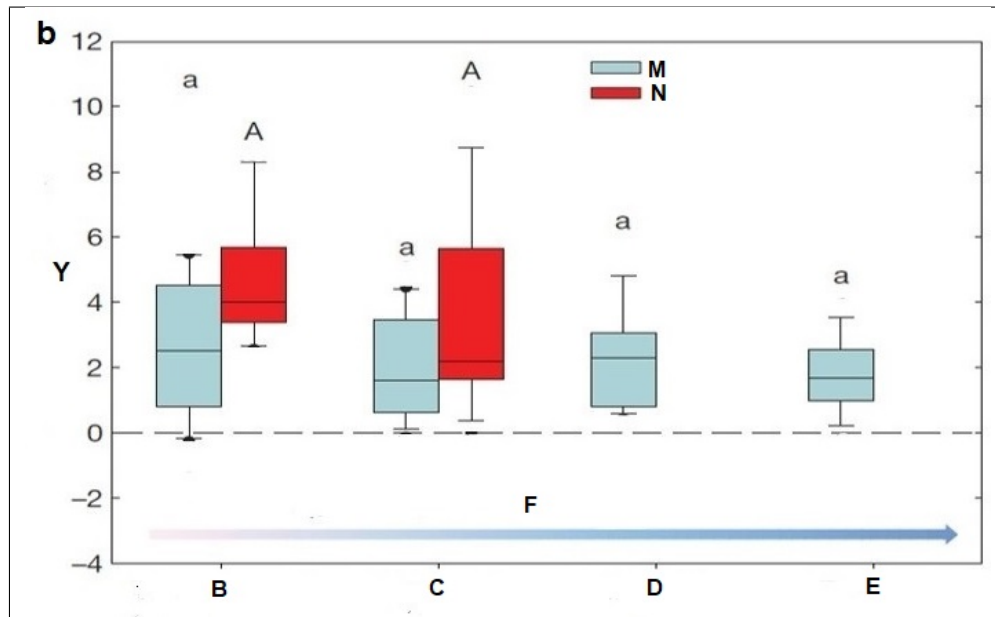


Figure b	
Y	Safety margin ψ_{88} (MPa)
B	Mediterranean and Woodland
C	Temperate forest
D	Tropical seasonal forest
E	Tropical rain forest
F	Increasing mean annual precipitation
M	Angiosperms
N	Gymnosperms

Figure b. Box plot of hydraulic safety margins for angiosperm and gymnosperm species across forest biomes.

Boxes show the median, 25th and 75th percentiles, error bars show the 10th and 90th percentiles. Gymnosperm species were not represented in tropical forests. Bars marked with the same lowercase letter(s) are not significantly different. In addition, bars marked with the same uppercase letter(s) are not significantly different.

True or False?

Q.28.1 After maturity, xylem structure can no longer acclimate to environmental stress to reduce risk of embolism. 1.0pt

Theory 1



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Q1-58

English (Official)

Q.28.2 Gymnosperms show greater hydraulic safety margins than angiosperms.	1.0pt
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Q.28.3 The safety margin quantifies the degree of conservatism in a plant's hydraulic strategy (plants with low safety margins experience higher risk of hydraulic failure)	1.0pt
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Q.28.4 There is global convergence in the vulnerability of forests to drought (all forest biomes are approximately equally vulnerable to hydraulic failure regardless of their current rainfall environment).	1.0pt
--	-------



Q.29

Water deficit (insufficient water availability) occurs in most natural and agricultural habitats and is caused mainly by periods without precipitation. When plant cells experience water deficit, cell dehydration occurs. Cell dehydration leads to plant water stress, which adversely affects many basic physiological processes.

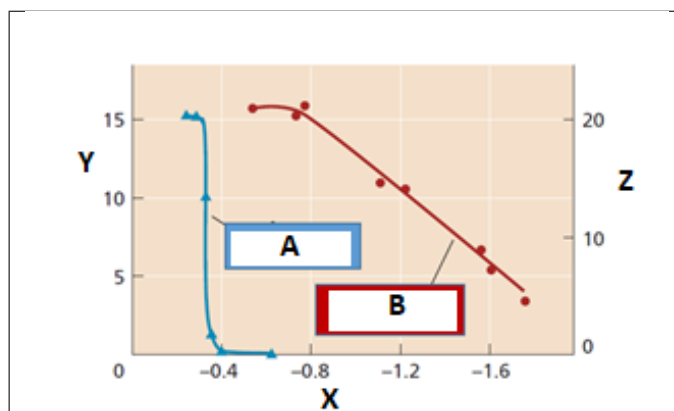


Figure 1. Effects of water stress on photosynthesis and leaf expansion of sunflower (*Helianthus annuus*).

X	Leaf water potential (MPa)
Y	Leaf expansion rate (percent increase in leaf area per 24h)
Z	Photosynthesis rate ($\mu \text{ mol } \text{CO}_2 \text{ m}^{-2} \text{ s}^{-1}$)
A	Leaf expansion
B	Photosynthesis

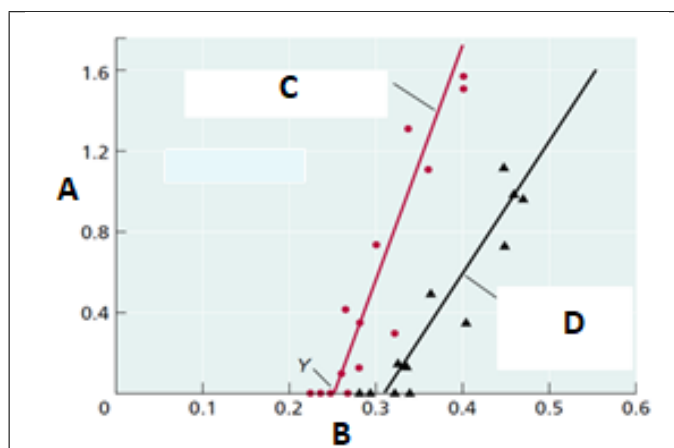


Figure 2. Sunflower (*Helianthus annuus*) plants were grown either with ample water, or with limited soil water to produce mild water stress. After re-watering, plants of both treatment groups were stressed by the withholding of water, and leaf growth rates (GR) and turgor (ψ_p) were periodically measured.

Theory 1



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Q1-60

English (Official)

A	Leaf growth rate ($mm.h^{-1}$), GR
B	Turgor (MPa), ψ
C	Plant 1
D	Plant 2
Y	X-intercept

True or False ?

Q.29.1 Photosynthetic rate is not as responsive to mild water stress as leaf expansion, because photosynthesis is much less sensitive to turgor than is leaf expansion. 1.0pt

Q.29.2 As stomata close during early stages of water stress, water-use efficiency may increase (i.e., more CO_2 may be taken up per unit of water transpired) because stomatal closure inhibits transpiration more than it decreases intercellular CO_2 concentrations. 1.0pt

Q.29.3 Growth slows down when stress reduces turgor. Turgor needs to decrease to zero to eliminate leaf expansion. 1.0pt

Q.29.4 Plant 1 was pre-stressed by growing it with limited soil water to produce mild water stress. Plant 2 was grown with ample water. 1.0pt



Q.30

Wheat is grown on more land area than any other food crop, and it receives about 20% of the world's Nitrogen fertiliser.

In the well-drained soils usually used to grow wheat, NO_3^- is a major N-fertilizer form. If rising atmospheric CO_2 levels significantly affect NO_3^- photoassimilation by wheat, alternative nitrogen fertilisers should be prepared.

Bloom et al. (2012) grew wheat seedlings in controlled environment chambers where CO_2 was controlled at ambient or elevated levels (360 or 700 $\mu\text{mol mol}^{-1}$), and the plants received either 0.2 mM NH_4^+ or 0.2 mM NO_3^- as the N source.

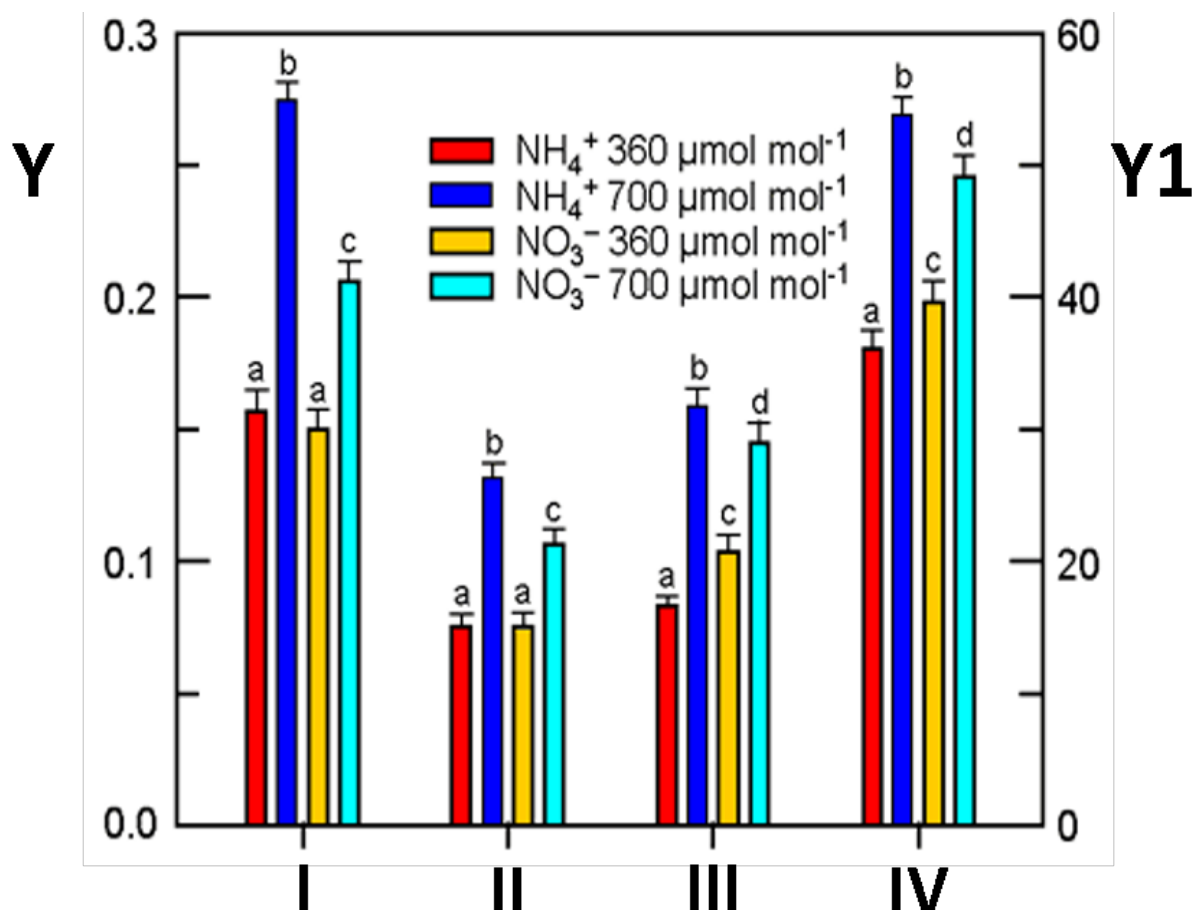


Figure 1. Biomass (g dry mass) and leaf area (cm^2), per plant, of wheat seedlings grown for 14 days in controlled environment chambers. Treatments labeled with different letters differ significantly ($P < 0.05$).



	Figure 1
Y axis	Biomass (g dry mass)
Y1 axis	Leaf area (cm^2). for 14 days in controlled environment chambers.
I	Shoot
II	Stem
III	Root
IV	Leaf area

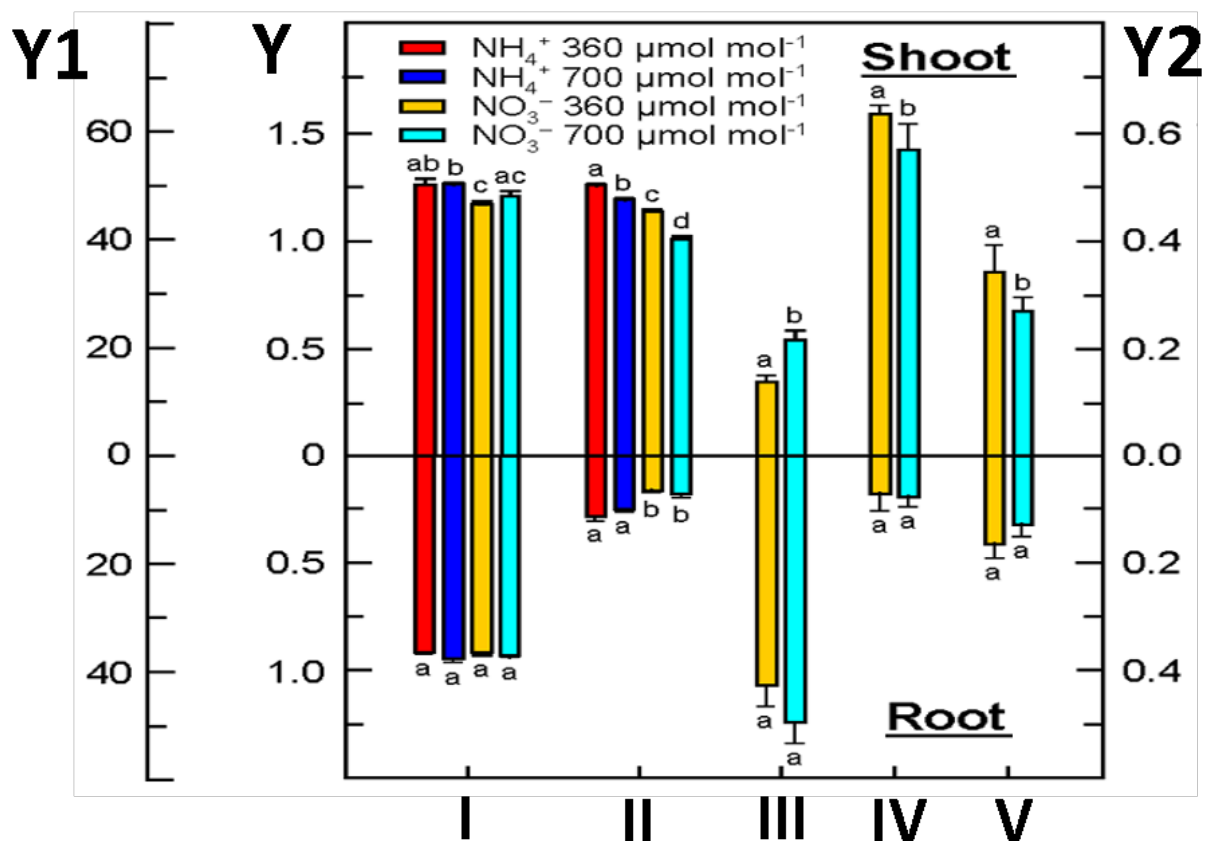


Figure 2. Total N concentration, protein concentration, NO_3^- concentration, NO_3^- reductase activity, and NO_2^- reductase activity in the shoot (top panel) or root (bottom panel) of wheat grown for 14 days in controlled environment chambers. Treatments labeled with different letters differ significantly ($P < 0.05$).

Theory 1



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Q1-63

English (Official)

	Figure 2
Y	NO_3^- concentration ($mg\ g^{-1}$)
Y1	Nitrogen or protein concentration ($mg\ g^{-1}$)
Y2	Enzyme activity
I	Total N
II	Protein
III	NO_3^-
IV	NO_3^- reductase Activity
V	NO_2^- reductase activity

True or false?

Q.30.1 Whether the form in which N was supplied affects shoot and stem growth depends on ambient CO_2 levels. 1.0pt

Q.30.2 The plants receiving NH_4^+ were more responsive to CO_2 enrichment than those receiving NO_3^- . 1.0pt

Q.30.3 Under the two CO_2 regimes, the N absorption per unit plant mass remained unchanged. 1.0pt

Q.30.4 The fate of N , after it was absorbed, was similar under ambient and elevated CO_2 as demonstrated by the balance of inorganic and organic N. 1.0pt

Q.30.5 *In vitro* shoot activities of NO_3^- reductase and NO_2^- reductase changed compared to roots in the different CO_2 regimes. 1.0pt

Q.30.6 The results suggest that rising atmospheric CO_2 will favor taxa that either prefer NH_4^+ as a nitrogen source, or assimilate NO_3^- primarily in their roots. 1.0pt



Q.31

In the following questions, a statement of assertion is followed by a statement of reason.

Mark the correct choice as:

- "a" If **both** Assertion and Reason are true, **and** the Reason is the correct explanation of Assertion.
- "b" If **both** Assertion and Reason are true, **but** Reason is not the correct explanation of Assertion.
- "c" If Assertion is true, but Reason is false.
- "d" If the Assertion is false.

Q.31.1 Assertion: Water is oxidized to oxygen during the light-dependent reactions of photosynthesis. 1.0pt

Reason: Water oxidation is carried out by the photosystem I complex.

Q.31.2 Assertion: Cytokinin exhibit polar transport in plants. 1.0pt

Reason: By using the polar transport system, cytokinin movement can be maintained regardless of changes in phloem transport caused by carbohydrate and mineral sinks and sources.

Q.31.3 Assertion: There is a meristematic phase of growth, both at the root apex and at the shoot apex, because the cells are constantly dividing. 1.0pt

Reason: There is a lot of protoplasm in the cells of this region, but no nucleus.

Q.31.4 Assertion: A plant exposed to high salinity stress exhibits reduced transpiration rate than a plant growing under normal conditions. 1.0pt

Reason: Water conduction in plant tissues is regulated by an equilibrium between water absorbed by the roots and water transpired from the leaves.

Q.31.5 Assertion: Plants produce many phenolic compounds that play an important role in their defense responses. Any manipulation in the production of phenolic compounds through genetic engineering would always lead to drastic retardation in plant growth and development. 1.0pt

Reason: Phenolic compounds are primary metabolites that regulate the cell growth and development at many stages.

Q.31.6 Assertion: It is **not** possible for plants to utilize atmospheric nitrogen for their metabolism. As a result, they require nitrogen-fixing microorganisms (e.g. rhizobia) in the soil to provide nitrogen in usable form. 1.0pt

Reason: The nitrogen fixed by Rhizobium is used in their own metabolism and becomes available to plants and fungi only when they die and decay.



Q.31.7 Assertion: Plant cells may die if they are exposed to severe abiotic stress like heat, salinity, drought etc. for a long period. 1.0pt

Reason: In response to abiotic stresses, among other pathologies, plants produce reactive oxygen species (ROS), which are highly reactive and toxic.

Q.31.8 Assertion: Sepals, petals, stamens and pistils are parts of a flower. 1.0pt

Reason: The petiole and lamina are parts of the stem.

Q.31.9 Assertion: Green leaves make their energy-rich compounds by the process of photosynthesis. 1.0pt

Reason: Plants used CO_2 and water in the presence of sunlight make energy-rich compounds.

Q.31.10 Assertion: Hydroponically grown plants (grown in the absence of soil) are grown in a nutrient solution in which air is bubbled. 1.0pt

Reason: The bubbling solution increases the relative humidity within the plant chamber which is needed for plant growth.

Q.31.11 Assertion: All cells of a plant have almost identical DNA, but there are different cell types and tissues within a plant. 1.0pt

Reason: Factors such as internal environment, hormones, light/dark etc. Determine which subset of the genome is expressed.

Q.31.12 Assertion: In general, dicotyledonous mesophytes leaves have fewer stomata and thicker cuticle on their upper surface, compared to their lower surface. 1.0pt

Reason: The upper surface of the leaves is exposed to greater light intensity.

Theory 1



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United Arab Emirates 2023

A2-1

English (Official)

Question title

Q.1 (4 pt)

Q.2 (4 pt)

Q.3 (4 pt)

Q.4.1 (0 pt)

Q.4.2 (0 pt)

Q.4.3 (0 pt)

Q.5 (10 pt)

Q.6.1 (3 pt)

Q.6.2 (3 pt)

Q.6.3 (3 pt)

Q.7.1 (1 pt)

Q.7.2 (4 pt)

Q.8.1 (3 pt)

Q.8.2 (2 pt)

Q.8.3 (3 pt)

Q.9 (0 pt)

Q.10 (5 pt)

Theory 1



34th International
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United Arab Emirates 2023

A2-2

English (Official)

Q.11 (4 pt)

Q.12.1 (3 pt)

Q.12.2 (1 pt)

Q.12.3 (3 pt)

Q.12.4 (1 pt)

Q.13 (3 pt)

Q.14.1 (3 pt)

Q.14.2 (3 pt)

Q.15.1 (3 pt)

Q.15.2 (5 pt)

Q.16.1 (3 pt)

Q.16.2 (3 pt)

Q.16.3 (3 pt)

Q.17.1 (3 pt)

Q.17.2 (3 pt)

Q.17.3 (3 pt)

Q.18 (7 pt)

Theory 1



34th International
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United Arab Emirates 2023

A2-3

English (Official)

Q.19.1 (3 pt)

Q.19.2 (3 pt)

Q.19.3 (4 pt)

Q.20 (4 pt)

Q.21 (4 pt)

Q.22.1 (2 pt)

Q.22.2 (1 pt)

Q.22.3 (1 pt)

Q.23.1 (2 pt)

Q.23.2 (2 pt)

Q.23.3 (2 pt)

Q.23.4 (2 pt)

Q.24.1 (2 pt)

Q.24.2 (2 pt)

Q.24.3 (2 pt)

Q.24.4 (3 pt)

Q.25.1 (3 pt)

Theory 1



34th International
Biology Olympiad
United Arab Emirates 2023

A2-4

English (Official)

Q.25.2 (1 pt)

Q.25.3 (1 pt)

Q.25.4 (3 pt)

Q.26.1 (2 pt)

Q.26.2 (2 pt)

Q.26.3 (3 pt)

Q.26.4 (2 pt)

Q.27.1 (3 pt)

Q.27.2 (1 pt)

Q.27.3 (1 pt)

Q.28 (4 pt)

Q.29 (4 pt)

Q.30 (6 pt)

Q.31 (12 pt)

IBO Theory Paper 1 Answer Key

Q.1 (19)

1 = D

2 = C

3 = A

4 = B

Matching and reasoning type of question using four distinctive types of the energy sources typical for distinct the muscle contraction modes

- a) aerobic oxidation: muscle glycogen, plasma glucose or liver glycogen (D) – rapid energy source after ATP, creatin phosphate and muscle glycogen are consumed
- b) aerobic oxidation: adipose tissue triglycerides and plasma fatty acids (C) – the slowest energy source (involving the most complex chemical transformation) but with the highest capacity and load
- c) ATP + creatine phosphate (A) – the first immediate source of energy for the muscle action, which could be consumed in approx. 1 min
- d) anaerobic oxidation: muscle glycogen (B) – utilized after A – limited source of energy due to limited storage capacity of the muscle ~~for glycogen~~

Q.2 (18)

- 1 = A
- 2 = D
- 3 = B
- 4 = C

Matching type of question using four distinctive types of the smooth muscle relaxation/contraction modes

- a) sphincters (A) – sphincters need to be actively relaxed from the contracted state to allow transporting function
- b) oesophagus, urinary bladder (D) – both are normally relaxed, after signalization they contract
- c) blood vessels, airways (B) – typically partly contracted with an ability to moderately modulate contraction (e.g. regulating the blood pressure)
- d) stomach, intestines (C) – phasically active tissues with peristaltics – periodically contracting the relaxed muscle

Q.3 (110)

3.1 T

3.2 F

3.3 T

3.4 F

- a) True, RBC is depleted and lymphocytes are smallest white blood cells without granules.
- b) False, RBC is smaller, than lymphocytes, so the resting RBC was excluded from analysis by FSC-threshold. Monocytes are shown in area 2.
- c) True, granulocytes are bigger and more granular than lymphocytes.
- d) False, because lot of blood cell molecules have conjugated double bonds and the fluorescent properties (for example, hem in hemoglobin).

Q.4 (3)

- 4.1 20 days
- 4.2 33.6°C
- 4.3 24°C

Q.5 (102)

- 5.1 T
- 5.2 F
- 5.3 T
- 5.4 F
- 5.5 F
- 5.6 T
- 5.7 F
- 5.8 T
- 5.9 T
- 5.10 F

Answers

Teaching university and medical students shows knowledge of osmoregulation is high, but understanding is usually very poor. Students can often answer correctly many aspects, but are incapable of working out the effects of a novel situation.

Part 1

This part assesses understanding of principles of homeostasis, using fluid handling as an example.

The red group behaves intuitively. They lose water via sweat, giving them increasing blood osmolarity, and decreasing blood volume / blood pressure / cardiac output. They are unable to replace this water, so these symptoms escalate. The body restrains sweating to preserve fluid, so their body temperature increases. ADH acts to preserve water by concentrating urine.

The blue group is able to replace some water by drinking. Therefore, their symptoms progress more slowly. However, they are unable to replace the salts which are lost in sweat (nb, sweat is much less salty than blood), therefore their osmolarity drops when they drink. The body operates a compromise between the drive to replace fluid volume, and the drive to preserve osmolarity - a phenomenon known as 'voluntary dehydration'. Therefore, they soldiers still slowly decay.

The black group is able to replace lost salt and water fully, so normal homeostasis is not compromised.

- **True** - the blue group must drink water to preserve blood volume. Allowing a decline in osmolarity assists them to drink more. (camels at watering holes allow a huge drop in osmolarity)
- **False.** Although their osmolarity declines, they drink less. The black group drinks more, but also consumes salt, so osmolarity is stable. This can be seen in the gradually

deteriorating cardiac output and temperature of the blue group, showing they are not drinking enough water.

- **True.** Red and Blue groups exhaust at the same, low cardiac output, but different temperatures and osmolarity. (Circulatory failure is the proximate cause of death for most people in most situations...)
- **False.** The camels are unable to replace water or salt. They follow the red trajectory. *(Note - humps do not contribute water (or salt)-this is an obviously incorrect myth. Fat is hydrophobic and is not associated with water or salt. Respiring fat will release some metabolic water, but fat is extremely energy dense, and can only be respired to create excess heat. The need to sweat to overcome this heat consumes an order of magnitude more water than the fat releases).*
- **False.** The ultimate problem for people in the desert is water loss via sweating. Food does not help replace this. Salt loss via sweat is much lower than water loss, and eating alone exacerbates osmolarity problems.

Part 3

This part requires detailed understanding of cause and effect.

- **True** - ADH drives the kidneys to conserve fluid.
- **False** - ADH drives the kidneys to produce salty urine, leaving the blood diluted. Note, ADH is not being regulated properly here, so the normal cause-effect is inverted.
- **True** - ADH drives the kidneys to conserve fluid.
- **True** - ADH drives the kidneys to conserve fluid and presses on blood vessels, both increasing blood pressure and therefore cardiac output
- **False** - Severe spikes in blood sugar drive thirst and increase blood volume, like ADH, but also causes dilute urine, and more salty blood.

Q.6 (103)

- 6.1 7.5 L
6.2 200 ml
6.3 30 ml

Inulin is small and will be freely filtered.
Dextran will is large so will not be excreted at all.

Pigs were given 0.75 mol, which gives a peak concentration of 0.1 M. Therefore $0.1 \text{ (M)} = 0.75 \text{ (mol)} / x \text{ (L)}$.

$$X \text{ (L)} = 0.75 \text{ (mol)} / 0.1 \text{ (mol/L)} = \underline{\underline{7.5 \text{ (L)}}}$$

The chance of a molecule being cleared per unit time must be renal clearance (ml/min) / total distribution volume (10 000 ml).

$$K \text{ (/min)} = y \text{ (ml/min)} / 10\,000 \text{ (ml)}$$

$$Y \text{ (ml/min)} = 10\,000 \text{ (ml)} * \ln[A_0 \text{ (M)} / A \text{ (M)}] / T \text{ (min)}$$

The steepest curve must be for PAH, as it is cleared completely.

$$\text{TRF (ml/min)} = 10\,000 * \ln(0.1 / 0.05) / 34.5 = 10\,000 * 0.693 / 34.7 = 199.71 \sim \underline{\underline{200 \text{ ml/min}}} \text{ (nb, same answer is arrived at using precise } \ln(2) \text{ rather than approximation)}$$

The less steep curve must be inulin, so represent GFR.

By the same calculation, GFR = 30 ml/min

NB, these ratios of total volume to TRF to GFR are approximately biologically correct.

- 7.5 L
200 ml
30 ml

Q.7 (91)

7.1 A

Q7.2.1 – True.

Q7.2.2 – True.

Q7.2.3 – False.

Q7.2.4 – False

MCQ:

Q7.1 Asgardarchaeota is the closest to Eukaryotes on the tree and hence the most promising group to study. Indeed, this is the group actively studied now to shed light on the origin of Eukaryotes.

Statements:

Q7.2.1 – True. The key property we expect from the “Host” is the ability for some form of endocytosis or at least partial engulfment of the “symbiont”. In eukaryotes this ability is linked to dynamic actin-based cytoskeleton which is involved in supporting elaborate and also dynamic cellular shapes. Although actin homologs are found in almost all domains of life, complex and dynamic actin cytoskeleton is rare so observing it would add support for a given group being closer to the “Host”.

Q7.2.2 – True. The logic is the same as in A but the statement is sort of more simple – it doesn’t require knowledge of the mechanism behind endocytosis/cell shape change.

Q7.2.3 – False. The described chemistry of the cellular membrane is typical for almost all Archaea and very different from the “classical” bacterial/eukaryotic version based on fatty acids linked to glycerol-3-phosphate via ester bonds. So this finding won’t make an Archaeal group stand out in terms of higher similarity to the “Host”. Indeed, the opposite would be true: if the imaginary group had “bacteria-type” lipids that would give an explanation why Eukaryotes also have the “bacteria-type” lipids.

Q7.2.4 – False. Flagellin-based flagella are typical of bacteria. Finding those won’t add evidence for the discovered group being evolutionary closer to the “Host”.

References:

Rodrigues-Oliveira T et al. Actin cytoskeleton and complex cell architecture in an Asgard archaeon. *Nature* 2023.

<https://www.nature.com/articles/s41586-022-05550-y>

Stairs CW, Ettema TJG. The Archaeal Roots of the Eukaryotic Dynamic Actin Cytoskeleton. *Current Biology*, 2020.

<https://www.sciencedirect.com/science/article/pii/S0960982220302815#bib4>

Villanueva, L., von Meijenfeldt, F.A.B., Westbye, A.B. *et al.* Bridging the membrane lipid divide: bacteria of the FCB group superphylum have the potential to synthesize archaeal ether lipids. *ISME J* **15**, 168–182 (2021).
<https://www.nature.com/articles/s41396-020-00772-2>

Q.8 (99)

8.1

	Gram-positive (A)	Gram-negative (B)
A typical diderm		X
A typical monoderm	X	
A monoderm with no peptidoglycan on the surface		X

A typical diderm (like *E. coli*) is Gram-negative – the stain cannot penetrate the OM and the peptidoglycan layer is thin.

A typical monoderm (like *B. subtilis*) is Gram-positive as nothing shields the peptidoglycan layer.

A monoderm without peptidoglycan (like *Mycoplasma*) will be Gram-negative as there is nothing the stain can bind to.

8.2

	Monophyletic (A)	Paraphyletic (B)	Polyphyletic ©
Monoderms			X
Diderms		X	

Neither monoderms nor diderms in Firmicutes are monophyletic. The first group is polyphyletic and the second one paraphyletic.

8.3.1 T

8.3.2 F

8.3.3 F

A – True. The sentence “...genes associated with the outer membrane are shared between Negativicutes and Halanaerobiales due to vertical transmission and not due to horizontal gene transfer” is basically saying that the most recent common ancestor of Negativicutes and Halanaerobiales had the outer membrane. And the MRCA of those two groups is also the MRCA of all Firmicutes.

B – False. The most parsimonious explanation is that the outer membrane was lost only once in the clade consisting of Bacillales and Lactobacillales, before the split of these two groups. A scenario of each of them losing the outer membrane independently requires two such events and hence is less parsimonious.

C – False. It is likely that the outer membrane evolved as a protection against penicillin-like antibiotics. Observing some groups losing the outer membrane does not disprove this idea – perhaps those groups did not face such a strong antibiotic pressure. In summary, there is no evidence that the OM did not originate as protection against penicillin-like antibiotics.

Reference

Muñoz-Gómez, S. A. & Roger, A. J. 2016. Phylogenomics: Leaving negative ancestors behind. *eLife* 5: e20061.

<https://elifesciences.org/articles/20061>

Q. 9 (27)

9.1 F

9.2 T

9.3 F

9.4 F

9.5 F

Q.9.1 PVX-POL-GFP itself can independently move through plasmodesmata. **(F)**

To study transport function of ORFs protein products the PVX-POL-GFP construct should be transport-deficient. Only fluorescence of single cells can be seen in panels (A), (B), and (C) in the Figure.

Q.9.2 ORF4 necessary for the transport of virus RNA into neighboring cells.

. See panel A in the Figure.

Q.9.3 This data is sufficient to conclude that ORF3 is necessary and sufficient for the transport of virus RNA through plasmodesmata. **(F)**

There are no any data to make such conclusion.

Q.9.4 This data is sufficient to conclude that ORF2 and ORF3 necessary and sufficient for the transport of virus RNA through plasmodesmata.

Q.9.5 ORF4, in combination with ORF2 and ORF3, significantly reduces transport of PVX-POL-GFP into neighboring cells. **(F)** - See panel D

Q.10 (39)

10.1 F

10.2 T

10.3 T

10.4 T

10.5 T

Reference

Garcia et al. (2016) A common bacterial metabolite elicits prion-based bypass of glucose repression. eLife 5:e17978.

Correct answers and comments

1. False – *One of the hallmarks of prion proteins is – as mentioned in the stem – “cytoplasmic and non-Mendelian inheritance of a conformational feature of the protein”. Although the statement meets the other hallmark “loss of physiological function of the protein”, as a whole, it should be considered false.*
2. True – *The highest occurrence of [gar–] (or the lowest occurrence of [GAR+] cells) is observed at 0% of lactic acid in a medium. As lactic acid concentration grows, fraction of [gar–] gets lower.*
3. True – *The [GAR+] prion is inherited in non-Mendelian manner. Based on information given in the stem, it should be considered true.*
4. True – *Culture of S. cerevisiae in filtered bacterial medium without bacterial culture is one of the controls in the experiment presented in panel A This control enables to exclude the influence of chemicals included in the bacterial medium on yeast phenotypes.*

True – *Students need to know that low molecular weight compounds easily diffuse in solid media*

Q.11 (90)

11.1 F

11.2 T

11.3 T

11.4 F

- a) False; there is protein expression according to Fig1A.
- b) True; there is a nucleic acid packaged in the capsids according to Fig1B. It is transcribed by reverse transcriptase according to Fig1C thus it is RNA.
- c) True; mutations to Lysine are generally selected in packaging efficiency according to Fig2. Also DNA-binding proteins found in nature are generally positively charged. This is in fact the reason that addition of Btat made a viable capsid from I53-50 which can be seen in experiment in Fig1.
- d) False; for instance in the heat map on Figure 2 there are some cells which show deleterious effects of mutation to K (Lysine) mainly in sites 74, 94, 95, and 98. Adding positive charge into the capsid is GENERALLY beneficial but not always, as there are higher order interactions in a protein sequence.

Q.12 (32)

12.1 Answer = 27

Average number of amino acids per protein = $50,000 / 110 = 454.454...$

*Total number of amino acids = $20,000 * 454.454... = 9090909$*

*Total number of base pairs = $9090909 * 3 = 27,272,727$*

(note, this answer is robust to rounding at previous stages).

12.2 Answer = A

12.3 Answer = 50

Humans have 4 bases, necessitating a triplet code to specify 20 amino acids ($4^3=64$; $4^2=16$)

The alien has 6 bases, so can use a doublet code to specify 20 amino acids ($6^2=36$)

Therefore 100 million bases can specify $100/2 = 50$ million amino acids.

12.4 Answer= E

Q.13 (35)

Answer: 6

Solution:

Based on OD: $0.024/8 \times 100 = 0.3\%$ is ratio of 23s rRNA to total genome. Then, 3.3×10^6 dalton of total genome is 23s rRNA. Then, based on MW of 23 rRNA, 6 copy of it exists.

Q.14 (117)

ANSWERS:

14.1 695 origins

14.2 8.64×10^6 nucleotides

EXPLANATION:

Students have to know that the human genome is **diploid** and, therefore, contains $2 \times 3 \times 10^9$ nucleotide pairs.

Students have to know that each **origin** gives **2 replication forks**, therefore, the rate of replication in the origin will be **200 nucleotides per second**.

Students have to know that **12 hours** contain $12 \times 60 \times 60$ seconds.

Therefore, each **origin** for **12 hours** will replicate $200 \times 12 \times 60 \times 60$ nucleotides.

Calculate the number of origins: $2 \times 3 \times 10^9 / 200 \times 12 \times 60 \times 60 = 694.44$ or **695 origins**.

The second question is necessary, because the first answer can be obtained from the wrong assumption: $1 \times 3 \times 10^9 / 100 \times 12 \times 60 \times 60 = 694.44$ or 695 origins.

Q.15 (47)

Explanations

15.1 135

15.2.1 F

15.2.2 T

15.2.3 F

15.2.4 F

15.2.5 F

Q.15.1 At 30°C, the proportion of individuals that will be females is about 90%, which will amount to **135** hatchlings. A slight margin of error can be considered and values between 134 and 136 eggs will be accepted.

Q.15.2.1 **False.** Species 1 is more vulnerable as it has a steeper slope, indicating rapid change in the proportion of female hatchlings with relatively small changes in temperature.

Q.15.2.2 **True.** Dark-coloured substrates on beaches absorb more heat, making them warmer than light- coloured substrates, raising incubation temperatures and encouraging the production of more female hatchlings.

Q.15.2.3 **False.** Rising temperatures will not affect operational sex ratios in the short term because, as mentioned in the stem of the question, female sea turtles mate once every three years, storing the sperm that they acquire within their bodies during this period, while the males mate every year. And hence, even with the absolute rise in the number of females, there will initially be enough males to fertilise the increased number of females. Moreover, the age at first breeding of sea turtles tends to be prolonged, typically ranging from 10 to 25 years. Thus, females-biased hatchlings will begin to influence the operational sex ratios beyond 10 years.

Q.15.2.4 **False.** Rising temperatures during climate change will directly affect the absolute sex ratio at hatching while their influence on operational sex ratios will be more indirect and come into effect at a later stage.

Q.15.2.5 **False.** Metabolic heat is the heat derived from metabolic activity in the eggs and hence, not immediately affected by external temperatures.

References

Blechsmidt et al. 2020. Climate change and green sea turtle sex ratio—preventing possible extinction. *Genes* 11(5): 588.

Laloë et al. 2014. Effects of rising temperature on the viability of an important sea turtle rookery. *Nature Climate Change*, 4(6): 513-518.

Q.16 (41)

16.1 93 – 94

16.2 63.0 – 63.5

16.3 670 – 685

Answers:

- 1) Jerboa is a small size animal with mass 100-times less than honey badger, so we use exponent $2/3$. It consume $100^{2/3} = 10 \times 10^{1/3} = 21.5$ times less energy than honey badger, $2000 \text{ kJ} / 21.5 = 93 \text{ kJ}$. (Appropriate range 93 – 94 kJ).
- 2) Camel is a large size animal with mass 100-times more than honey badger, so we use exponent $3/4$. It consume $100^{3/4} = 10 \times \sqrt[4]{10} = 31.6$ times more energy than honey badger, $2 \text{ MJ} \times 31.6 = 63.2 \text{ MJ}$. (Appropriate range 63.0 – 63.5 MJ).
- 3) $63200 \text{ kJ} / 93 = 680$ (Appropriate range 670 – 685).

Q.17 (111)

There are nine species in sample A, seven species in sample B while six species are common to both communities.

Q.17.1 $DSC = 2 \times 6 / (9+7) = 0.75$

Q.17.2 $JI = 6 / (7+9-6) = 0.6.$

Q.17.3.1 True, Because $A+B > (A \cap B)$

Q.17.3.2 True, similarity indices between rivers i and iii is higher than between rivers i and ii.

Q.17.3.3 False, because discriminative capacity is higher for JI, not for DSC.

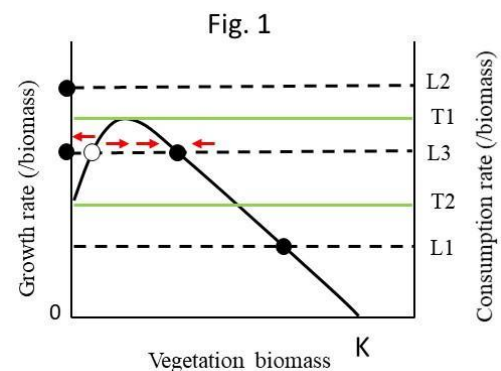
Q.18 (40)

- 18.1 T
- 18.2 F
- 18.3 T
- 18.4 F
- 18.5 F
- 18.6 T
- 18.7 F

Answer Key and explanations

The point of this question is to focus on the equilibrium state determined by the balance between the growth rate of vegetation biomass and the consumption rate of biomass by livestock.

When livestock density is low, and hence the consumption rate is low (L1), there is only one stable equilibrium point of biomass, but above a certain consumption level (L3 in Fig. 1), there are two equilibrium points. However, the lower equilibrium is unstable (white circle). A further increase in the consumption rate (L2) results in a single stable equilibrium point with no vegetation. Importantly, the tipping point of vegetation recovery (T2) was lower than that of vegetation disappearance (T1). This is because the lower equilibrium point was unstable, making it impossible to establish vegetation up to T2.



A. True

When plant productivity is low, the rate of vegetation increase is low. This is represented by the solid blue line in Fig. 2 below. Tipping point T1 can be reached at lower consumption rates (or livestock density).

B. False

When plant resource competition is weak, the density effect weakens, and the negative slope of the growth rate with increasing biomass is less steep. The red line in Fig. 2 corresponds to this point. The tipping point T1 does not change (it might increase slightly, but never decreases).

C. True

Severe soil degradation induces a steeper decrease in vegetation biomass, as represented by the brown line in Fig. 2. Tipping point T2 is lowered because the growth rate is lower without vegetation.

D. False

If many plants are unpalatable to livestock, the vegetation biomass should increase at a given level of livestock density. In other words, the consumption rate of vegetation by livestock decreases, as represented by the green dashed line in Fig. 2. Consequently, vegetation is maintained at a higher livestock density, and T1 increases as a result.

E. False.

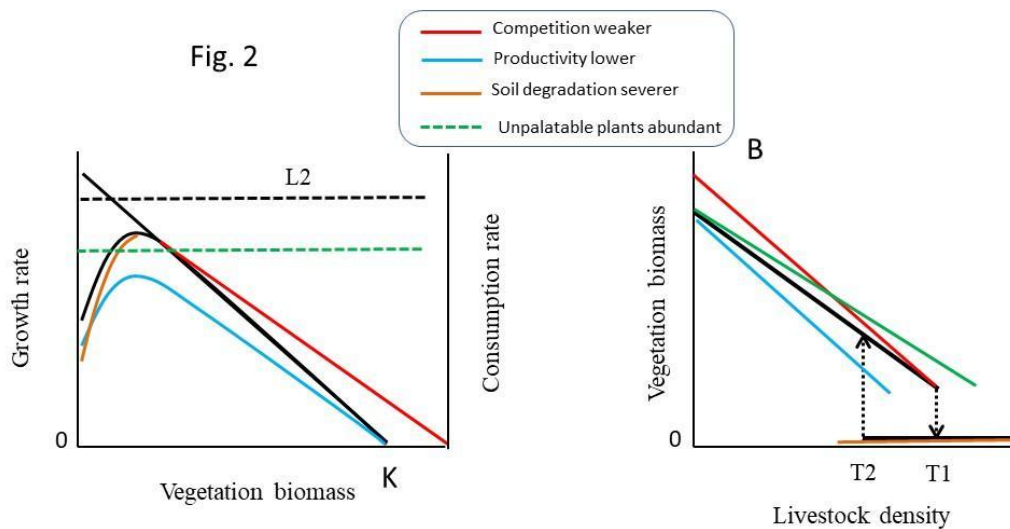
The tipping point is represented by line C. Refer to Fig 1 (explanations)

F. True.

The tipping point is represented by line E. Refer to Fig 1 (explanations)

G. False.

The point is L1 intersects at the point of stable equilibrium. Refer to Fig 1 (explanations)



Q.19 (104)

19.1 385

19.2 364

19.3.1 T

19.3.2 F

19.3.3 T

19.3.4 F

1. The energy saved by the bird in foraging time

= less energy spent in foraging – the energy spent in resting for the same time

= (1.3 h x 500 calories) – (1.3 h x 200 calories)

= 395 calories

2. The energetic cost of defence

= energy spent in defence – energy saved by not sitting for the same time

= (0.28 h x 3000 calories) – (0.28 h x 400 calories)

= 728 calories

Note that the daily energy spent by the sunbird in calories in the following activities under the two situations are:

When not defending a territory:

Foraging = 4 h x 500 cal = 2000 cal

Perching = 20 h x 200 cal = 4000 cal

When defending a territory,

Foraging = 2.70 h x 500 cal = 1350 cal

Defence = $0.28 \text{ h} \times 1500 \text{ cal} = 420 \text{ cal}$

Perching = $21.02 \text{ h} \times 200 \text{ cal} = 4204 \text{ cal}$

Q.19.3.1 Statement 1 is true because under the conditions specified above, the bird will indeed defend a territory even though its net perching cost actually increases during territorial defence.

Q.19.3.2 Statement 2 is false because the bird will actually show territorial defence if it reduces the amount of time spent perching under these conditions.

Q.19.3.3 Statement 3 is true because the birds will be territorial if the cost of foraging per hour, when not defending a territory, is higher than the cost of defence.

Q.19.3.4 Statement 4 is false because the birds will show territorial defence when the net costs, incurred by defence, are lower than when not defending it.

References

Gill, F. B. and Wolf, L. L. 1975. Economics of feeding territoriality in the golden-winged sunbird.
Ecology 56: 333-345

Krebs, J. R. and Davies, N. B. 1997. *Behavioural Ecology: An Evolutionary Approach*, 4th Edn,
Blackwell Scientific Publications, Oxford

Q.20 (50)

20.1 T

20.2 F

20.3 F

20.4 T

1. TRUE. In Figure 1B, individual songs of *F. hypoleuca* from the same location (population) cluster together, that is, they have more similar songs.
2. FALSE. (a) If this was true, we would expect significant differences in the responses of the nestlings to the calls of the two species in areas where they co-exist (the right panel of Figure 2) but not in areas where only *F. hypoleuca* is found (left panel of Figure 2); and (b) nestlings respond rather poorly to songs of individuals from the other populations of the same species (Figure 3) which should not be observed in case the songs preference had evolved to prevent cross-species hybridization.
3. FALSE. This is linked to the observation that the nestlings did not necessarily react better to songs that were similar to those of their social fathers, as indicated in the last part of the question stem. This might be inconclusive but, if anything, provides evidence against learning from their social fathers. The nestlings could learn from any song they hear around them or the songs they learn could even be innate. But there is definitely no conclusive evidence that the song patterns are learnt specifically from their social fathers.
4. TRUE. As the birds appeared to discriminate between songs at a dialect level, differences in dialects could result in a reproductive barrier: the stronger the difference in songs there is, the less likely mating is to occur between them and hence less likely gene flow is to happen. And gene flow barriers over time lead to genetic divergence due to drift.

Reference

Wheatcroft, D. et al. 2022. *Current Biology* 32: 5153–5158.
<https://www.cell.com/action/showPdf?pii=S0960-9822%2822%2901605-0>

Q.21 (107)

Answers

A – 2, B – 4, C – 1, D – 3

References

Dugatkin, L. A. 1992. Sexual selection and imitation: females copy the mate choice of others.
American Naturalist 139: 1384-1389

Witte, K. 2006. Learning and mate choice. In: *Fish Cognition and Behaviour* (eds. Brown, C., Laland, K. and Krause, J.). Blackwell Publishing, Oxford

Q.22 (54)

22.1.1 = C

22.1.2 = B

22.2 = B

22.3 T

The analysis tests the student's understanding of correlation between phenotypic and DNA markers. The student has to first infer the outcome of PCR of the two alleles. PCR of the mutant allele will result in a larger fragment (amplicon). Further, this method can identify both the alleles in a heterozygous individual. The student thus has to infer that homozygous round will show the smaller fragment only, heterozygous will show both the fragments while the homozygous wrinkled will show only the larger fragment.

1. Thus, in cross one observes three types of progeny, only larger fragment (9), both the fragments (14) and only smaller fragment (7). The observed ratio is ~1:2:1. This can result from a cross between parents as represented in Panel C. [$Rr \times Rr = RR (1) : Rr (2) : rr (1)$]

In cross two one observes two types of progeny, both fragments (13) or only larger fragment (17). The observed ratio is ~1:1. This can result from a cross between parents as represented in Panel B. [$rr \times Rr = Rr (1) : rr (1)$]

Cross I: $Rr \times Rr$

Cross II: $rr \times Rr$

2. Wrinkled. The band is larger, so it is the allele with insertion (r). Only 1 band, so homozygous for wrinkled seeds.

3. TRUE. Heterozygotes are round hence having active SBE1 needed to produce starch and leading to the round phenotype while insertion homozygotes are wrinkled because they lack SBE1 activity.

Q.23 (55)

This is an example of paternal imprinting. This can be concluded by comparing the progeny of II-2 and II-3 with that of II-5 and II-6. While children from the former and the latter parents carry the mutant allele, the children from the former show the disorder.

23.1.1 True. All individuals will carry an imprinted allele.

23.1.2 True. See explanation above.

23.2 0.25. As both parents are heterozygous (Xx and Xx), the probability of the child being xx is 0.25.

23.3 0.50. The child will receive an imprinted allele from the father. From the mother there is a 50% chance that the child receives the mutant allele.

23.4 0.25. The probability of the child being a son is 0.5. The probability that it will show the disorder is 0.5 (reason, see Q 3). Thus the overall probability is $0.5 \times 0.5 = 0.25$

Q.24 (63)

1.

Relationship	IBD1	IBD2	T	F
Monozygotic twins	0	100		X
Parent-offspring	100	0		X
Full-siblings	50	25	X	
Half-siblings	50	0	X	
Grandparent-grandchild	50	0	X	

24.4 TRUE

24.5 FALSE

24.6 TRUE.

For monozygotic twins at any place in the genome both chromosomes are identical so at any position twins are IBD2 – 100% of their genome is IBD2. There is no biological variation.

Each individual has one haploid genome from each of the parents so all the genome is IBD1 between a parent and an offspring (assuming the parents are unrelated and hence don't share IBD). No biological variation – you have exactly one haploid genome shared with one parent.

Full siblings can have some regions in the genome where they got the same chromosomal chunk from both parents (in 25%) which is IBD2. The same probability is of both chromosomes being different (IBD0). The remaining is IBD1 – 50%. You can think of it this way: at a locus parents have the following genotypes: A1A2 and A3A4. Then there is a 25% chance of the offspring having identical genotypes (for instance A1A3) which will be IBD0. There is also a 25% chance of having no alleles in common (A1A3 and A2A4) – this is IBD0. And the remaining 50% will be represented by cases of one allele shared and the other not (A1A3 and A1A4 for example). But now there is variation – due to random segregation siblings can share slightly more or slightly less. Think of it that way: there is an extremely low but non-zero probability of two siblings having all of their genome IBD0.

Half-siblings can't share IBD2 because they share only one parent. But as each of the half-siblings have 100% of their genome in IBD1 state with the shared parent and there is random segregation there is 50% chance of a given locus being IBD1 between half-siblings.

Parent-offspring share 100% IBD1, in one generation this is “diluted” two times so
Grandparent-grandchild share 50% of the genome IBD1. Again, some stochasticity is involved.

24.4 TRUE

There is one round of recombination between a parent and an offspring (an offspring's chromosome is IBD with one of the parent across all its length but it switches from one parental chromosome to another due to recombination so the length of each segment is defined by recombination rate) but two independent recombination rounds that “separate” two siblings.

24.5. FALSE

As we trace the family tree back into the past we observe increasing stochasticity in the amount of DNA one inherits from his/her ancestors X generations ago. At bigger X we get disproportionately a lot of DNA from some ancestors and truly 0 from others. On top of that, there is the phenomenon of pedigree collapse: if we just think in 2^X terms, we will soon reach a paradox that one had more ancestors than there were people on Earth at that time: this is resolved by the same person being your ancestor along multiple lines in the pedigree

24.6. TRUE.

If a population has a smaller long-term population size it means the pool of possible ancestors is smaller – the same individual in the past has higher chances of being the ancestor of the two randomly picked individuals. Hence, they will have a higher chance of having inherited some DNA from the same ancestor.

Q.25 (52)

25.1 0.058

25.2 = C

25.3 = C

25.4.1 F

25.4.2 F

25.4.3 F

1. 0.058

The degree of sequence difference between the alleles is as follows:

$$A-B = 4/40 = 0.1$$

$$A-C = 2/40 = 0.05$$

$$B-C = 6/40 = 0.15$$

Next, we calculate the frequency of each combination of alleles, multiply them by their differences and sum all the products (combinations of the same alleles are included to illustrate the principle):

$$2 \cdot 0.5 \cdot 0.3 \cdot 0.1 + 2 \cdot 0.5 \cdot 0.2 \cdot 0.05 + 2 \cdot 0.3 \cdot 0.2 \cdot 0.15 + 0.5^2 \cdot 0 + 0.3^2 \cdot 0 + 0.2^2 \cdot 0 = 0.058$$

Note that some webpages forget multiplying by 2. This is essential though – nucleotide diversity is defined as average difference between two sequences, not two different alleles. Hence, pairs of the same sequence should be included in the denominator. In a way, nucleotide diversity is an extension of expected heterozygosity that takes the difference between alleles into account.

2. Answer C is true.

First, Cheetahs are well-known for their very low effective population size. Second, it is very hard to imagine why would cheetahs differ so drastically from other mammals including felids in their mutation rate or efficiency of selection. Rapid adaptation could decrease nucleotide diversity locally but not genome-wide.

3. MCQ:

Answer C is true.

The drop in nucleotide diversity in the crop is observed in the upstream region of the gene. Mutations here are not causing amino acid substitutions or premature stop codons. It is also highly unlikely to affect splicing. But it can indeed affect transcription of the gene.

- A. **False.** Purifying selection decreases nucleotide diversity by removing sequence variants from the gene pool. For the statement to be true the nucleotide diversity should be lower in the wild plant which is not the case.
- B. **False.** See above.

Two kinds of F1 selfing will take place

(i) $AaBb \times AaBb$

$A_B_$ (Male fertile, Herbicide resistance) 9

$aa\ B_$ (Male fertile, Herbicide resistance) 3

$A_bb_$ (Male sterile, Herbicide resistance) 3

$aabb$ (Male fertile, Herbicide sensitive) 1

(ii) $aaBb \times aa\ Bb$

$aaB_$ (Male fertile, Herbicide resistance) 12

$aabb$ (Male fertile, Herbicide sensitive) 4

3 out of 32 progeny are male sterile, i.e. 9.4% is male sterile (**rounded to 9**)

27 out of 32 progeny are herbicide resistant i.e. 84.4% is herbicide resistant (**rounded to 84%**)

From the above:

26.1 0%

26.2 100%

26.3 15%

26.4 90%

Q.27 (60)

Q27.1 False

Q27.2 False

Q27.3 False

Q27.4 B

Q27.5 B

Yellow dots tend to be further along x, than orange, than red, therefore $TT > CT > CC$ in terms of size.

It can be easily seen that there is significant overlap between the red and yellow dots, so the two genotypes are not fully separated. Secondly, on average, the orange heterozygotes tend to have intermediate sizes so there can be no simple dominance relationship.

It can be seen that dogs of the same genotype (heterozygote) vary from 2 kg – 35 kg, across the large majority of the size range. Similarly, the other genotypes also spread across the majority of the size range. Therefore, genotype is not explaining the majority of size variation. The environment and/or other genes must be causing large effects.

The trend line between IGF1 in serum and size is positive.

Wolves appeared from other canids, and then dogs appeared from wolves. Dogs possess C and T alleles. Wolves also possess C and T alleles (although predominantly T). Wider canids almost entirely possess C alleles. Therefore, the parsimony principal, with fewest separate origins for the same allele, suggests T first appears in wolves, before the evolution of dogs. This is also intuitive, and fits with the size of different canids (northern wolves being notably larger).

Q.28 (70)

28.1 T

28.2 T

28.3 T

28.4 T

Explanation:

- A. True: Because xylem conduits are dead at maturity.
- B. True: That the linear relationship between Ψ_{min} and Ψ_{pot} of gymnosperms is farther away from 1:1 line than angiosperms indicated greater hydraulic safety margins (than angiosperms).
- C. True: The lower safety margins, the closer Ψ_{min} and Ψ_{pot} = large amounts of embolism and thus the more risk of hydraulic failure.
- D. True: These findings on Safety margins provide insight into why drought-induced forest decline is occurring not only in arid regions but also in wet forests not normally considered at drought risk. Safety margins are largely independent of mean annual precipitation.

Choat et al. 2012. Nature 491: 752-755. doi:10.1038/nature11688

Q.29 (72)

29.1 T
29.2 T
29.3 F
29.4 F

- A. True: Process 1 is leaf expansion which is driven by turgor, and thus very sensitive to turgor loss.
- B. True: During early stages of water stress, water-use efficiency may increase because transpiration is more reduced than intercellular CO₂ concentrations (and thus photosynthesis).
- C. false: Y is the x-intercept of the graph (= growth/expansion approach zero).
- D. False: Plant 1 was grown with ample water and thus has higher m, lower Y compared to plant 2.

Taiz L., and Zeiger E. 2002. Plant Physiology. 3rd edition.

Q.30 (70)

30.1 T

30.2 T

30.3 T

30.4 F

30.5 T

30.6 T

Explanation:

- A. True: As shown in Figure 1.
- B. True: Leaf area in the elevated CO_2 treatment relative to the ambient CO_2 treatment increased 49% under NH_4^+ nutrition, but only 24% under NO_3^- nutrition. Total plant biomass increased 78% under NH_4^+ nutrition, but only 44% under NO_3^- nutrition.
- C. True: As shown in Figure 2, Shoot and root N concentrations were similar under the two CO_2 regimes. Total N. (Shoot N: ab:b, c:a) (Root N: a:a, a:a).
- D. False: They differed as demonstrated by the balance of inorganic and organic N! As shown in Figure 2. (Protein=organic N, Shoot=abcd, Root=aabb) (NO_3^- =inorganic N, Shoot=ab, Root= aa).
- E. True: As shown in Figure 2, (Shoot NR, and NiR: ab, ab) (Root NR, and NiR: aa, aa)
- F. True: The results support a hypothesis that elevated CO_2 inhibits shoot NO_3^- photoassimilation ($\Rightarrow$ good option is to change to taxa that prefer NH_4^+ as a nitrogen source), but not in the root ($\Rightarrow$ good option is to change to taxa that assimilate NO_3^- primarily in their roots).

https://learninglink.oup.com/access/content/taiz-plant-physiology-6e-student-resources/taiz-plant-physiology-6e-essay-13-1-elevated-co2-and-nitrogen-photoassimilation?previousFilter=tag_chapter-13

Q.31 (81)

31.1 = c
31.2 = d
31.3 = c
31.4 = a
31.5 = d
31.6 = c
31.7 = a
31.8 = c
31.9 = a
31.10 = c
31.11 = a
31.12 = a

1. ANSWER: (c)

Water splitting during the light reactions involves Photosystem II. Photosystem I is not involved in this process.

2.

Answer: (d)

Polar transport in plants is only exhibited by auxins, not cytokinins.

3.

Answer: (c)

Many regions of the plant consist of meristematic tissue, including the root apex and shoot apex. New cells are produced by mitotic divisions of meristematic cells. These cells are composed of cellulosic walls, contain a large nucleus, and are rich in protoplasm. During this phase, cells are forming or dividing.

4.

Answer: (a)

Since the presence of high salt concentration limits the water uptake by the roots, the plant cells would exhibit lower transpiration rates in order to avoid water loss and preserve water content in the cells.

5. .

Answer: (d)

An organism produces phenolic compounds as secondary metabolites, small organic molecules that are not essential for growth, development, or reproduction.

6. Answer: (c)

Rhizobium bacteria are nitrogen fixing organisms that live symbiotically, growing inside tissues of host ferns and seed plants. They convert atmospheric nitrogen into nitrates which are essential for the growth of plants.

7. Answer: (a)

ROS are produced in the cells as a result of abiotic stresses as they cause damage to proteins, lipids, carbohydrates, and DNA eventually leading to cell death.

8. Answer: (c)

Petiole and lamina are parts of a leaf, not stem.

9. Answer: (a)

Plants use light energy and water and perform the light reactions in thylakoids to form ATP and NADPH that are then used in the dark reactions (Calvin cycle) to produce sugars (food) in stroma. In addition to ATP and NADPH, CO₂ is also required in the Calvin cycle.

10. Answer: (c)

The bubbling of the solution is done to provide oxygen to the plant cells. Water and nutrient solutions do not have enough oxygen to sustain aerobic respiration.

11. Answer: (a)

Factors such as internal environment, hormones, light/dark etc. may influence the expression of different subsets of genetic information from the genome, resulting in differentiation and development.

12. Answer: (a)

Because of the greater light intensity and heat absorption on the upper surface of the leaf, the upper surface has fewer stomata than the lower surface and a thicker cuticle than the lower surface.