
HL Paper 3

c. Outline how variations in specific molecules can lead to phylogeny.

[3]

d. Outline the value of classifying organisms.

[2]

Markscheme

c. a. phylogeny is the evolutionary line of descent;

b. the study of similar molecules in two different species; (e.g. *mitochondrial DNA* / *hemoglobin* / *Cytochrome c*)

c. the greater the differences, the longer the time span since the two species had a common ancestor;

d. variation can be due to mutations;

e. mutations are chance events so caution must be taken when interpreting these;

d. a. organization of data helps to identify organisms;

b. suggests evolutionary links;

c. suggests the closeness of a relationship the more similar the characteristics are;

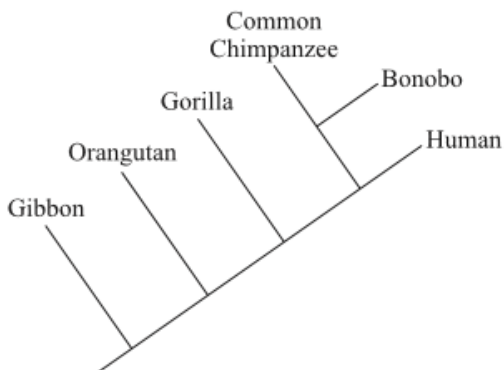
d. allows prediction of characteristics shared by members of a group;

Examiners report

c. Candidates had trouble with the question regarding how variations in molecules can lead to phylogeny, confusing the study of evolutionary relationships with the actual development of the relationships themselves.

d. [N/A]

The diagram below is a cladogram.



a. State a function of each of the following parts of the human brain.

[2]

(i) Cerebellum

(ii) Hypothalamus

b (i) Identify the **two** most closely related organisms.

[1]

b (ii) Identify the species to which the Bonobo is most distantly related.

[1]

c. Describe **one** type of barrier that may exist between gene pools.

[3]

Markscheme

a. (i) (coordinates) unconscious motor functions/balance and movement

(ii) (maintains) homeostasis/thermoregulation/appetite/thirst / coordinates endocrine systems / secretes hormones/regulating factors

b (i) (common) chimpanzee and bonobo

b (ii) gibbon

c. named barrier;

description of its action;

results in terms of gene pools;

e.g.:

behavioural barrier;

different populations mate at different times of year thus preventing interbreeding;

allele frequencies become different in the two gene pools/separates gene pools / sympatric speciation;

Examiners report

a. The vast majority of candidates provided correct answers.

b (i) This part presented a cladogram of larger primates and the two subparts were interpreted correctly by the vast majority of candidates.

b (ii) This part presented a cladogram of larger primates and the two subparts were interpreted correctly by the vast majority of candidates.

c. This part required candidates to name a barrier that may exist between gene pools and describe its action and the results in terms of gene pools.

Mixed results were obtained here, although many candidates gained all the marks. Some candidates confused between types of barrier and types of evolution (e.g. geographic vs allopatric), were vague about its action and could not relate to gene pools.

- b. Define analogous characteristics using **one** example to illustrate your answer. [1]
- c. Outline **two** pieces of evidence that support the endosymbiotic theory for the origin of eukaryotes. [2]
- d. List **two** anatomical features that define humans as primates. [2]

Markscheme

- b. analogous structure similar in appearance/function but with different evolutionary history e.g. wing of bat and wing of bird;
- c. smaller/70S ribosomes in mitochondria/chloroplasts (as in prokaryotes);
circular DNA in mitochondria/chloroplasts (as in prokaryotes);
mitochondria/chloroplasts have double membrane;
similar size/shape of mitochondria/chloroplasts to prokaryotes;
- d. opposable thumb;
large range of shoulder movement;
good vision / stereoscopic vision / overlapping field view;
large brain relative to body size;
tailless primate;
Y-5 cusps of molars;

Examiners report

- b. Those that knew the correct definition did well.
- c. The main pieces of evidence supporting the endosymbiotic theory for the origin of eukaryotes seen were double membranes and the presence of circular DNA.
- d. The most popular answers here were those of humans having an opposable thumb and stereoscopic vision. Many though only gained one mark point here with the answer of opposable thumb.

-
- a. Distinguish between innate and learned behaviour. [1]
 - c. Distinguish between analogous and homologous structures. [2]

Analogous structures	Homologous structures

Markscheme

- a. innate behaviour is independent of experience/environmental conditions/inherited
while learned behaviour is influenced by experience/environment / *OWTTE*

c.

<i>Analogous structures</i>	<i>Homologous structures</i>
same function	(same or) different function;
differ in (fundamental) structure	similar in (fundamental) structure;
not common ancestry/convergent evolution	common ancestry/divergent evolution;

Examiners report

- a. Many gave vague answers to this section and did not make reference to the role of the environment or experience in distinguishing between the two types of behaviour. Candidates should not describe "learned" behaviour as that which we learn.
- c. The table was given so that candidates could easily distinguish between analogous and homologous structures clearly but some still did not compare like points.

Discuss the relationship between cladograms and the classification of living organisms.

Markscheme

classification traditionally based on morphology;

cladistics (strength) based on molecular differences/base sequences/amino acid sequences;

cladistics (weakness) is based on probability but improbable events do occur, so relationships can be wrong;

clade includes ancestral species/descendants from that species;

members of clade share set of features not found in more distant relatives;

cladogram is a tree-like diagram where nodes/branches represent the splitting of (two) new groups from a common ancestor;

different cladograms can represent same relationships in a group;

cladogram timescale not necessary;

classification based on cladograms is often same as traditional classification;

in some groups cladograms have led to revised classification;

Accept any of the above points shown in a clearly annotated diagram.

Examiners report

Many answers had content that did not match well with the markscheme, making this the hardest question in the exam, as very few candidates scored full marks. Often vague statements were given, not distinguishing between the fundamental differences between cladogram and traditional methods of classification. There was no clear idea about what/how/why cladograms were done, and the differences were between them and traditional classification. Many candidates believe that cladograms are the source of data, not their presentation.

State **two** characteristics that permit the classification of microbes into domains.

Markscheme

cell wall structure/composition / whether the cell wall contains peptidoglycan;

size of / 70S or 80S ribosomes;

(base sequence in) ribosomal RNA/rRNA;

whether there are introns;

whether there are histone proteins;

membrane structure / ether or ester bonds (in membrane lipids);

Examiners report

This posed few problems for well-prepared candidates, though (a) and (b) were not known by all.

Explain cladistics as a method of classifying organisms.

Markscheme

a. cladistics uses cladograms/tree diagrams;

b. show clades/branches (in parallel) that begin at a point/node;

c. each clade includes a (common) ancestral organism/node and all its descendents;

- d. members of a clade share derived/inherited characteristics;
- e. clades are nested/subsets of larger clades;
- f. cladograms show evolutionary history/origin of organisms / phylogeny;
- g. branch length (of clade) can indicate (relative) amount of genetic change/time;
- h. clades based on (objective) molecular analysis/genetic evidence / differ in amino acid sequences/DNA base changes/mutations;
- i. fewest number of differences/maximum parsimony determines branch separation;
- j. predictability of DNA base changes/mutation rates suggests evolutionary timelines;
- k. problems arise when gene change varies (greatly) from one gene to the next;
- l. cladograms may not match traditional/Linnaean classification;
- m. (mismatch) prompts re-examination of data / reclassification of a group;

Some of the above points may be included in a correctly annotated diagram clearly stating above points.

Examiners report

This was probably the most poorly answered of the longer response questions on this paper. Candidates did not seem to have enough knowledge about cladistics to allow them to respond adequately and marks above 2 or 3 were rarely seen. As they were unable to communicate ideas on clades clearly they waffled and were repetitive. Better candidates were able to discuss cladograms to some degree. Better teaching of this topic is required.

Explain the biochemical evidence for the common ancestry of living organisms.

Markscheme

- DNA/RNA found in all living organisms/genetic code is universal;
- amino acids all L- not D- isomers;
- same 20 amino acids/proteins found in all living organisms;
- involves comparing similarities and differences in the amino acid sequence of the same molecule;
- e.g. hemoglobin;
- involves comparing base sequences of variable regions of DNA;
- e.g. mitochondrial DNA;
- the more similar the base/amino acid sequence, the more closely related;
- comparing amino acid sequences that result in the phenotype/comparing DNA sequences that result in the genotype;
- evidence for molecular evolution in drug resistance;

Examiners report

[N/A]

Discuss the use of cladograms in phylogenetic studies.

Markscheme

- a. a cladogram is a diagram which shows shared characteristics/phylogenetic relationships;
- b. phylogeny is the study of evolutionary origins/ancestry;
- c. clade is a group of (all) organisms that evolved from a common ancestor;
- d. evidence from biomolecules/DNA/RNA/protein/cytochromes;
- e. cladograms can be compared with other representations of phylogenetic relationships/may confirm fossil/anatomical evidence;
- f. organisms placed close together in a cladogram are closely related evolutionarily;
- g. there may be more than one possible cladogram (for a particular group) raising questions about evolutionary relationships;
- h. divisions between clades/nodes suggest the sequence in which groups diverged;
- i. cladograms can be used to estimate time since groups diverged;
- j. cladograms are often similar to classification based on other evidence/traditional methods;
- k. cladograms may lead/have led to reclassification of a group;

Examiners report

Although this was a popular option, candidates did not do very well on it.

While some candidates had an idea that cladograms were used to show evolutionary relationships, they were not able to clearly indicate what clades were and how cladograms were used. Some candidates confused cladograms with dichotomous identification keys. Candidates seldom received more than 3 out of 6 marks for this question.

Explain the biochemical evidence for the common ancestry of organisms on Earth.

Markscheme

- all organisms use DNA as genetic material;
- same four (nucleotide) bases makes up DNA in all organisms;
- number of mutations reflect differences between organisms;
- all organisms use the same genetic code / minor differences;
- genetic code is degenerate/OWTTE;
- all organisms use the same 20 amino acids;
- function of proteins constant between species;
- protein/molecule examples; (*eg hemoglobin, cytochrome, chlorophyll*)
- only left-handed amino acids have been observed in living organisms;
- although right-handed amino acids will have been available;

only right-handed glucose/carbohydrates used in organisms;

similarities in glycolysis/metabolic pathways;

all use RNA/same enzymes in transcription/translation;

Examiners report

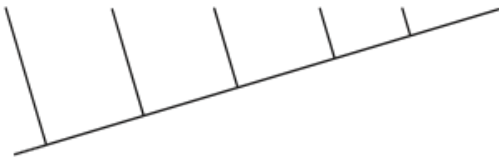
Candidates had more difficulty with this question than with questions requiring longer answers in the other options, but many nevertheless provided good answers and managed to gain all the marks; those who were less successful confused biochemical evidence with origins of life.

a. The table shows certain characteristics present (+) or absent (-) in six organisms.

[3]

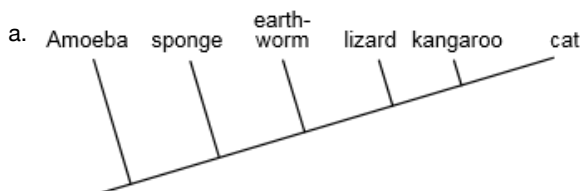
	Segmented	Jaws	Hair	Placenta	Multicellular	Limbs
Amoeba	-	-	-	-	-	-
Cat	+	+	+	+	+	+
Earthworm	+	-	-	-	+	-
Kangaroo	+	+	+	-	+	+
Lizard	+	+	-	-	+	+
Sponge	-	-	-	-	+	-

Using the data, label the cladogram with the names of the organisms.



c. A species is often defined as a group of similar individuals that interbreed in nature and produce fertile offspring. Discuss some problems with the use of this definition. [2]

Markscheme



Award [1] for the correct position of any two organisms.

Award [1 max] if the correct order is reversed horizontally (ie from cat on the left to Amoeba on the right).

- c. a. not all organisms can be defined in this way / does not take into account hybrids/ microorganisms/plants;
 - b. (even if able to interbreed) may have differences in DNA/protein;
 - c. does not apply to bacteria/other organisms that reproduce asexually;
 - d. in sympatric/allopatric isolation members of the same species do not interbreed;
 - e. (in some species) significant differences in morphology can occur within the same species eg: sexual dimorphism/metamorphosis/ring species;
- Accept any other correct answer.

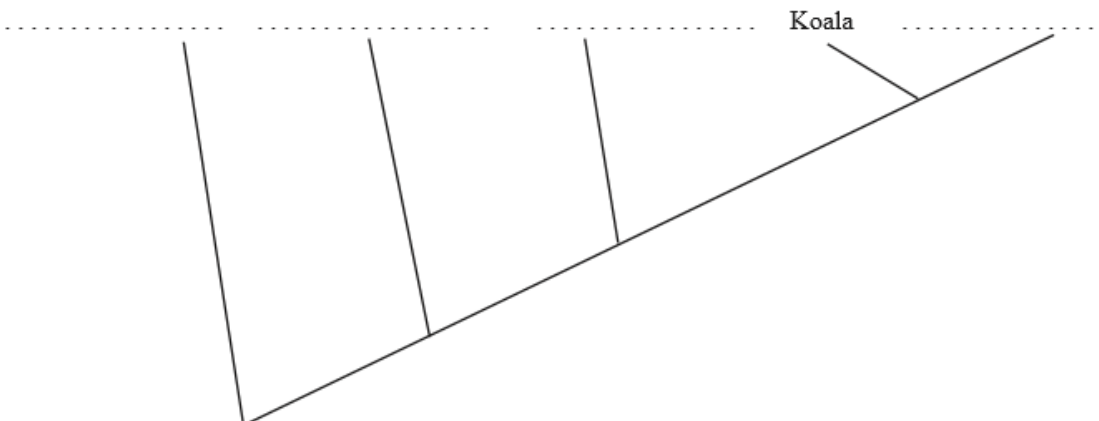
Examiners report

- a. The majority of candidates could label the cladogram correctly, although a certain number did it backwards.
- c. Many candidates presented a good discussion about the use of species definition, but many others could not express their ideas clearly enough or only had a vague idea.

- a. Define the term *clade*. [1]
- b. Distinguish between analogous and homologous structures, giving an example of each. [2]
- c. The table below lists five animals along with four morphological characteristics. A plus sign (+) indicates that the animal has this characteristic [2] while a minus sign (-) indicates that the characteristic is absent.

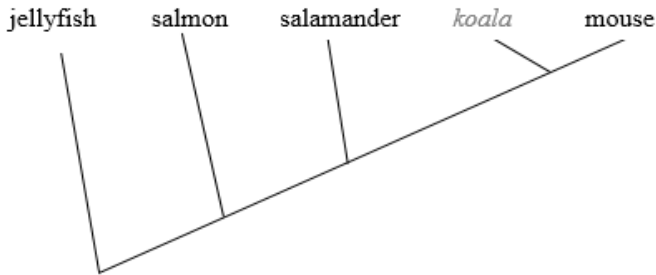
Animal	Jaws	Limbs	Hair	Placenta
Salamander	+	+	-	-
Mouse	+	+	+	+
Jellyfish	-	-	-	-
Koala	+	+	+	-
Salmon	+	-	-	-

Based on the features above, a student constructed a cladogram. State the names of the organisms missing in the following cladogram.



Markscheme

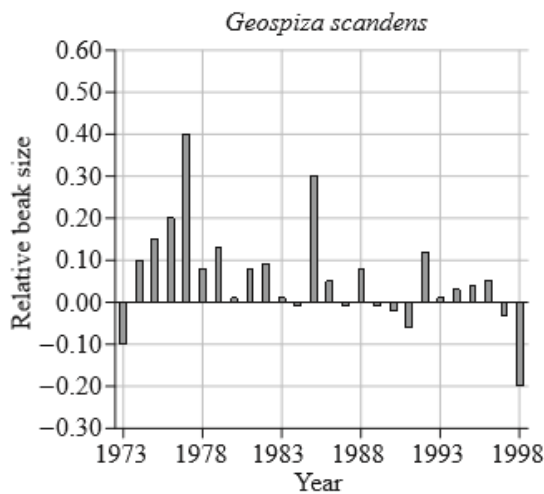
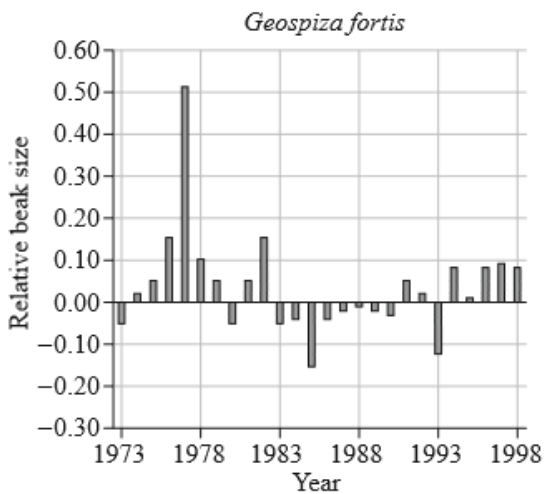
- a. a group of related organisms sharing a common ancestor / a group of organisms containing an ancestor and all of its descendants / *OWTTE*
- b. homologous structures evolved from a common ancestor while analogous structures did not;
example of homologous and example of analogous; (*both needed*)
- c. *Two correct labels for [1].*



Examiners report

- a. Many were able to get mark for the definition of clade but others were omitting the idea of common ancestry.
- b. This was fairly well done with many getting both marks. The most common example used for homologous structure was the pentadactyl limb with various examples for analogous structures such as insect and bird wings.
- c. Virtually all candidates were able complete the cladogram for 2 marks.

A study of two populations of Darwin's finches, medium ground finch (*Geospiza fortis*) and cactus finch (*Geospiza scandens*), was undertaken between 1973 and 1998 on the Galápagos Islands. The graphs below show the mean beak size in each year from 1973 to 1998 compared with the long-term mean size.



- a. State the year in which *G. fortis* had the greatest change in relative beak size. [1]
- b. Compare the trends in relative beak size of *G. fortis* and *G. scandens*. [3]
- c. Outline possible reasons for the trends in relative beak size in finches. [2]

Markscheme

- a. 1977 / 1978

N.B. Some responses are interpreting this as a change between years.

- b. both species increased (relative) beak size at the beginning of the study/ between the years 1973/1974 to 1977/1978;
no similarity in trend for both species after 1977/1978/1979 / no relationship between the two species in the years of increase and decrease;
more occurrence of decrease in (relative) beak size in *G. fortis* whereas *G. scandens* showed more increases in (relative) beak size;
G. fortis shows wider fluctuation in (relative) beak size than *G. scandens*;
Do not accept year by year comparisons.

- c. changes in environment/rainfall/ocean currents/migration / drought;
change in food supply;
hybridization/crossbreeding between species;
natural selection / selection pressure;

Examiners report

- a. N/A
- b. The lack of sufficient explanation in the question, "mean beak size" for each species or for the two species together, led to a wide variety of answers that scored poorly. Many also quoted values for individual years which did not describe a "trend."
- c. Factors contributing to different beak size between species were stated (different food sources) instead of reasoning which factors cause that a given species change its size.

Antibiotics are sometimes given orally to poultry to prevent disease that may lead to reduced growth. Antibiotic resistance of bacteria from turkeys and chickens bred for meat and from egg laying hens was measured.

Excrement was collected and *Escherichia coli* bacteria were isolated. These bacteria were tested for resistance to a range of antibiotics and the results are shown below.

Number of antibiotics to which <i>E. coli</i> are resistant	Turkeys <i>n</i> = 43	Chickens <i>n</i> = 45	Egg laying hens <i>n</i> = 20
0	7	9	13
1	8	5	3
2	7	7	0
3	2	7	3
4	5	7	1
≥5	14	10	0

[Antibiotic resistance of faecal *Escherichia coli* in poultry, poultry farmers and poultry slaughterers. A. E. van den Bogaard, N. London, C. Driessen, E. E. Stobberingh. *Journal of Antimicrobial Chemotherapy*, 47, June 1, 763–771. 2001, Oxford University Press.]

- a. Calculate the percentage risk of bacteria becoming resistant to more than five kinds of antibiotics in turkeys and egg laying hens. [1]
- Turkeys:
- Egg laying hens:
- b. Compare the incidence of drug resistance in bacteria from chickens and egg laying hens. [2]
- c. Discuss the hypothesis that giving antibiotics increases antibiotic resistance in poultry bacteria. [2]
- d. Suggest how antibiotic-resistant bacteria are passed from animals to humans. [1]
- e. Outline the mechanism of the action of antibiotics. [2]
- e. Outline the mechanism of the action of antibiotics. [2]

Markscheme

- a. *turkeys*: 33/32.6/32.56 %
- egg laying hens*: 0 %
- Both needed to award the mark.*
- b. a. none of the egg laying hens have bacteria resistant to 5 or more antibiotics while (10) chickens have bacteria resistant to 5 or more antibiotics;
- b. 13/65 % of the egg laying hens have no resistant bacteria while 9/20 % of the chickens have no resistant bacteria;
- c. both have approximately same percentage/number of *E. coli* resistant to 1 or 3 antibiotics;
- d. egg laying hens have less incidence of antibiotic-resistant bacteria than chickens;
- c. a. hypothesis supported for poultry raised for meat but not for egg-laying;
- b. turkeys and chickens always have bacteria resistant to more antibiotics than egg laying hens;
- c. antibiotic-resistant bacteria are still found in egg laying hens even though antibiotics are rarely given;
- d. antibiotic-resistant strains (of bacteria) may have arisen by other means/other than by poultry being given oral antibiotics;
- d. from fecal matter to man handling the chickens / by accidental hand to mouth contact / contaminated dust / eating raw meat;
- e. a. inhibition of synthesis of walls;
- b. inhibition of protein synthesis;

c. inhibition of nucleic acid synthesis;

e. a. inhibition of synthesis of walls;

b. inhibition of protein synthesis;

c. inhibition of nucleic acid synthesis;

Examiners report

a. Many could calculate the percentages correctly, but demonstrated a total lack of understanding of the data. There was quite a bit of confusion about the poultry being resistant to bacteria rather than the bacteria found in the poultry being drug resistant.

b. Many could calculate the percentages correctly, but demonstrated a total lack of understanding of the data. There was quite a bit of confusion about the poultry being resistant to bacteria rather than the bacteria found in the poultry being drug resistant.

c. Many could calculate the percentages correctly, but demonstrated a total lack of understanding of the data. There was quite a bit of confusion about the poultry being resistant to bacteria rather than the bacteria found in the poultry being drug resistant.

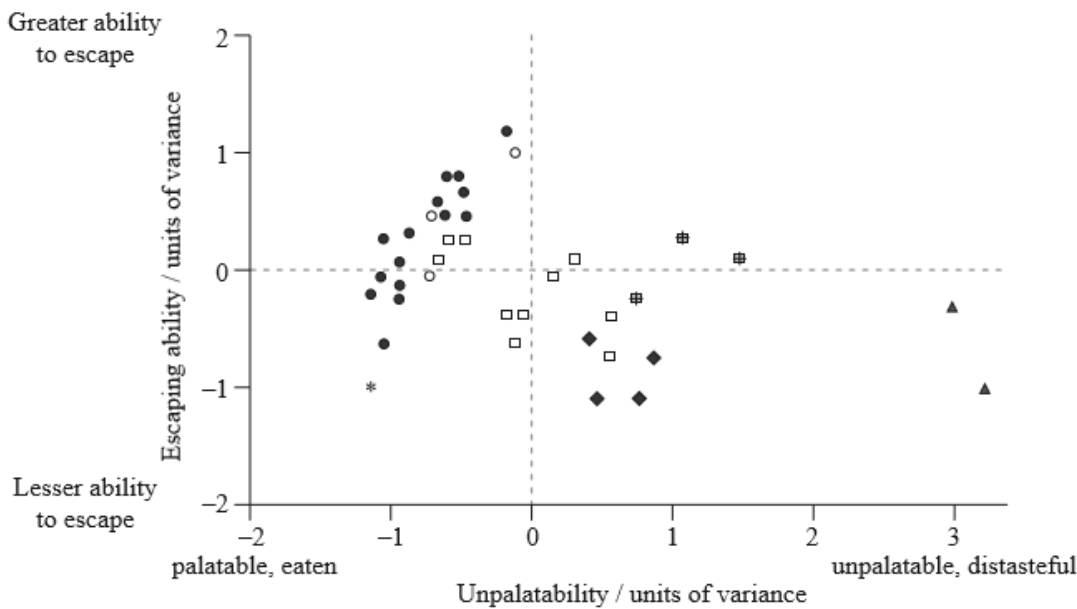
d. Many could calculate the percentages correctly, but demonstrated a total lack of understanding of the data. There was quite a bit of confusion about the poultry being resistant to bacteria rather than the bacteria found in the poultry being drug resistant.

e. Many could calculate the percentages correctly, but demonstrated a total lack of understanding of the data. There was quite a bit of confusion about the poultry being resistant to bacteria rather than the bacteria found in the poultry being drug resistant.

e. Many could calculate the percentages correctly, but demonstrated a total lack of understanding of the data. There was quite a bit of confusion about the poultry being resistant to bacteria rather than the bacteria found in the poultry being drug resistant.

Butterflies have evolved different methods of defence against bird attacks. The relative escaping ability and unpalatability (distastefulness) of different tropical butterfly families and subfamilies was investigated in the presence of wild kingbirds, *Tyrannus melancholicus*, a natural predator of butterflies.

Each symbol on the graph represents a different species within a (sub)family.



Key:	● Limenitidinae	* Nymphalidae	■ Danainae	▲ Papilionidae
	○ Charaxinae	□ Heliconiinae	◆ Ithomiinae	

['Palatability and escaping ability in Neotropical butterflies: tests with wild kingbirds (*Tyrannus melancholicus*, Tyrannidae).'] *Biological Journal of the Linnean Society*, 59, pp. 351–365, Carlos E.G. Pinheiro. ©1996 Linnean Society. Reproduced with permission of Blackwell Publishing Ltd.]

- State which butterfly (sub)family contains the species with the greatest escaping ability. [1]
- Suggest one feature of butterfly wings that might help a butterfly to escape from a predator. [1]
- (i) Explain how the ability of a butterfly to escape from predators could increase by natural selection. [3]
- (ii) The graph shows that distasteful butterflies tend to have a lower ability to escape from predators than palatable butterflies. Suggest reasons for this trend. [2]

Markscheme

- Limenitidinae
- large wing size / camouflage/cryptic coloration / warning coloration / mimicry / powerful wing muscles / high flight speed / erratic flight pattern / OWTTE
- (i) natural selection favours survival of better-adapted individuals;
better-adapted butterflies have greater ability to escape predation;
and survive to reproduce;
allowing them to pass their characteristics/alleles/genes to offspring;
over generations, the number of butterflies with best-escaping ability increases in the population / frequency of alleles/genes for better escaping ability increases in the population/gene pool;

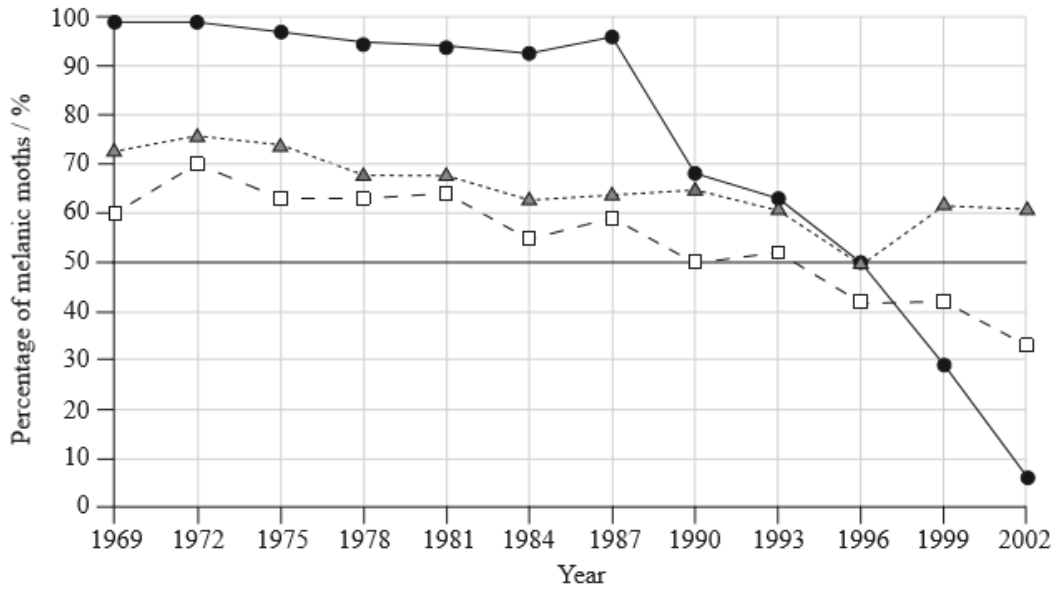
- c (i) palatable butterflies with high escaping ability can survive to pass on genes / palatable butterflies with low escaping ability are eaten and their genes are lost;
- unpalatable/distasteful butterflies, regardless of escaping ability, are not eaten/are avoided by predators;
- such butterflies survive to pass on their genes to the next generation;

Examiners report

- a. This part required candidates to read the highest escaping ability correctly, which was done by the vast majority of candidates.
- b. The vast majority of candidates suggested a plausible feature that could increase the escaping ability among butterflies, most mentioning camouflage.
- c (i) This part seemed more challenging for candidates who nevertheless managed to gain marks. In (i), stating the principles of natural selection clearly in terms of adaptation, survival, reproduction and relating to populations and/or gene pools was the most difficult part, with many answers failing to include the words *adaptation*, *population* and *gene pool*.
- c (ii) In (ii), many candidates managed to state that unpalatable butterflies were not eaten by predators, but had much difficulty to figure out that it was regardless of escaping ability; many answers had a lamarckian connotation, stating that butterflies who could not escape had to evolve to become unpalatable, which is incorrect. Furthermore, candidates largely failed to explain palatable butterflies here. Very few marking points were awarded for “palatable butterflies with high escaping ability can survive to pass on genes / palatable butterflies with low escaping ability are eaten and their genes are lost.”

A study of the changing frequencies of the melanic (dark) and non-melanic (light) forms of three moth species *Biston betularia*, *Odontoptera bidentata* and *Apamea crenata* was carried out in the north of England. Moths were captured using mercury vapour light traps throughout the flying season. All three of the moth species fly at night and rest in the day, when they would be vulnerable to predation by birds, if visible. *B. betularia* rests on tree branches and there is evidence that the change from melanic to non-melanic forms was associated with black soot disappearing from these branches as air pollution was reduced and pale coloured lichens started to grow. *O. bidentata* rests under the leaves of trees or in cracks in tree bark. *A. crenata* rests in long grasses. The graph shows the percentage of melanic moths caught between 1969 and 2002.

Key: ● *B. betularia*
 ▲ *A. crenata*
 □ *O. bidentata*



- a. Identify the year with the highest frequency of the melanic form of *O. bidentata*. [1]
- b. Estimate the percentage of **non-melanic** forms of *A. crenata* in 1978. [1]
- c (i) Compare the trends for the three moth species during the study. [3]
- c (ii) Suggest reasons for the differences in trends. [2]

Markscheme

- a. 1972
- b. 32 (units not required) (Allow answers in the range 31–33)
- c (i) Award [2 max] if at least 1 similarity and 1 difference not given.

Similarities:

in all species, melanics show a decline / non-melanics an increase in frequency;
 up to 1987 percentage of melanics stable/slight decline for all three species;

Differences: Both parts of comparison required for [1].

after 1987 percentage of *B. betularia* melanics declines sharply whereas percentage for the other species declines slowly;
 at start of investigation/1969/up to 1987 (very) few (less than 10 %) non-melanic forms of *B. betularia* whereas the percentage much higher (more than 20 %) for the other two species / converse;
 melanic forms of *B. betularia* and *O. bidentata* drop below 50% (by 1996) but *A. crenata* does not;

- c (ii) change from polluted (industrial) environment to clean (post-industrial);
- change in tree species allowing different habitats for resting moths;
- change in predators as climate/habitats change;

changing selection pressures/mutation/migration/genetic drift;

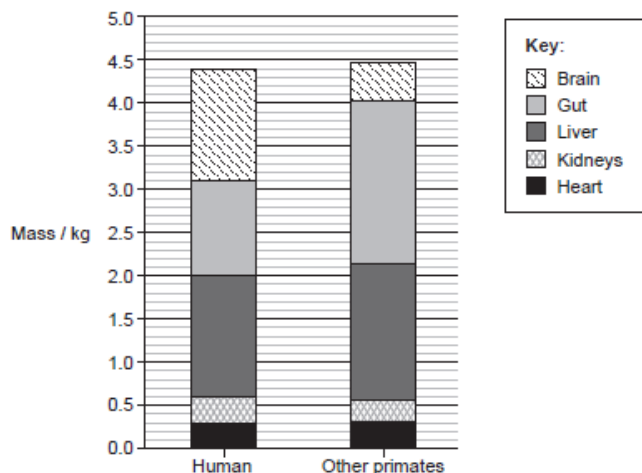
grass grows quickly/colour not influenced by pollution so least change in/less selection pressure on *A. crenata*;

Examiners report

- a. Almost every candidate was able to identify 1972 as the year with the highest frequency of the melanic form of *O. bidentata*.
- b. Many obtained one mark for correctly estimating the percentage of non-melanic moths in 1978.
- c (i) This part proved more discriminating. For (i), many candidates obtained one mark for indicating that in all species, melanics showed a decline. However, most did not compare the trends but simply stated what was happening for each of the three moth species over time. They also did not connect the fall in percentage melanics with a rise in percentage of nonmelanic forms of the species but instead incorrectly stated that the species number fell. .
- c (ii) Many were able to suggest the trends were due to a change from the polluted environment to a cleaner one for one mark but did not get a second point.

Researchers investigating human evolution recorded energy use for the brain, gastrointestinal tract (gut), liver, kidneys and heart as a percentage of total energy used in the human body. They found that these organs use around 70 % of the body's energy although they account for only about 7 % of body mass. They also compared the mass of each of these organs in humans with other modern primates, each with a body mass of 65 kg as shown in the bar chart.

Human organs	Brain	Gut	Liver	Kidneys	Heart
Energy use as percentage of total for body / %	16	15	19	8	11



[Source: adapted from LC Aiello, (1997), *Brazilian Journal of Genetics*, 20, Issue 1]

- a. Calculate the percentage of the total body mass made up by the human brain. [1]
- b. Compare the mass of human organs with the mass of other primate organs. [2]

- c. Using information from the table and the graph, identify the human organ which uses the greatest amount of energy per kilogram of body tissue. [1]
- d. Explain the differences between the organ size of humans and other primates in terms of trends in human evolution and their causes. [4]

Markscheme

a. $\left(\frac{1.3}{65} \times 100 =\right) 2(\%)$

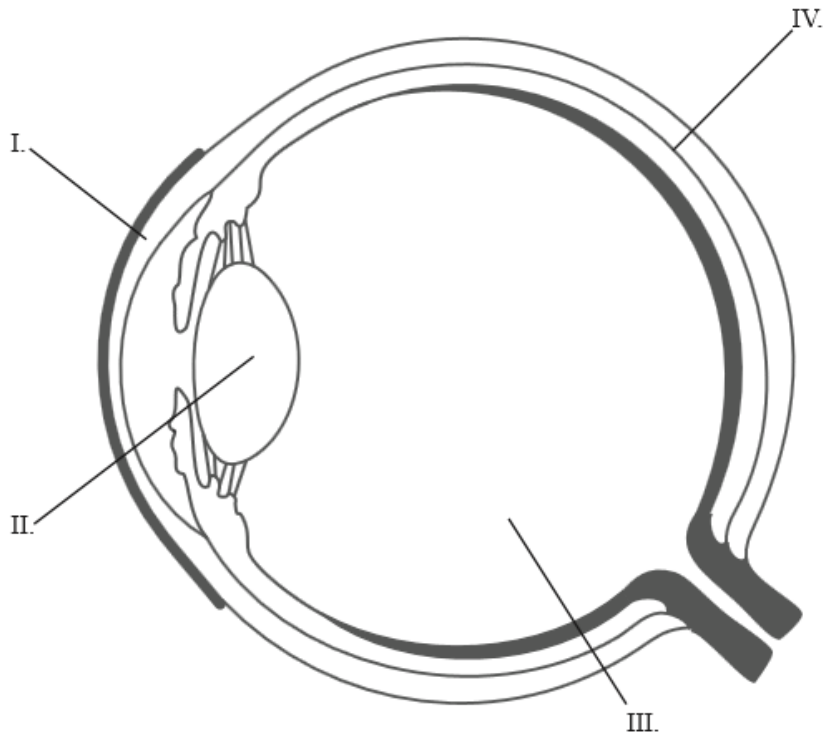
- b. a. total organ mass (approximately) same for both;
- b. very little difference in mass in heart/kidney/liver;
- c. human brain has greater mass than the primate brain;
- d. human gut has lower mass than the primate gut;
- c. heart
- d. a. brain size increased during hominid evolution / *OWTTE*;
- b. change in diet from mostly vegetarian to more protein-rich/meat eating diets;
- c. eating meat/protein allows larger brain growth / change in diet corresponds to the start of increase in hominid brain size;
- d. larger brains require more energy;
- e. larger gut necessary for plant material digestion;
- f. smaller gut is sufficient for meat/cooked food;

Examiners report

- a. The majority of candidates could interpret the data correctly, although there were some erroneous calculations and identifications of liver instead of heart as the organ using the greatest amount of energy per kilogram of body tissue (due to calculation issues). Most candidates displayed some knowledge when explaining the different organ sizes, but their understanding of cause and effect was sometimes not that clear.
- b. The majority of candidates could interpret the data correctly, although there were some erroneous calculations and identifications of liver instead of heart as the organ using the greatest amount of energy per kilogram of body tissue (due to calculation issues). Most candidates displayed some knowledge when explaining the different organ sizes, but their understanding of cause and effect was sometimes not that clear.
- c. The majority of candidates could interpret the data correctly, although there were some erroneous calculations and identifications of liver instead of heart as the organ using the greatest amount of energy per kilogram of body tissue (due to calculation issues). Most candidates displayed some knowledge when explaining the different organ sizes, but their understanding of cause and effect was sometimes not that clear.
- d. The majority of candidates could interpret the data correctly, although there were some erroneous calculations and identifications of liver instead of heart as the organ using the greatest amount of energy per kilogram of body tissue (due to calculation issues). Most candidates displayed some knowledge when explaining the different organ sizes, but their understanding of cause and effect was sometimes not that clear.
-

a. The diagram below represents the human eye. State the names of structures I, II, III and IV.

[2]



I.

II.

III.

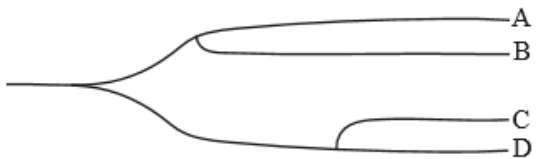
IV.

b. Outline the evidence provided by DNA for the common ancestry of living organisms.

[2]

c. The cladogram below shows the classification of species A to D. Deduce how similar species A is to species B, C and D.

[2]



d. Suggest **two** reasons for using cladograms for the classification of organisms.

[2]

Markscheme

a. I. cornea;

II. lens;

III. vitreous humour;

IV. choroid; (Accept sclera as line is on the border between these two)

Two correct for [1] and four correct for [2].

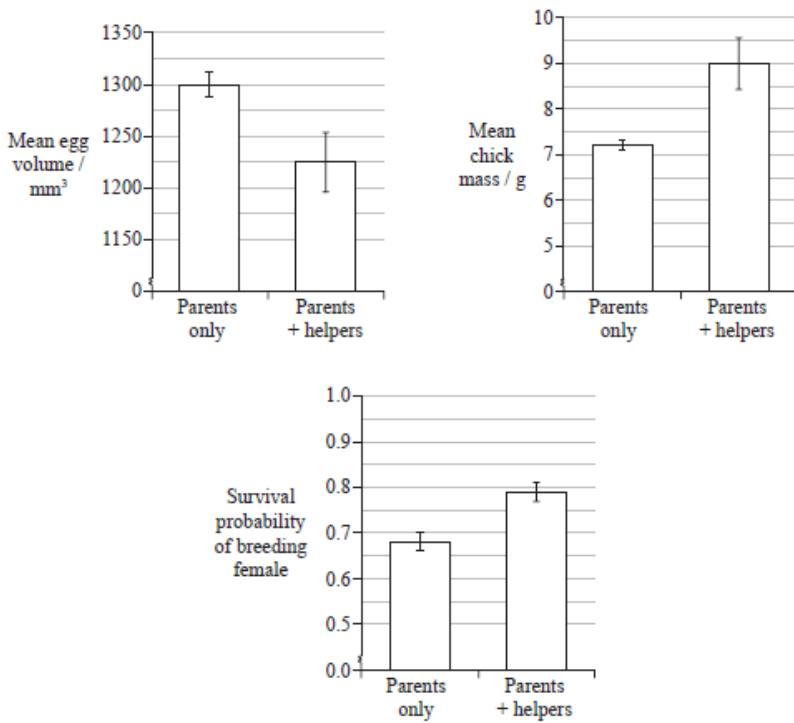
- b. all living organisms use DNA as genetic/hereditary material;
genetic code is (almost) universal;
idea that mutations accumulate gradually in DNA;
- c. A is most similar to B;
A is equally similar to C and D;
A is least similar to both C and D;
- d. methods used to prepare cladograms use a different approach from traditional classification/taxonomy;
show ancestral relationships;
reflect how recently two groups shared a common ancestry;
cladograms are (objective/accurate because they are usually) based on molecular differences;
they should be considered as a good complement to traditional classification;

Examiners report

- a. Candidates did surprisingly poorly on this simple task of naming the structures of the eye. The label line for IV was on the border of the choroids and the sclera, and thus either one was accepted as correct.
- b. This was poorly done. Some correctly indicated that DNA was the genetic or hereditary material for all living organisms and that the genetic code is universal. Many wrote about pentadactyl limbs, DNA being made of 20 amino acids or about chimps and humans which did not get marks.
- c. Many candidates correctly interpreted the cladogram, deducing that A and B were most similar. Some were able to get a second point.
- d. Many were able to get one mark for indicating that cladograms showed ancestral/evolutionary relationships but only a few got the second mark for another reason for using cladograms.

Cooperative breeding in birds occurs when more than two birds of the same species help to rear the young from one nest. For the Australian superb fairy-wren (*Malurus cyaneus*), mature non-breeding birds help to protect and rear the young, although they are not parents of any of them.

The bar charts below show the effect of the presence of helpers on mean egg volume, mean mass of six-day-old chicks and the probability of survival of the breeding females until the next breeding season.



[Source: From A F Russell, et al., (2007), *Science*, 317, pages 941-944. Reprinted with permission from AAAS.]

- a(i). State the effect of the presence of the helpers on mean chick mass. [1]
- b. Calculate the percentage decrease in mean egg volume found in the presence of helpers as compared to the parents only. Show your working. [2]
- c. With reference to the data, suggest why the activity of the helper affects the probability of survival of the breeding female until the next breeding season. [2]
- d. Cooperative breeding is an altruistic behaviour. Outline the evolution of altruistic behaviour. [2]

Markscheme

- a(i). (mean) chick mass increases in presence of helpers
- b. $\frac{1300-1225}{1300} \times 100\%$ or other correct calculation;
5.8%;
Accept the correct answer if it is not rounded up to 5.8% or if it is rounded up to 6%.
- c. with helper, smaller egg volume;
less resources from mother to produce egg/rear young;
more resources toward survival of mother;
- d. (altruistic) behaviour is inherited;
adaptations/behaviours that help the colony survive at expense of individual;
selected for (natural selection);
will be more likely to be passed on;

b. Explain what the branching off points represent in the cladogram of these fungi. [1]

c. There are several methods of introducing DNA into a cell in the laboratory. Outline the introduction of recombinant DNA in plant cell protoplasts. [2]

Markscheme

a. a. identify a start codon and stop codon

b. identify base sequences for a gene/that could code for a polypeptide

c. possible correlation with existing open reading frames in databases

b. a. represent common ancestors shared by the organisms that emanate from the point

b. indicates time since divergence

c. indicates number of differences in DNA

c. a. plant cells made into protoplasts by removing their cell wall / use cellulase to produce protoplasts

b. physical methods such as electroporation /microinjection/biolistics

c. chemical methods such as liposomes/calcium chloride/polyethylene glycol «PEG»

d. vectors such as *Agrobacterium*/tobacco mosaic virus

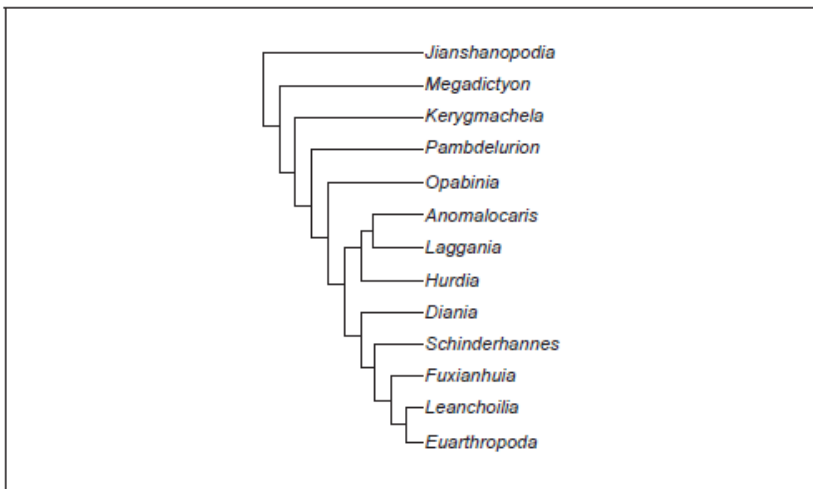
Examiners report

a. [N/A]

b. [N/A]

c. [N/A]

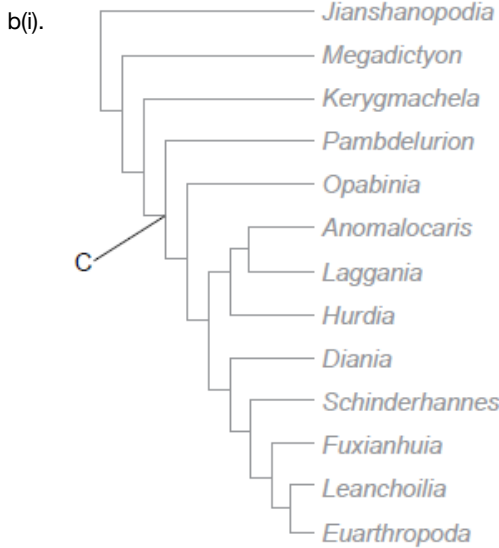
The diagram shows part of a cladogram for invertebrate species from the Cambrian age.



b(i) On the cladogram, label with the letter C the point that shows the most recent common ancestor of *Pambdelurion* and *Fuxianhuia*. [1]

b(ii) Identify which **two** species evolved most recently. [1]

Markscheme



Letter C must point to/be at the node/junction.

b(ii) Leanchoilia and Euarthropoda

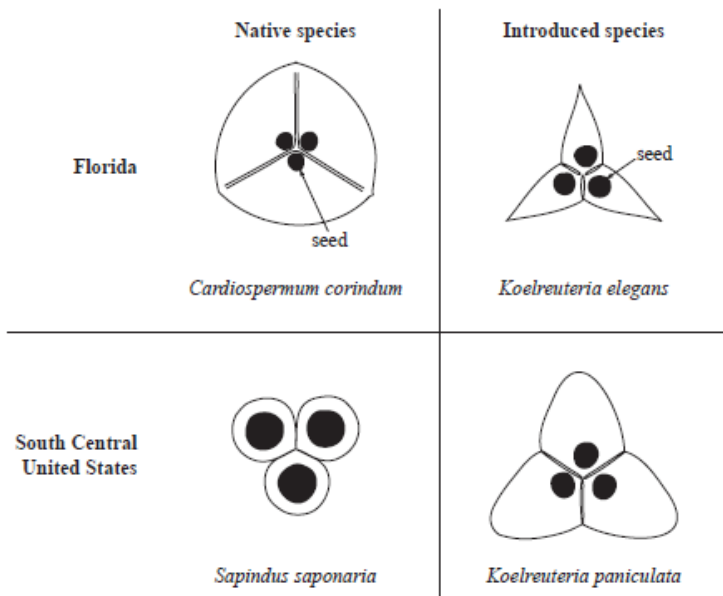
Examiners report

b(i) A large number of candidates had some difficulty labelling the common ancestry in the cladogram correctly, either because their label was not precise enough, even if they understood it (e.g. label at the right of *Pambdelurion*), or because they could not interpret it at all. It was easier for them to identify the two species that evolved more recently at the bottom of the cladogram, although some might have done it by chance due to their position on the cladogram.

b(ii) A large number of candidates had some difficulty labelling the common ancestry in the cladogram correctly, either because their label was not precise enough, even if they understood it (e.g. label at the right of *Pambdelurion*), or because they could not interpret it at all. It was easier for them to identify the two species that evolved more recently at the bottom of the cladogram, although some might have done it by chance due to their position on the cladogram.

The soapberry bug (*Jadera haematoloma*) feeds on the seeds of plants from the soapberry family (Sapindaceae). It does this by penetrating the fruit containing the seeds with mouthparts called the proboscis.

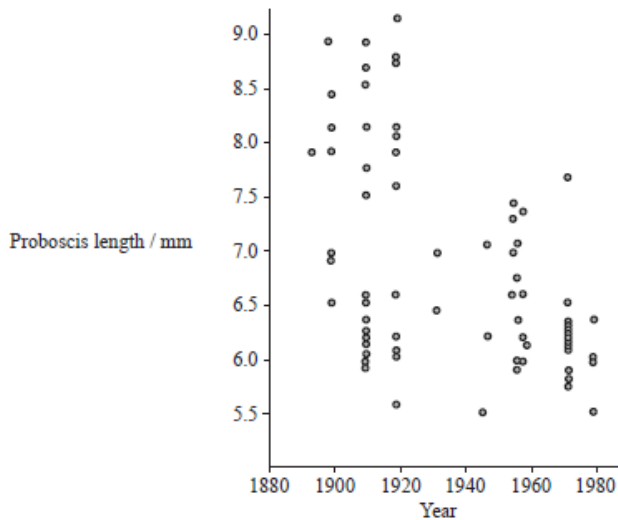
The diagrams below show sections through the fruits taken from four members of the Sapindaceae family.



[Source: Adapted from S P Carroll and C Boyd, "Host race radiation in the soapberry bug: Natural history, with the history", *Evolution*, Vol 46, pages 1052-1069. © John Wiley & Sons]

In Florida, *Cardiospermum corindum* is native to the area while *Koelreuteria elegans* is a species that was introduced in the 1890s and is now common in Florida. In the South Central United States, *Sapindus saponaria* is native while *Koelreuteria paniculata* is an introduced species which has become more common over the past 70 years.

The graph below shows proboscis lengths of samples of adult female soapberry bugs in Florida between 1880 and 1980.



[Source: Adapted from S P Carroll and C Boyd, "Host race radiation in the soapberry bug: Natural history, with the history", *Evolution*, Vol 46, pages 1052-1069. © John Wiley & Sons]

a(i). Outline the trends in proboscis length in soapberry bugs shown in the graph. [2]

b. Suggest, giving a reason, the expected trend in the proboscis length of the soapberry bug in the South Central United States over the past 70 years. [2]

Markscheme

a(i). proboscis length has decreased;

proboscis length has become less variable;

b. introduced fruit has a thicker flesh;

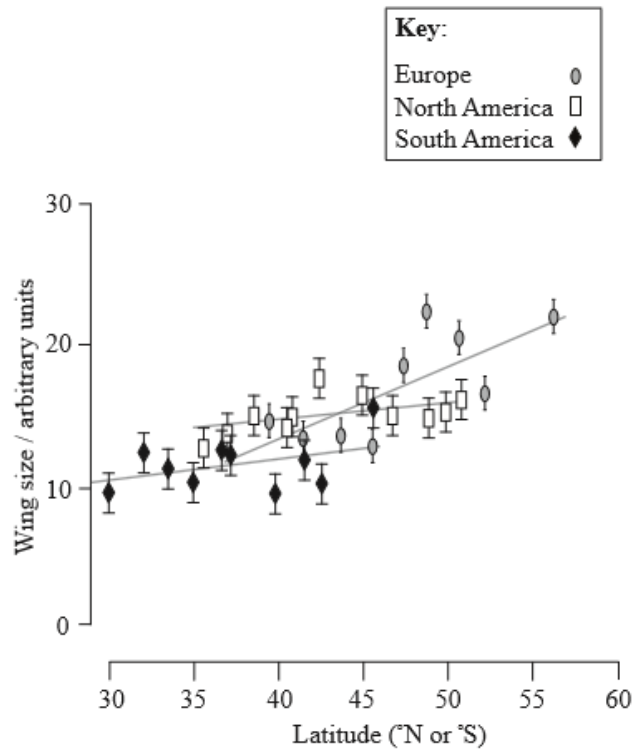
expect proboscis to get longer;

Examiners report

a(i).The trend required was often seen, the change in the variation of the data however, was rarely stated.

b. This was mostly very well answered with many students successfully suggesting that the proboscis length would increase over time due to the distance of the seeds from the outside of the fruit.

Drosophila subobscura (shown in photograph below) is a species of fruit fly native to Europe. The sample on the left is from Spain, latitude 39°, and the one on the right is from Denmark, latitude 56°. The species was introduced into both South America and North America approximately 20 years ago. The graph below shows the wing size in arbitrary units of *D. subobscura* at different latitudes in the three locations.



[Source: R.B. Huey, *et al.*, (2005), *Species Invasions; Insights into Ecology, Evolution and Biogeography*, pages 139–164]

[Source: G.W. Gilchrist, *et al.*, (2004), *Evolution*, **58**, pages 768–780]

[Source: M. Vellend, *et al.*, (2007), *Trends in Ecology and Evolution*, **22** (9), pages 481–488]

- a. Identify the relationship between wing size and latitude shown by *D. subobscura* in Europe. [1]
- b (i) Compare the data for wing size of *D. subobscura* in North and South America with wing size in Europe. [2]
- b (ii) Suggest **one** reason for the differences. [1]
- c. Predict, with a reason, what might happen to *D. subobscura* in the future as a result of its introduction to new areas. [2]

Markscheme

a. as latitude increases so does wing size / direct relationship / positive correlation

(do not accept directly proportional as line does not pass through the origin)

b (i) at higher latitudes/above 45° European species have larger wings than American species/largest wing sizes seen in European flies;

European flies show more variation than American flies (steeper curve);

at lower latitudes/below 45° North American flies have larger wings than European species;

South American flies have smaller wing size than European/ N. American flies;

b (ii) American species show less variation because they have had less time to diverge / evolve;

size of American flies closer to that of flies recently introduced/founder effect / European founder population from low latitudes;

American flies exposed to different selective pressures;

c. isolated populations diverge (genetically) / separation of gene pools;

may become a new species / allopatric speciation;

wing size will follow same trend as in Europe as population spreads (to higher latitudes because larger size favored by higher latitudes/colder climate);

wing size may stay small due to smaller gene pool/different climate;

Examiners report

a. Almost every candidate was able to identify the relationship shown in the graph. Candidates sometimes confused latitude with altitude which caused problems when answering the other sections of D1.

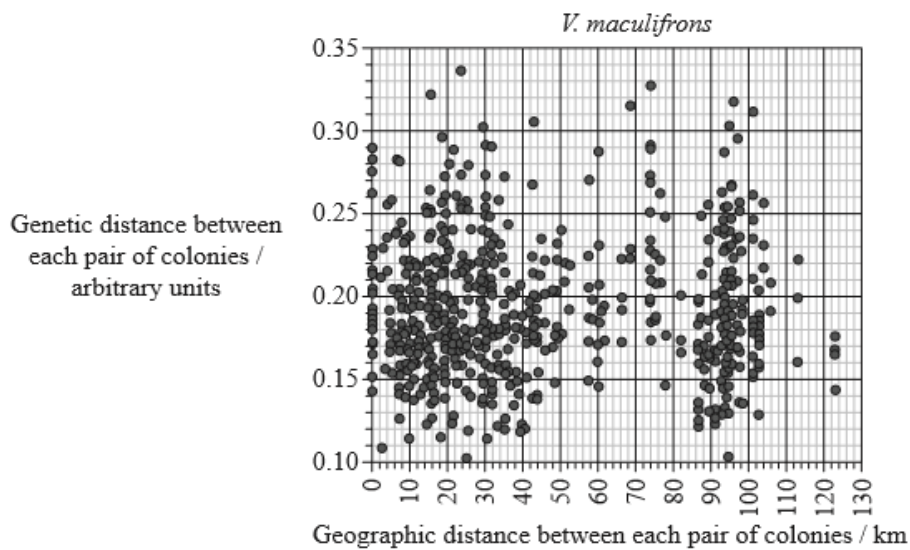
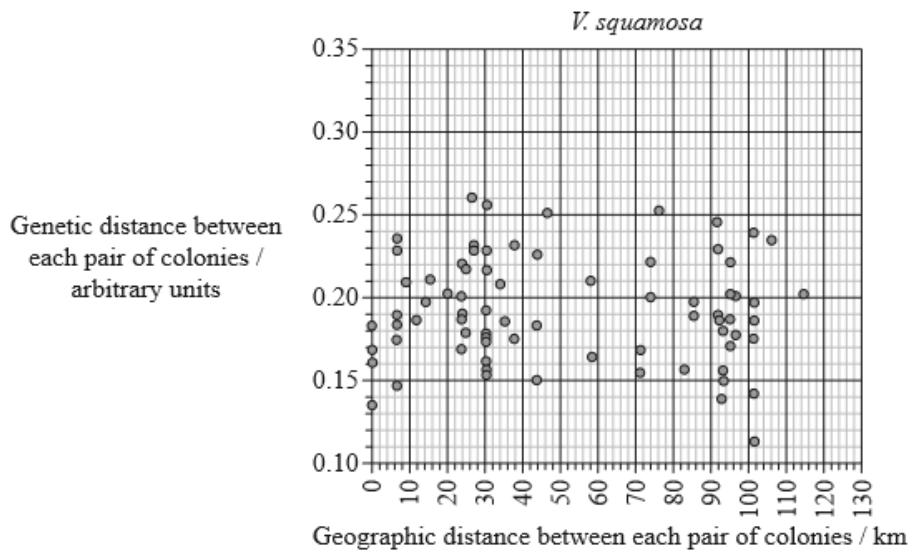
b (i) Many obtained one mark for correctly indicating that the European flies showed more variation than the American flies but few were able to get a second point in (i) or to suggest an acceptable reason for this in (ii). Those that did answer (ii) got a mark for understanding the role of selection pressures. Candidates need to be sure to make comparisons when asked rather than write descriptions.

b (ii) Many obtained one mark for correctly indicating that the European flies showed more variation than the American flies but few were able to get a second point in (i) or to suggest an acceptable reason for this in (ii). Those that did answer (ii) got a mark for understanding the role of selection pressures. Candidates need to be sure to make comparisons when asked rather than write descriptions.

c. Many were able to get one mark for indicating that a new species may form and some indicated this was a result of separation of gene pools due to geographic isolation.

A study was undertaken of the evolution of two species of wasps, one the parasite of the other. The parasite queen, *Vespula squamosa*, kills the host queen, *Vespula maculifrons*, and takes over her role in the colony. Data was compiled for 13 colonies of *V. squamosa* and 37 colonies of *V. maculifrons* to analyse the genetic structure of the two species.

Each point on the graphs represents the genetic distance and geographic distance between a pair of colonies. The genetic distance indicates the number of differences in specific DNA markers between a pair of colonies. The results are shown below.



Source: "Genetic structure and breeding system in a social wasp and its social parasite" by Hoffman EA, Kovacs JL, Goodisman MAD, *BMC Evolutionary Biology* (2008) 8:239. © 2008 Hoffman et al; licensee BioMed Central Ltd

- a (i) Determine the greatest genetic distance between any pair of colonies of *V. squamosa*. [1]
- a (ii) Identify the greatest geographic distance between any pair of colonies of *V. maculifrons*. [1]
- b. Describe the relationship between the geographic distance and genetic distance in the two species. [1]
- c. Compare the two species in terms of genetic distance between the pairs of colonies. [2]

Markscheme

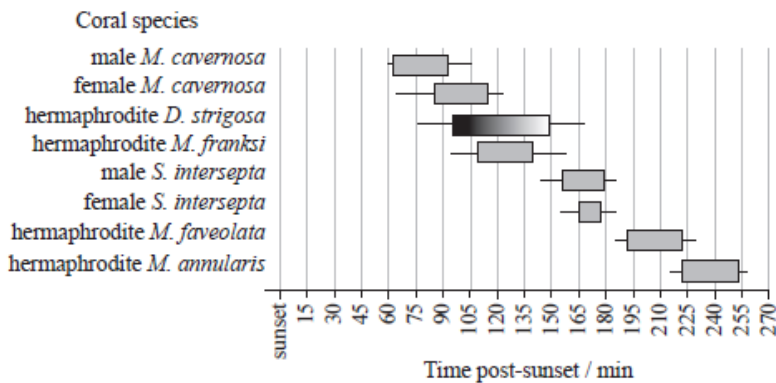
- a (i) 0.26 (arbitrary units) (*units not required*)
- a (ii) 123 km (*accept answers in the range of 122 km and 124 km*)
- b. none / low correlation / non-significant / OWTTE;
less data/fewer results/less variation at 60/70 km distance;

- c. both show genetic differences (between all pairs of colonies);
- both have (highly) variable/wide range of genetic distance;
- similar mean/average genetic distance;
- V. maculifrons* has a greater range than *V. squamosa*; (*vice versa*)

Examiners report

- a (i) Parts (a) (i) and (ii) were intended to key the candidates in to the data and give two relatively easy marks. Most scored them, but those that did not often then scored poorly on the rest of this question.
- a (ii) Parts (a) (i) and (ii) were intended to key the candidates in to the data and give two relatively easy marks. Most scored them, but those that did not often then scored poorly on the rest of this question.
- b. Part (b) was perhaps slightly misleading, given that the expected answer is that there is not clear relationship between genetic and geographic distance in the pairs of colonies.
- c. Some candidates overcomplicated their answers to (c) by including differences in geographic distance. This was not intended and the two available marks could be scored relatively easily by giving similarities and differences between the two species in the genetic difference between pairs of colonies.

Corals can be male, female or hermaphrodite (both male and female) and the release of their gametes is called spawning. Data was collected to study the spawning behaviour in the Gulf of Mexico of three genera of coral: *Montastraea*, *Stephanocoenia* and *Diploria*. The spawning behaviour is expressed in minutes post-sunset. Peak spawning windows are shown as grey bars and the range as black bars.



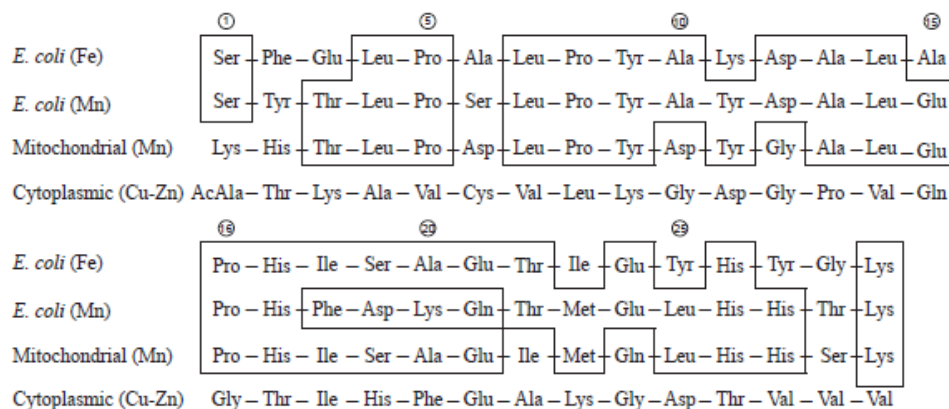
[Adapted from P. D. Vize, J. A. Embesi, M. Nickell, D. P. Brown and D. K. Hagman (2005) "Tight temporal consistency of coral mass spawning at the Flower Garden Banks, Gulf of Mexico, from 1997–2003." *Gulf of Mexico Science*, 1, pp. 107–114. © 2005 by the Marine Environmental Sciences Consortium of Alabama. Used with permission.]

Superoxide dismutase is an enzyme used by cells to protect themselves against oxidative damage. These enzymes can have different metals as part of their structure.

A study to compare two dismutases from *Escherichia coli* bacteria and two dismutases from eukaryotic cells was undertaken. The following enzymes were used:

- *E. coli* dismutase with iron (Fe)
- *E. coli* dismutase with manganese (Mn)
- eukaryotic mitochondrial dismutase with manganese (Mn)
- eukaryotic cytoplasmic dismutase with copper-zinc (Cu-Zn).

The following shows part of the amino acid sequences of these enzymes. Boxes enclose identical amino acids in the sequence of the two *E. coli* and mitochondrial dismutases.



[H. M. Steinman and R. L. Hill (1973) "Sequence homologies among bacterial and mitochondrial superoxide dismutases". PNAS journal (USA), 70 (12), pp. 3725—3729. Used with the permission of the authors.]

- State the range of the time of spawning for the male *M. cavernosa*. [1]
- State how many amino acids are in the same position in the *E. coli* (Fe), *E. coli* (Mn) and the mitochondrial dismutase sequences shown. [1]
- State the amino acids which are present in the same position in at **least one** bacterial dismutase and in **both** eukaryotic dismutases. [1]
- Compare the *E. coli* (Mn) and the mitochondrial dismutases. [2]
- The sequences of the two bacterial dismutases and the mitochondrial dismutase show a high degree of homology. Discuss how this supports the endosymbiotic theory for the origin of mitochondria. [2]

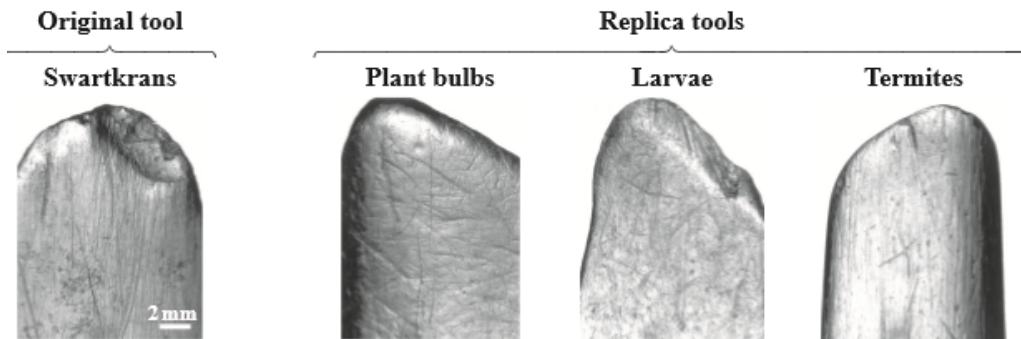
Markscheme

- from 60 to 105 minutes (post-sunset) / 45 minutes
- 11
- Ile and Glu (*both needed to award the mark*)
 - share 17 (out of 29) amino acids in common / more amino acids similar than different;
 - both have Mn in the enzyme (as cofactor);
 - greatest difference between them is from amino acid 18 to 22;
 - mitochondrial has Gly (position 12) while *E. coli* (Mn) never has Gly;
 - Leu is most common amino acid in both appearing four times / other valid comparison;
- endosymbiotic theory states bacteria were engulfed by organisms to become mitochondria;
 - sequence comparison between mitochondrial and bacterial dismutase supports this hypothesis;
 - more similarity in the amino acid sequence between mitochondrial and bacterial dismutase than between mitochondrial and cytoplasmic dismutase;

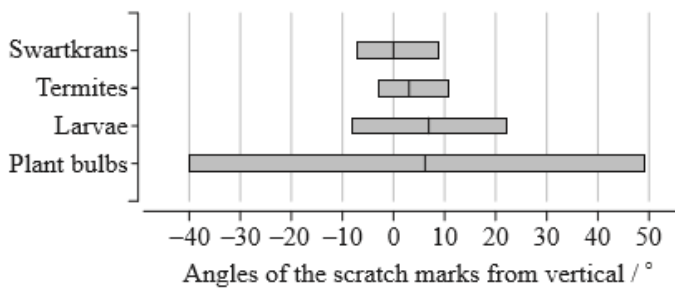
Examiners report

- a. Most candidates performed well in the data analysis with (e) being the best discriminator of the better candidates.
- a. Many candidates responded correctly to (a).
- b. Many candidates responded correctly to (a) and (b), although some candidates only stated one of Ile and Glu.
- c. [N/A]
- e. Many candidates were familiar with the endosymbiotic theory and gained marks in (e).

Bone tools found in the Swartkrans site in South Africa were thought to be used by *Australopithecus robustus* when digging for food. Using replica tools, researchers dug around plants for bulbs, dug in soil for larvae and dug in termite mounds for termites. They compared the scratch marks found on the replica tools with those on the original Swartkrans tool to predict the food eaten by *A. robustus*.



The graphs below show the ranges of angles from the vertical position of the scratch marks and the ranges of widths of the scratch marks on each tool. The solid line on each bar represents the mean value for the range.



[Source: Lucinda R. Backwell and Francesco d'Errico, "Evidence of termite foraging by Swartkrans early hominids", *PNAS* 98 (4), 1358–63. Copyright 2001, National Academy of Sciences, USA.]

- a. State the greatest angle from the vertical of the scratch marks on the tool used on termite mounds. [1]
- b. Calculate the difference in the angle between the mean values for the Swartkrans tool and the tool used to dig for plant bulbs. [1]
- c. Compare the width of scratch marks on the tool used to dig for larvae with the Swartkrans tool. [2]
- d. Using evidence from the photographs and the graphs, suggest what the researchers' main conclusion was. [2]
- e. *A. robustus* was thought to have coexisted with *Homo habilis*, both becoming extinct at the same time. State approximately how many years ago *A. robustus* became extinct. [1]

Markscheme

- a. 11° (accept answers in the range of 10.5° to 11.5°)
- b. 6° (accept answers up to 7°) (working not required)
- c.
 - a. mean/average of Swartkrans less than larvae;
 - b. range of Swartkrans less than larvae;
 - c. no overlap between the two in terms of widths of scratch marks / widest Swartkrans less width than the narrowest larvae;

Do not accept answers stating numerical values only.
- d. *from the photograph:*
 - a. (*A. robustus*) ate termites because the pattern of scratch marks on the tool are of similar angle;

from the graph:

 - b. (*A. robustus*) ate termites because the ranges of widths/means of angles/widths are more similar;
- e. 1.4 to 1.8 million years ago (accept answers within this range)

Examiners report

- a. Many candidates had difficulty to relate to the means when comparing the tools. References to photographs, if any, remained too vague to earn any mark in most cases. The vast majority of candidates ignored the approximate date of extinction of *H. robustus*.
- b. Many candidates had difficulty to relate to the means when comparing the tools. References to photographs, if any, remained too vague to earn any mark in most cases. The vast majority of candidates ignored the approximate date of extinction of *H. robustus*.
- c. Many candidates had difficulty to relate to the means when comparing the tools. References to photographs, if any, remained too vague to earn any mark in most cases. The vast majority of candidates ignored the approximate date of extinction of *H. robustus*.
- d. Many candidates had difficulty to relate to the means when comparing the tools. References to photographs, if any, remained too vague to earn any mark in most cases. The vast majority of candidates ignored the approximate date of extinction of *H. robustus*.
- e. Many candidates had difficulty to relate to the means when comparing the tools. References to photographs, if any, remained too vague to earn any mark in most cases. The vast majority of candidates ignored the approximate date of extinction of *H. robustus*.

