

Organisms (Unity and diversity) practice questions

16 questions • 51 marks • mark scheme at the back

For IB Diploma Biology, Standard Level and Higher Level (first assessment 2025). **HL only** is additional higher level content, for HL students only.

Name

Total / 51

Diversity of organisms **Spec A3.1**

1 PAPER 1A STYLE [1 mark]

Which is the correct way to write the binomial of the grey wolf?

- A. ☐ Canis Lupus
- B. ☐ canis lupus
- C. ☐ *Canis lupus*
- D. ☐ *Lupus canis*

2 PAPER 1A STYLE [1 mark]

Which statement about chromosome numbers is correct?

- A. ☐ All mammals have 46 chromosomes in their body cells.
- B. ☐ Diploid cells have an even number of chromosomes.
- C. ☐ Species with more chromosomes are more complex.
- D. ☐ Chimpanzees have fewer chromosomes than humans.

3 PAPER 1A STYLE [1 mark]

What is the main source of genome diversity between individuals of the same species?

- A. ☐ Differences in the number of genes
- B. ☐ Single-nucleotide polymorphisms
- C. ☐ Differences in chromosome number
- D. ☐ Differences in the genetic code

4 PAPER 2A STYLE [4 marks]

(a) State the biological species concept. [1] (b) Outline why it can be an arbitrary decision whether two populations are the same species or different species. [3]

5 PAPER 2A STYLE**[4 marks]**

Humans have 46 chromosomes and chimpanzees have 48. Evaluate the evidence for the hypothesis that human chromosome 2 arose from the fusion of two chromosomes found in a shared primate ancestor.

6 PAPER 1B STYLE**[5 marks]**

The table shows approximate haploid genome sizes taken from a genome database. (a) Calculate how many times larger the genome of *Paris japonica* is than the human genome. [1] (b) Using the data, evaluate the hypothesis that genome size increases with the complexity of an organism. [3] (c) Suggest one reason why some plants have much larger genomes than humans. [1]

Approximate haploid genome sizes		
Organism	Group	Genome size / million base pairs
<i>Escherichia coli</i>	bacterium	4.6
<i>Saccharomyces cerevisiae</i>	fungus (yeast)	12
<i>Drosophila melanogaster</i>	insect	180
<i>Arabidopsis thaliana</i>	flowering plant	135
<i>Homo sapiens</i>	mammal	3,100
<i>Triticum aestivum</i>	flowering plant	16,000
<i>Paris japonica</i>	flowering plant	149,000

Answer =

[3 marks]

[illegible]

[6 marks]

[illegible]

[4 marks]

[illegible]

Classification and cladistics

Spec A3.2

HL only

10 PAPER 1A STYLE

[1 mark]

HL only

What does a node on a cladogram represent?

- A. ☐ A species alive today
- B. ☐ A hypothetical common ancestor
- C. ☐ A mutation in a single base
- D. ☐ The time since a species became extinct

11 PAPER 1A STYLE

[1 mark]

HL only

Which evidence led to the classification of all organisms into three domains?

- A. ☐ Comparisons of cell wall structure
- B. ☐ Base sequences of ribosomal RNA
- C. ☐ Numbers of chromosomes
- D. ☐ Fossils of the earliest cells

12 PAPER 1A STYLE

[1 mark]

HL only

Why can the molecular clock only give an estimate of when two clades diverged?

- A. ☐ Sequence differences stop accumulating once two clades have diverged.
- B. ☐ Only amino acid sequences, not base sequences, can be used.
- C. ☐ Mutation rates are affected by generation time, population size and selective pressure.
- D. ☐ The number of sequence differences decreases as time passes.

13 PAPER 2A STYLE

[4 marks]

HL only

(a) Outline the need for classification of organisms. [2] (b) Explain one advantage of classifying organisms according to evolutionary relationships. [2]

HL only

The table shows the number of amino acid differences in a protein between four species, P, Q, R and S (practice data). (a) Identify the two most closely related species. [1] (b) Assuming differences accumulate at 1 difference per 10 million years, estimate when P and S diverged. [1] (c) Deduce the sequence in which the species diverged, and describe the most probable cladogram. [2] (d) Suggest why the estimate in (b) may be inaccurate. [1]

Amino acid differences between species				
	P	Q	R	S
P	-	9	10	12
Q	9	-	3	8
R	10	3	-	7
S	12	8	7	-

Answer =

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HL only

A cladogram shows a root leading to node 1, which splits into species A and node 2. Node 2 splits into species B and node 3. Node 3 splits into species C and species D. (a) State which node represents the most recent common ancestor of B and D. [1] (b) Deduce how many clades contain species B. [1] (c) Identify the species most closely related to C. [1]

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HL only

Discuss how cladistics has changed the classification of organisms.

[illegible]

Mark scheme

One mark for each point unless a maximum is given. Words in brackets are not needed for the mark.

1. [1]

C C: genus first with a capital letter, species name lowercase, in italics [1]

2. [1]

B B: chromosomes in diploid cells are in homologous pairs [1]

3. [1]

B B: members of a species share most of their genome; SNPs give some diversity [1]

4. [4]

- (a) a group of organisms that can breed and produce fertile offspring [1]
- (b) speciation is the splitting of one species into two or more [1]
- (b) speciation usually happens gradually / not by a single act [1]
- (b) non-interbreeding populations diverge / become more and more different in their traits [1]
- (b) no clear point at which they become separate species / intermediate stages exist [1]
- (b) interbreeding cannot be tested if populations are geographically separated OWTTE [1]
- max 4

5. [4]

- banding pattern of human chromosome 2 matches chimpanzee chromosomes 12 and 13 (2A and 2B) end to end [1]
- telomere sequences found near the middle of chromosome 2 / at the fusion point [1]
- remains of a second (inactive) centromere on chromosome 2 [1]
- gene order (largely) matches that on the two chimpanzee chromosomes [1]
- fusion explains reduction from 48 to 46 / 24 to 23 pairs [1]
- the hypothesis is testable / made predictions that could have been falsified [1]
- evidence supports but does not prove the hypothesis / fusion itself was not observed OWTTE [1]
- max 4

6. [5]

- (a) $149,000 \div 3,100 = 48$ (times) [1] Accept 48.1
- (b) supported: simplest organisms / bacterium and yeast have the smallest genomes [1]
- (b) not supported: plants such as wheat / *Paris japonica* have larger genomes than humans [1]
- (b) *Arabidopsis* and *Drosophila* have genomes of a similar size / same order of magnitude despite being very different organisms OWTTE [1]
- (b) conclusion: no close correlation between genome size and complexity / hypothesis not supported overall [1]
- (b) only one or a few species per group / small sample of species [1]
- (c) more non-coding / repetitive DNA [1] Accept extra copies of whole chromosome sets / polyploidy
- max 5

7. [3]

- sequencing is increasingly fast and cheap, so many genomes can be compared [1]
- current: research into evolutionary relationships between species / comparing numbers of base differences [1]
- current: finding SNPs / variation linked to traits or diseases [1]
- future: personalised medicine [1]
- choosing drugs / doses / predicting disease risk from an individual's genome [1]
- max 3

8. [6] HL only

- the biological species concept defines a species as organisms that can breed and produce fertile offspring [1]
- asexually reproducing organisms do not interbreed, so the concept cannot be applied [1]
- each clone / individual would be reproductively isolated, making every one a species OWTTE [1]
- bacteria reproduce asexually / by binary fission [1]
- bacteria exchange genes by horizontal gene transfer / plasmids [1]
- genes pass between different species, so species boundaries are blurred [1]
- interbreeding cannot be tested for fossils / geographically separated populations [1]
- members of a species have the same chromosome number [1]
- hybrids of parents with different chromosome numbers are unlikely to be fertile [1]
- chromosomes cannot pair in meiosis, so viable gametes are not produced [1]
- e.g. horse (64) × donkey (62) gives an infertile mule (63) [1]
- max 6

9. [4] HL only

- (a) each step has two contrasting descriptions / paired choices [1]
- (a) uses features that are easy to observe [1]
- (a) uses features that do not vary within a species / not size or colour [1]
- (a) each choice leads to another numbered step or a name [1]
- (b) water sample taken and DNA extracted [1]
- (b) barcode region copied by PCR and sequenced [1]
- (b) sequences compared with a reference database of barcodes to identify species [1]
- max 4

10. [1] HL only

B B [1]

11. [1] HL only

B B [1]

12. [1] HL only

C C [1]

13. [4] HL only

- (a) immense diversity of species / very large number of species [1]
- (a) classification makes diversity manageable / allows identification [1]
- (a) after classification, further study is facilitated / information about related species can be found [1]
- (b) all members of the group have evolved from a common ancestor [1]
- (b) characteristics of members can be predicted [1]
- (b) because characteristics are shared within a clade [1]
- (b) e.g. a species related to one that produces a useful drug may produce it too [1]
- max 4

14. [5] HL only

- (a) Q and R [1]
- (b) $12 \times 10 = 120$ million years ago [1]
- (c) P diverged first / P is the outgroup [1]
- (c) then S; Q and R share the most recent common ancestor [1]
- (c) cladogram: P branches from the root, then S, with Q and R as sister species at the last node [1]
- (d) mutation rate may not be constant / varies with generation time / population size / selective pressure [1] Accept: P-Q differences (9) give a different date (90 million years) for the same divergence, so rates differ between lineages
- max 5

15. [3] HL only

- (a) node 2 [1]
- (b) two (the clade from node 1 and the clade from node 2) [1] Accept three if B alone is counted as a clade
- (c) D [1]

16. [7] HL only

- traditional hierarchy of kingdom, phylum, class, order, family, genus, species [1]
- fixed ranks are arbitrary / do not reflect gradation of variation / do not always match patterns of divergence [1]
- cladistics uses unranked clades: an ancestor and all its descendants [1]
- evidence from base sequences of genes / amino acid sequences of proteins [1]
- sequence evidence is more objective than morphology [1]
- morphology can mislead because of convergent evolution [1]
- cladograms built using parsimony / fewest sequence changes [1]
- traditional groups found not to be clades were reclassified [1]
- e.g. figwort family / Scrophulariaceae: many species moved to other families [1]
- e.g. birds lie within the reptiles, so the class Reptilia is not a clade [1]
- rRNA base sequences led to three domains: Bacteria, Archaea, Eukarya (1977) [1]
- a new level above kingdoms / prokaryotes split into two domains [1]
- paradigm shift / earlier classifications falsified [1]
- but cladograms are hypotheses; different criteria / data can give different trees [1]
- max 7