Surname	StemUp Model Solution	Centre Number	Candidate Number
First name(s)			2

GCE A LEVEL

A400U20-1

O21-A400U20-1

FRIDAY, 15 OCTOBER 2021 – MORNING

BIOLOGY – A level component 2
Continuity of Life

2 hours

For Examiner's use only		
Question	**Maximum Mark**	**Mark Awarded**
1.	**12**	
2.	**11**	
3.	**17**	
4.	**12**	
5.	**18**	
6.	**10**	
7.	**11**	
8.	**9**	
Total	**100**	

A400U201
01

ADDITIONAL MATERIALS

In addition to this examination paper, you will need a calculator and a ruler.

INSTRUCTIONS TO CANDIDATES

Use black ink or black ball-point pen. Do not use gel pen. Do not use correction fluid.

Write your name, centre number and candidate number in the spaces at the top of this page.

Answer **all** questions.

Write your answers in the spaces provided in this booklet. If you run out of space, use the additional page(s) at the back of the booklet, taking care to number the question(s) correctly.

INFORMATION FOR CANDIDATES

The number of marks is given in brackets at the end of each question or part-question.

The assessment of the quality of extended response (QER) will take place in question **8**.

The quality of written communication will affect the awarding of marks.

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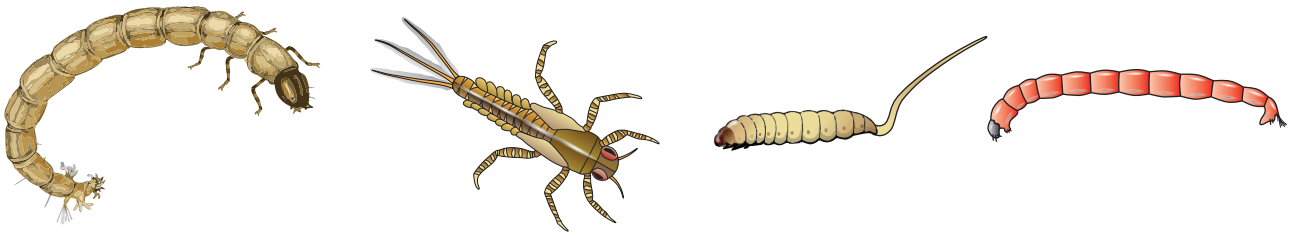
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Answer **all** *questions.*

1. Many insects lay their eggs in freshwater streams and rivers. At the larval stage many insects are difficult to identify accurately below the taxon Family. **Image 1.1** shows some insect larvae (not to the same scale).

Image 1.1



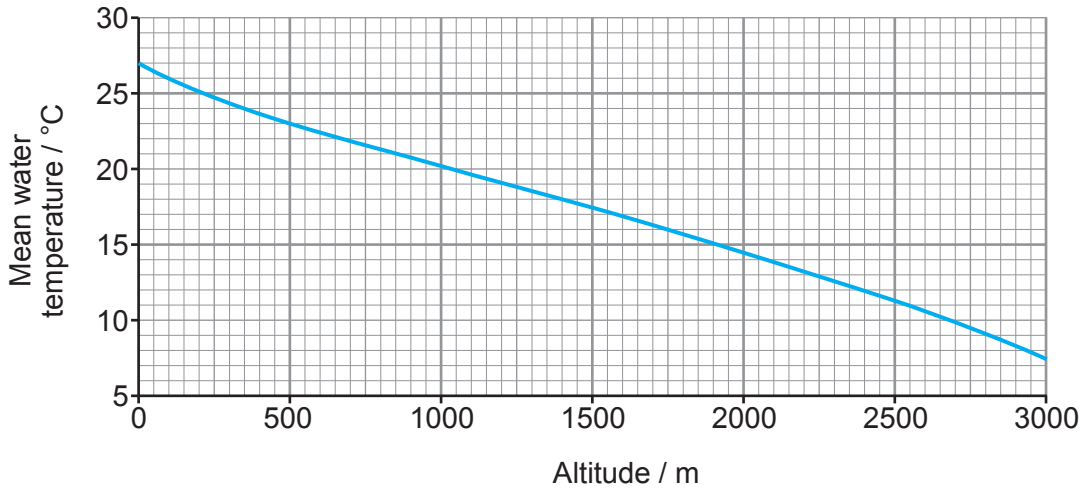
(a) Suggest how protein analysis could enable ecologists to classify the larvae to the individual Species instead of the Family. [2]

Compare the amino acid sequence (order) of a common protein in each larva against the known amino acid sequences of identified insect species.

The larvae shown in **image 1.1** are aquatic and their distribution is affected by a range of environmental factors including the temperature of the water.

To investigate the effect of temperature on the biodiversity of insects with aquatic larvae, a study was carried out at three different altitudes in a mountainous region of South America. **Image 1.2** shows how mean water temperature changes with altitude.

Image 1.2



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Data were collected from shallow streams at 350 m, 2 100 m and 3 000 m above sea level, that flowed over similar rocks and had a similar pH.

Five streams were sampled at each altitude. Areas of each stream were sampled using the following kick-sampling method:

- Place a 0.5 m^2 quadrat on the stream bed in the middle of the stream.
- Place a 0.5 m wide flat-bottomed net downstream of the quadrat.
- Disturb the area of the stream bed inside the quadrat for two minutes by kicking strongly.
- Transfer the organisms caught in the net to a container.
- Group the insect larvae into Orders and record the number of Families in each Order recorded.
- Working upstream, sample a further nine areas in each stream.

(b) (i) Explain why the ecologists worked upstream from the first sample. [2]

Organisms dislodged by kicking but not caught in the net would flow downstream.

Working upstream prevents them being caught in the next sample, so no more organisms are caught than are actually present there.

(ii) Suggest why the quadrats were placed in the middle of each stream. [1]

To minimise the effect of the banks, so that every sample had a similar flow of water and similar light.

A400U201 03

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Table 1.3 below shows the mean number of Families in the different Orders of insects per m^2 identified at each altitude tested.

Table 1.3

Order of insects	Number of Families identified at each altitude		
	350 m	2 100 m	3 000 m
Collembola	1	1	1
Plecoptera	1	1	1
Ephemeroptera	4	4	2
Odonata	4	1	0
Megaloptera	1	0	0
Hemiptera	4	0	0
Coleoptera	6	6	2
Trichoptera	8	9	6
Lepidoptera	1	1	0
Diptera	8	9	10

Table 1.4 shows the number of individuals of each Family found in the streams sampled at 3 000 m.

Table 1.4

Altitude = 3 000 m			
Insect Family	n	$(n–1)$	$n(n–1)$
Collembola	1	0	0
Plecoptera	1	0	0
Ephemeroptera	2	1	2
Odonata	0	–1	0
Megaloptera	0	–1	0
Hemiptera	0	–1	0
Coleoptera	2	1	2
Trichoptera	6	5	30
Lepidoptera	0	–1	0
Diptera	10	9	90
N	22	$\Sigma n(n–1)$	124
$(N–1)$	21		
$N(N–1)$	462		

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(iii) Use **table 1.4** and the formula below to calculate a Diversity Index *(D)* for the streams sampled at 3 000 m. [3]

$$D = 1 - \frac{\sum n(n-1)}{N(N-1)}$$ where N = total number of insect families; n = number of families per order of insect; Σ = sum of

$\Sigma n(n-1) = 2 + 2 + 30 + 90 = 124$

$N(N-1) = 22 \times 21 = 462$

$D = 1 - (124 \div 462) = 1 - 0.268 = 0.732$

D = 0.73

(iv) The Diversity Index was calculated for the other two altitudes. These are shown below.

350 m	D	=	0.87
2 100 m	D	=	0.81

Conclude and explain the effect of water temperature on the biodiversity of insects with aquatic larvae. [2]

The lower the temperature, the lower the biodiversity (D falls from 0.87 to 0.73).

Less kinetic energy, so slower enzyme action and metabolism, so fewer species survive.

(v) Identify **one** *other* abiotic factor which is affected by altitude and explain why this may reduce your confidence in your conclusion. [2]

Oxygen: at higher altitude there are lower oxygen levels, so less oxygen is dissolved in the water.

Lower diversity could be due to not enough oxygen for respiration, not temperature; only temperature was tested.

A400U201 05

12

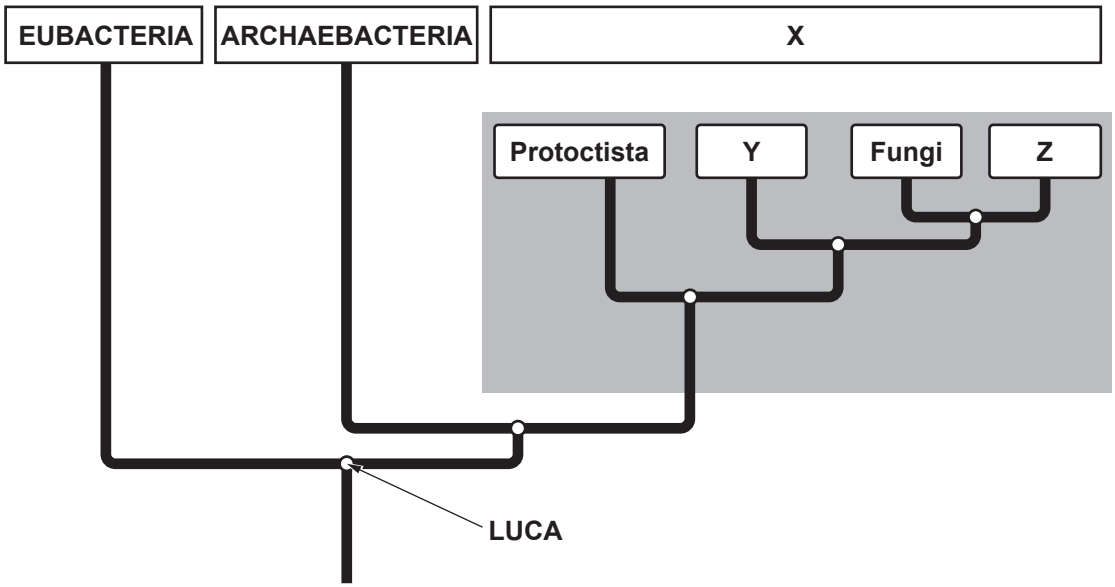
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2. Humans classify organisms into groups to determine their evolutionary relationships. **Image 2.1** represents our current understanding of how organisms are related.

Image 2.1



(a) (i) Name Domain **X** shown in **image 2.1** and describe how all the organisms in this Domain are different from those in the other Domains. [2]

Eukarya (Eukaryota).

All have cells with a nucleus, membrane-bound organelles and large (80S) ribosomes, which Bacteria and Archaea lack.

(ii) Organisms in Domain **X** are classified into smaller groups of more closely related organisms: Group **Y** are all phototrophic and Group **Z** are all heterotrophic.

Using this information, state the following:

I. the **level** of classification represented by groups **Y** and **Z**; [1]

Kingdom

II. the **names** of groups **Y** and **Z**; [1]

Y Plantae (plants)

Z Animalia (animals)

III. **one** *other* distinguishing feature of groups **Y** and **Z** used to place them in these groups. [1]

Y cellulose cell walls and chlorophyll (no nervous coordination)

Z no cell walls, no chlorophyll, centrioles and nervous coordination

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(b) The point labelled **LUCA** on the diagram stands for Last Universal Common Ancestor. Suggest how the role of ATP provides evidence that all organisms have evolved from this single common ancestor. [3]

ATP is used and produced by all living organisms, as the universal energy currency.

It is the common source of energy for nearly all biochemical reactions, e.g. active transport and synthesis, in every cell.

Such shared biochemistry is unlikely to have evolved separately many times, so all organisms must share common DNA (genes) inherited from LUCA.

The binomial system is used to give a scientific name to all organisms on Earth. However, scientific names change. For example, one species of bluebell, *Scilla italica*, has been reclassified as *Hyacinthoides italica*.

(c) (i) State the classification **levels** (taxa) given in the binomial name of an organism. [1]

Genus and species.

(ii) Explain why the reclassification of *Scilla italica* as *Hyacinthoides italica* demonstrates the tentative nature of classification. Suggest why its scientific name may change again in the future. [2]

Classification is based on evidence available and is not fixed; it may not reflect evolutionary relatedness.

It changed as new (DNA) evidence was found; further new evidence could move it again.

A400U201
07

11

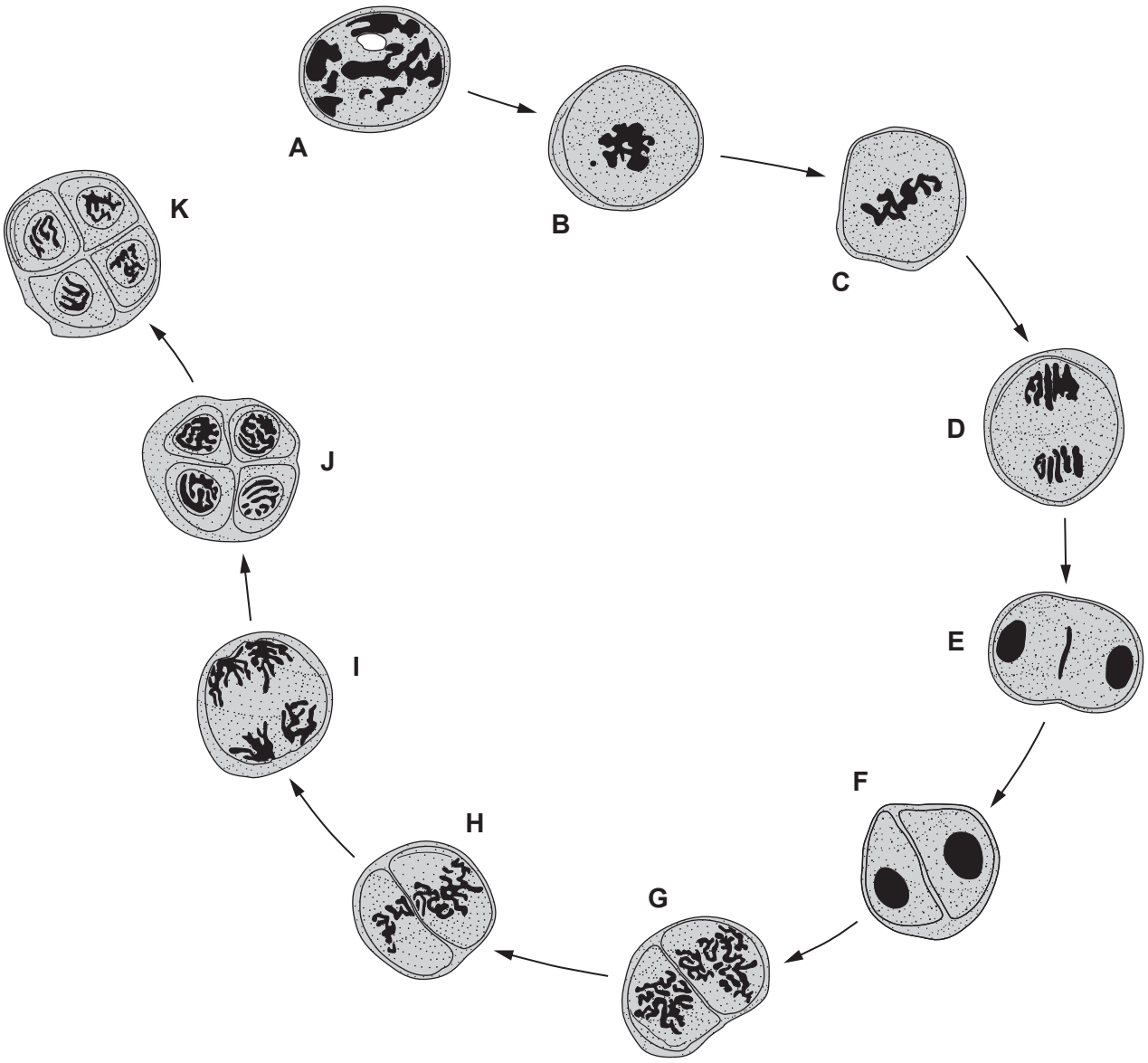
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3. Pollen grain formation in flowering plants involves both mitosis and meiosis. **Image 3.1** shows stages in the formation of pollen grains in a species of lily *(Lilium sp.)* by meiosis.

Image 3.1



(a) Using your knowledge of meiosis and pollen grain formation, identify which stage labelled **A** to **K** shows the following events: [3]

I. the chromosomes from each homologous pair (composed of two chromatids) are pulled to opposite poles; D

II. reformation of the nuclear membranes around the male gametic nuclei; J

III. pairs of homologous chromosomes forming bivalents are arranged across the equator of the spindle apparatus. C

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(b) Gametogenesis in male mammals follows a similar pattern to that shown in **image 3.1**.

(i) Describe **two** ways in which meiosis in an animal is different from meiosis in a plant. [2]

I. *Animal cells have centrioles which organise the spindle fibres;*

plant cells have no centrioles.

II. *In animals cytokinesis is by cleavage (cell membrane pinches in);*

in plants a cell plate forms and a new cell wall is made.

(ii) Name the cells produced in spermatogenesis in a mammal that are at the same stage of meiosis as the following stages in the formation of pollen grains in **image 3.1**. [3]

A *spermatogonia*

F *secondary spermatocytes*

K *spermatids*

(iii) In mitosis, the cells formed during cytokinesis would re-enter the cell cycle. Explain why this does not occur following the production of sperm cells. [1]

Sperm cells are fully differentiated (and haploid), so they cannot

re-enter the cell cycle and divide again.

(c) *Lilium sp.* have a diploid number of 12 chromosomes. The number of combinations of chromosomes in the gametes of a species can differ due to independent assortment of chromosomes and can be calculated as:

2^n where **n** = haploid number

In addition to crossing over, independent assortment also increases genetic variation.

(i) Calculate the number of different gametes that can be produced by *Lilium sp.* due to different combinations of chromosomes alone. [2]

haploid number n = 12 ÷ 2 = 6

$2^6 = 2 \times 2 \times 2 \times 2 \times 2 \times 2 = 64$

number of gametes = *64*

(ii) Name the stage(s) of meiosis where independent assortment can occur. [1]

Metaphase I (stage C) and metaphase II (stage H).

(iii) Apart from mutation, name **one** *other* source of genetic variation during sexual reproduction that does not result from meiosis. [1]

Random fertilisation (any male gamete can fuse with any egg).

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(d) Apple trees produce pollen grains that are chemically self-incompatible with their own stigmas. To produce apples their flowers must be pollinated by pollen from a different variety of apple tree.

Flowering, including pollen production and the development of receptive stigmas, is triggered in some varieties of apple by warmer air temperatures but in others is triggered by increasing day length between March and June.

Cross-pollination often occurs between a variety in which flowering is triggered by longer day length and a variety in which flowering is triggered by warmer temperatures.

Using this information, conclude why commercial apple growers in the UK are concerned that crossing the climate change boundary could result in a lower yield of apples. [4]

Crossing the climate change boundary increases atmospheric temperatures, so varieties triggered by warmer air temperatures will flower earlier in the year. Day length is not affected by climate change, so varieties triggered by day length still flower at the same time.

The two varieties therefore flower at different times: when one produces pollen, receptive stigmas are not present on the other, so cross-pollination cannot take place. Pollinating insects may also appear earlier, out of step with flowering.

This gives lower rates of pollination and fertilisation, so fewer apples develop and the yield is lower.

17

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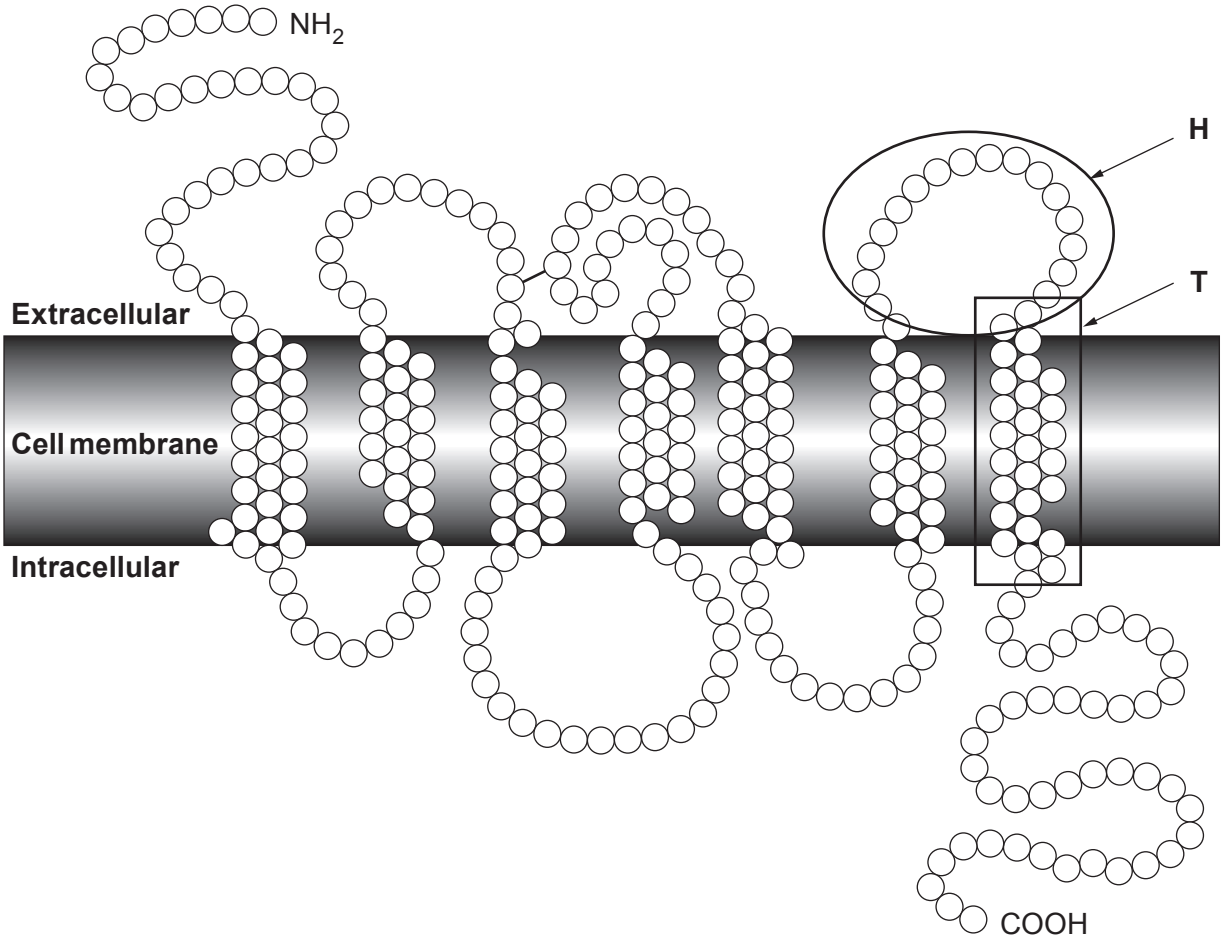
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4. RhD is a glycoprotein embedded in the cell membranes of red blood cells.

Image 4.1 shows the amino acids of the RhD glycoprotein and its position in the cell membrane of red blood cells.

Image 4.1



(a) (i) One trans-membrane part of the protein, labelled **T** on **image 4.1**, is in the form of an alpha helix. State the level of protein structure present in an alpha helix and describe how this structure is maintained. [2]

Secondary structure.

The helix is held by hydrogen bonds between the C=O of one amino acid and the N-H of an amino acid four further along the chain.

(ii) State whether the region of the protein labelled **H** on **image 4.1** contains amino acids which are hydrophobic or hydrophilic. Explain your answer. [2]

Hydrophilic.

Region H is outside the bilayer, in contact with water (aqueous solution); polar, so repelled by the hydrophobic fatty acid tails.

A400U201
11

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The presence or absence of the RhD protein is controlled by a gene with two alleles:
D – the presence of RhD, and **d** – the absence of RhD.

If a woman who is rhesus negative (genotype **dd**) becomes pregnant with a child who carries a dominant allele for RhD, the mother will develop an immune response against the RhD protein from the foetus. Antibodies against RhD can cross the placenta and potentially kill the foetus.

Pre-natal testing of the foetus to determine its blood group can now be carried out by analysing the mother's blood. Some foetal DNA passes into the mother's blood and if the allele for RhD is detected doctors know that the foetus is at risk.

(b) (i) Explain why a blood test is preferable to either sampling the amniotic fluid surrounding the foetus or sampling tissue from the placenta (chorionic villus sampling). [2]

A blood test is non-invasive: it does not involve taking tissue or fluid from the uterus, amnion or placenta, so there is no risk of the test causing a miscarriage or harm to the foetus, and no risk of infection.

(ii) In Europe, the proportion of the populations of both women and men who are rhesus negative is 0.16. Use the Hardy-Weinberg equations to answer the questions that follow.

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

I. Determine the proportion of the population in Europe who are homozygous dominant. [2]

$q^2 = 0.16$, so $q = \sqrt{0.16} = 0.4$

$p = 1 - q = 1 - 0.4 = 0.6$

$p^2 = 0.6^2 = 0.36$

Proportion of population who are homozygous dominant = 0.36

II. Determine the proportion of the population in Europe who are heterozygous for RhD. [1]

$2pq = 2 \times 0.6 \times 0.4 = 0.48$

Proportion of population who are heterozygous for RhD = 0.48

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III. State the percentage of men in Europe who could not produce a rhesus positive child with a rhesus negative woman. [1]

Percentage = 16%

(iii) The Hardy-Weinberg principle states that the frequencies of dominant and recessive alleles and genotypes will remain constant from one generation to the next under certain conditions which include:

- a large population;
- no selection for or against any phenotype;
- the population is isolated.

Pre-natal testing enables doctors to treat rhesus positive babies carried by rhesus negative mothers before or shortly after birth and save the lives of these children.

Using the information provided, conclude why the allele frequencies for **D** and **d** are not constant in Europe. [2]

There is selection: Rh positive children born to Rh negative mothers now survive, so are selected for.

The population is not isolated: immigration and emigration take place, bringing alleles in and out.

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5. Mendel investigated the inheritance of characteristics of pea plants. He formulated two laws of inheritance:

Law of segregation	During gamete formation, the alleles for each gene segregate from each other so that each gamete carries only one allele for each gene.
Law of independent assortment	Genes for different traits can segregate independently during the formation of gametes.

Mendel found that:

- the allele for tall plants (**T**) is dominant to that for short plants (**t**)
- the allele for purple flowers (**P**) is dominant to that for red flowers (**p**).

(a) (i) Based on these laws, state the phenotypes and the ratios you would expect in the offspring following a cross between the following parent plants:

I. both plants heterozygous for height of plant – **Tt**: [1]

Phenotypes tall short

Ratio 3 tall : 1 short

II. both plants heterozygous for height and flower colour – **Tt Pp**: [1]

Phenotypes tall, purple tall, red short, purple short, red

Ratio 9 tall, purple : 3 tall, red : 3 short, purple : 1 short, red

(ii) State what is meant by the term *linkage* and explain why Mendel's law of independent assortment only applies if the genes are not linked. [2]

Linkage: two (or more) genes are located on the same chromosome.

Linked genes are more likely to be passed into the same gamete together, so they cannot segregate independently; independent assortment only happens if the genes are on different chromosomes.

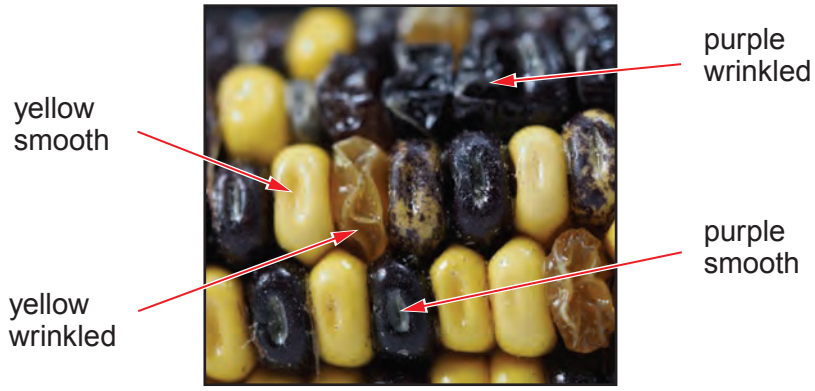
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(b) Corn cobs were produced by crossing parent plants that were heterozygous for both colour and appearance of the seeds. The phenotypes in the F_1 can be seen in **image 5.1**.

Image 5.1



Key: purple **A** – dominant smooth **B** – dominant
yellow **a** – recessive wrinkled **b** – recessive

Complete the following genetic cross to show how the different genotypes resulting in these phenotypes could have been inherited. [5]

Parent phenotypes: purple, smooth × purple, smooth

Parent genotypes: AaBb × AaBb

Gametes: AB Ab aB ab × AB Ab aB ab

F_1 phenotypes:	purple smooth	purple wrinkled	yellow smooth	yellow wrinkled
F_1 genotypes:	AABB	AAbb	aaBB	aabb
	AaBB	Aabb	aaBb	
	AABb			
	AaBb			

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15

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(c) The phenotypes of a sample of 400 seeds were recorded as shown in **table 5.2**.

Table 5.2

phenotype	number in sample
purple; smooth	201
purple; wrinkled	84
yellow; smooth	81
yellow; wrinkled	34

A Chi^2 test was carried out to determine whether the results of this cross followed Mendel's law of independent assortment.

(i) State the null hypothesis for this test. [1]

There is no significant difference between the observed and expected numbers of each phenotype; any difference is due to chance.

(ii) Complete the table below to calculate the Chi^2 statistic for these data. [3]

phenotype	observed numbers O	expected numbers E	$O-E$	$(O-E)^2$	$\frac{(O-E)^2}{E}$
purple; smooth	201	225	−24	576	2.56
purple; wrinkled	84	75	9	81	1.08
yellow; smooth	81	75	6	36	0.48
yellow; wrinkled	34	25	9	81	3.24
Total	400	400			$\sum$ = 7.36

$$\text{Chi}^2 = \sum \frac{(O-E)^2}{E}$$

Chi^2 = 7.36

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The probability table for the Chi^2 statistic is shown in **table 5.3** below.

Table 5.3

Degrees of freedom	Probability									
	0.90	**0.80**	**0.70**	**0.50**	**0.30**	**0.20**	**0.10**	**0.05**	**0.02**	**0.01**
1	0.02	0.064	0.15	0.46	1.07	1.64	2.71	3.84	5.41	6.64
2	0.21	0.45	0.71	1.39	2.41	3.22	4.61	5.99	7.82	9.21
3	0.58	1.01	1.42	2.37	3.67	4.64	6.25	7.82	9.84	11.34
4	1.61	2.34	3.00	4.35	6.06	7.29	9.24	11.07	13.39	15.09

(iii) Based on these data the hypothesis was accepted but with low confidence. Use your calculated value of Chi^2 and data from **table 5.3** to explain this conclusion.

[5]

The calculated Chi^2 value of 7.36 is less than the critical value of 7.82, at 3 degrees of freedom (4 phenotypes – 1) and a probability of 0.05. So the null hypothesis is accepted: there is no significant difference, the differences are due to chance and the results follow independent assortment (9:3:3:1). However, 7.36 is very close to the critical value of 7.82; it lies between 6.25 ($p = 0.10$) and 7.82 ($p = 0.05$). So there is a low probability, less than 0.10 (less than a 10% chance), that the differences were due to chance and not significant, so confidence in accepting the hypothesis is low.

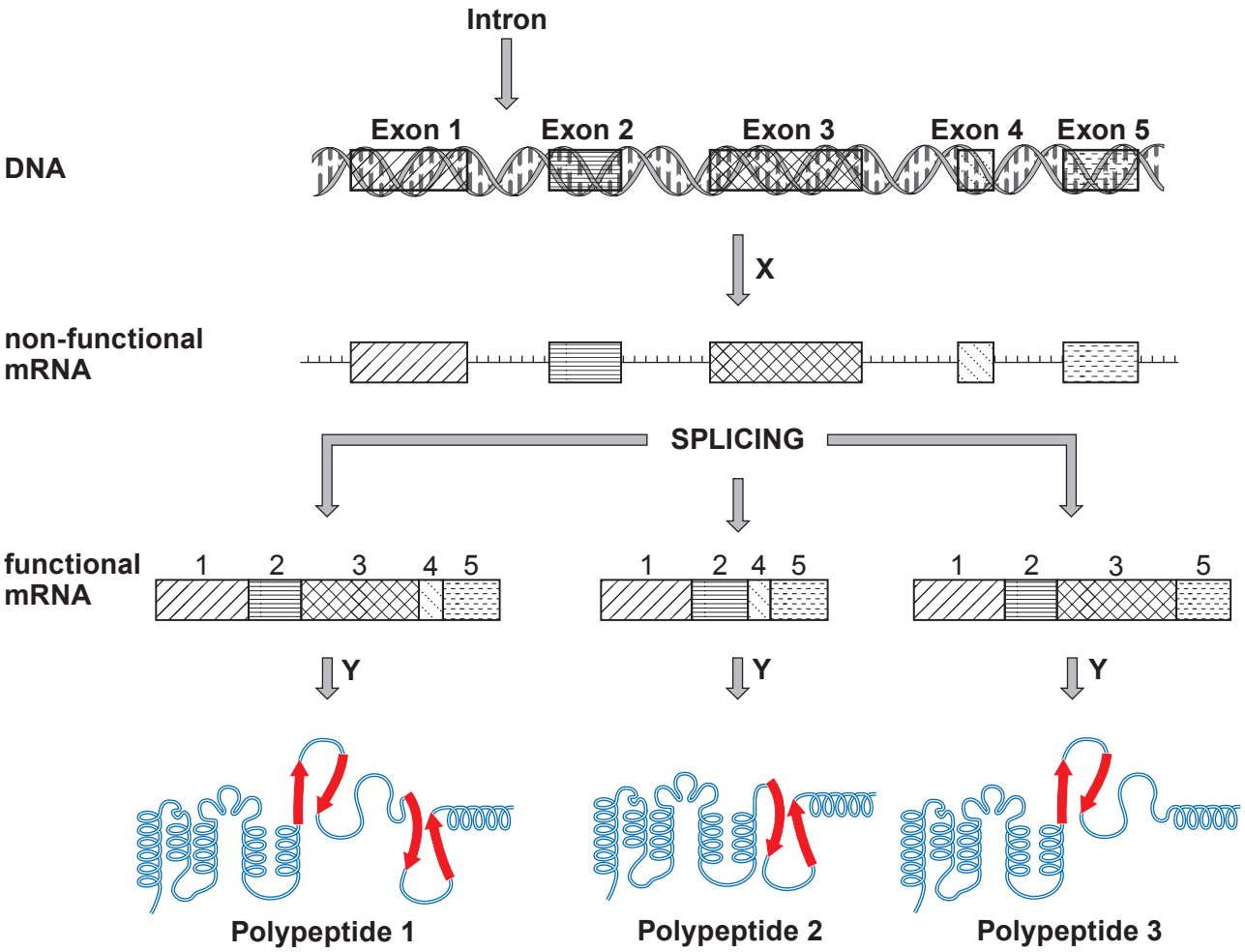
18

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6. Most genes are made up of **exons** and **introns**. It was originally believed that the genetic code for one protein was carried by a single gene. This theory was later changed to the 'one gene – one polypeptide' hypothesis.

Image 6.1 shows the process of converting the genetic code of a single gene into polypeptides.

Image 6.1



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(a) (i) Name processes **X** and **Y** involved in the production of polypeptides **1**, **2** and **3**. [1]

X *transcription*

Y *translation*

(ii) Explain how the information shown in **image 6.1** disproves the 'one gene – one polypeptide' hypothesis. [1]

Three different polypeptides (from three different mRNA molecules) are synthesised from the same gene, as the exons are spliced in different combinations.

(iii) Explain why a mutation in an exon might **not** affect the primary structure of a protein. [1]

The genetic code is degenerate: some amino acids have more than one codon, so the mutated triplet may still code for the same amino acid.

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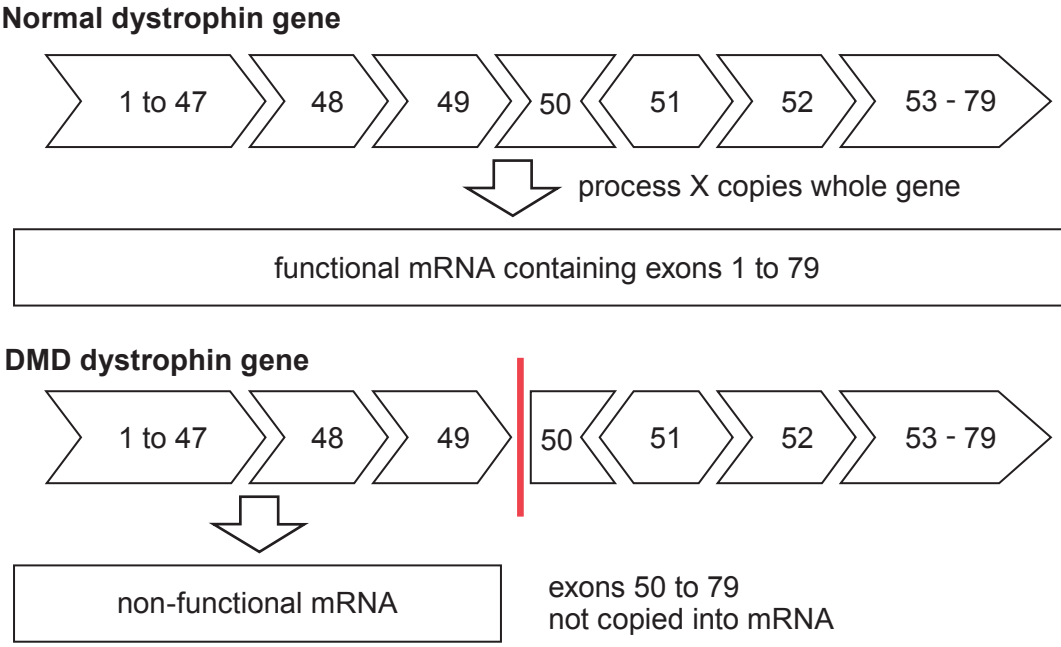
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(b) Muscular dystrophy is caused by mutations to the gene coding for dystrophin which is found in the cell membranes of muscle cells. The dystrophin gene is the largest gene found in the human genome containing 79 exons separated by introns.

In Duchenne Muscular Dystrophy (DMD) a mutation in exon 50 prevents synthesis of the functional form of dystrophin. This is shown in **image 6.2**. Note: the shapes of the exons show whether they are able to bind to each other during splicing.

Image 6.2



Describe how functional mRNA for dystrophin is produced and suggest why the mutation to exon 50 results in a shorter form of dystrophin in a person with DMD. [5]

In transcription the template strand of DNA is copied into mRNA by complementary base pairing.

RNA polymerase unwinds the DNA and joins free RNA nucleotides together.

This pre-mRNA contains both exons and introns; the introns are removed from the mRNA and the exons joined together by splicing to make functional mRNA.

In DMD the mutation in exon 50 means splicing can only take place up to exon 49, so the whole gene is not copied: exons 50 to 79 are missing.

So the mRNA is shorter and does not contain the code for the whole dystrophin molecule, so a shorter polypeptide is translated.

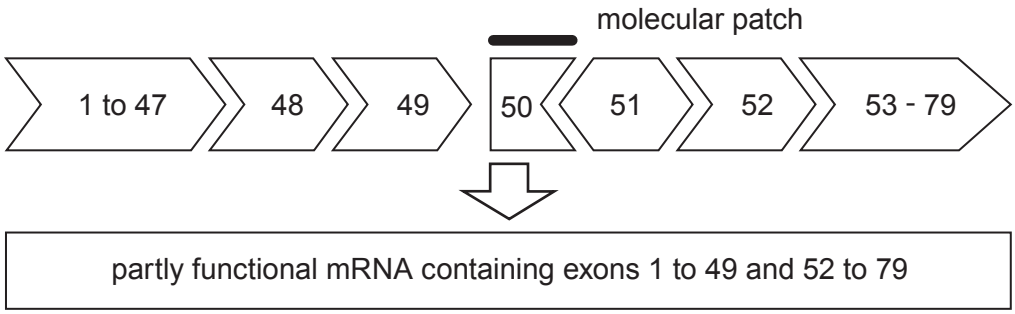
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(c) One type of therapy that has been trialled is the use of a **molecular patch** that binds to exon 50. This results in the synthesis of dystrophin which is only slightly shorter than normal and is almost fully functional as shown in **image 6.3**.

Image 6.3



(i) Suggest why the mRNA produced does not contain exon 51 even though the mutation is in exon 50. [1]

Exon 49 would have to join to exon 51, but their ends are not complementary, so exon 51 cannot bind to exon 49 during splicing.

(ii) Suggest why a person treated with a molecular patch to reduce the symptoms of DMD would still be able to pass on the mutation to the next generation. [1]

The patch only acts in somatic muscle tissue, not the germ line; it does not change the DNA base sequence, so the mutation is still present in the gametes.

10

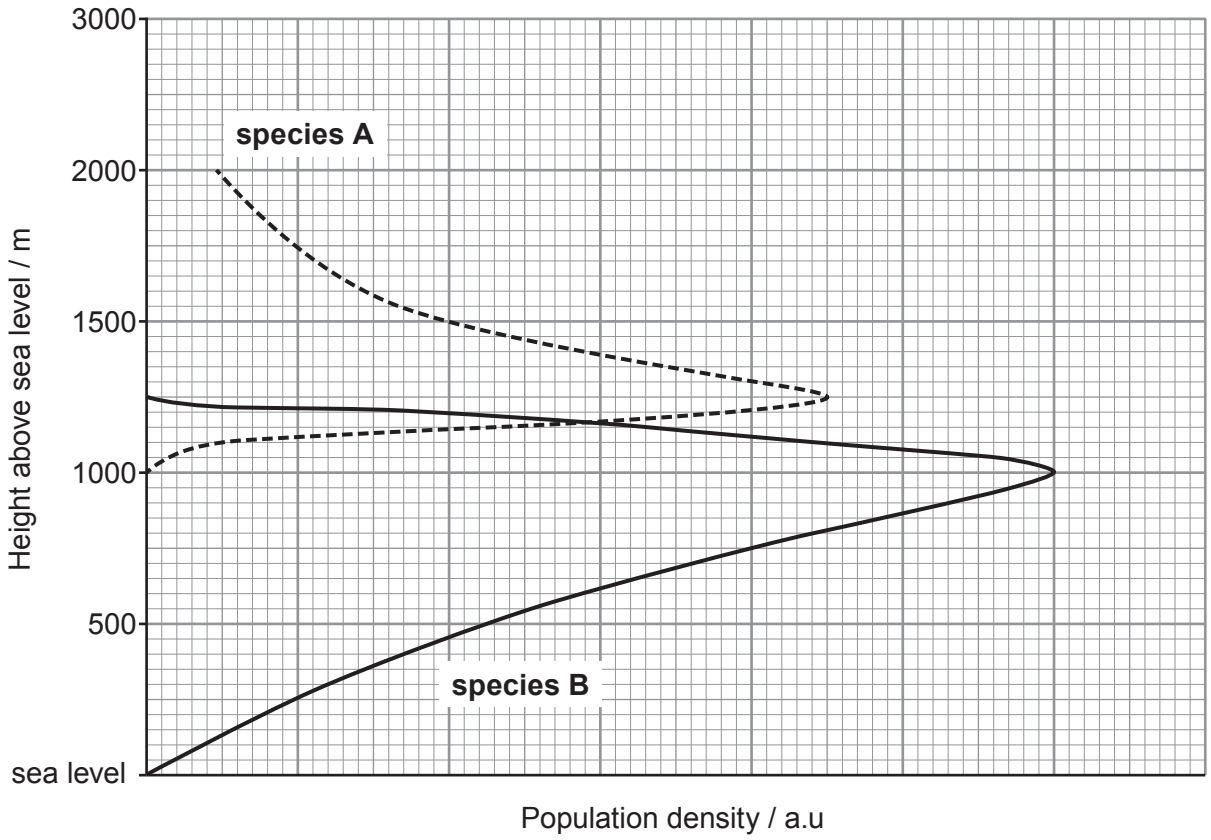
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7. **Image 7.1** shows the population densities of two species of closely related birds at different heights above sea level in a mountain range in the USA.

Image 7.1



(a) (i) State the main type of competition present: [1]

I. at 800 m *intraspecific*

II. between 1 000 m and 1 250 m *interspecific*

(ii) Identify **three** density dependent factors which could affect the distribution and population densities of these bird species between 1 000 m and 1 250 m above sea level. [2]

Food supply (insect prey), availability of nesting sites, and predators (also disease and parasites).

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(iii) Species **A** has haemoglobin with a slightly higher oxygen affinity than species **B**. Explain **one** advantage and **one** disadvantage of this to species **A**. [3]

Advantage: species A can live at higher altitude, where there is less oxygen, because its haemoglobin can absorb (load) more oxygen at the low partial pressure in the lungs.

Disadvantage: at lower altitudes, with higher oxygen levels, its haemoglobin does not release (unload) oxygen as easily to the respiring tissues.

(b) DNA analysis of the genes which code for haemoglobin has shown that the birds evolved into different species less than 10 000 years ago.

(i) Use the information given and your own knowledge to explain how **natural selection** could account for the evolution of these two species from their common ancestor. [3]

A mutation arose in the haemoglobin gene, giving a higher oxygen affinity.

Low oxygen at high altitude is a selection pressure, so birds with the mutation had an advantage and were more likely to survive and reproduce, passing on the allele for high oxygen affinity to offspring, so its frequency rose at high altitude (species A).

(ii) Explain why the evolution of these two species from the same common ancestor is an example of sympatric speciation. [2]

Both species evolved in and live in the same area (the same mountain range), and their ranges overlap between 1 000 m and 1 250 m.

There was no geographical (physical) barrier; only a reproductive (behavioural) barrier prevented interbreeding.

11

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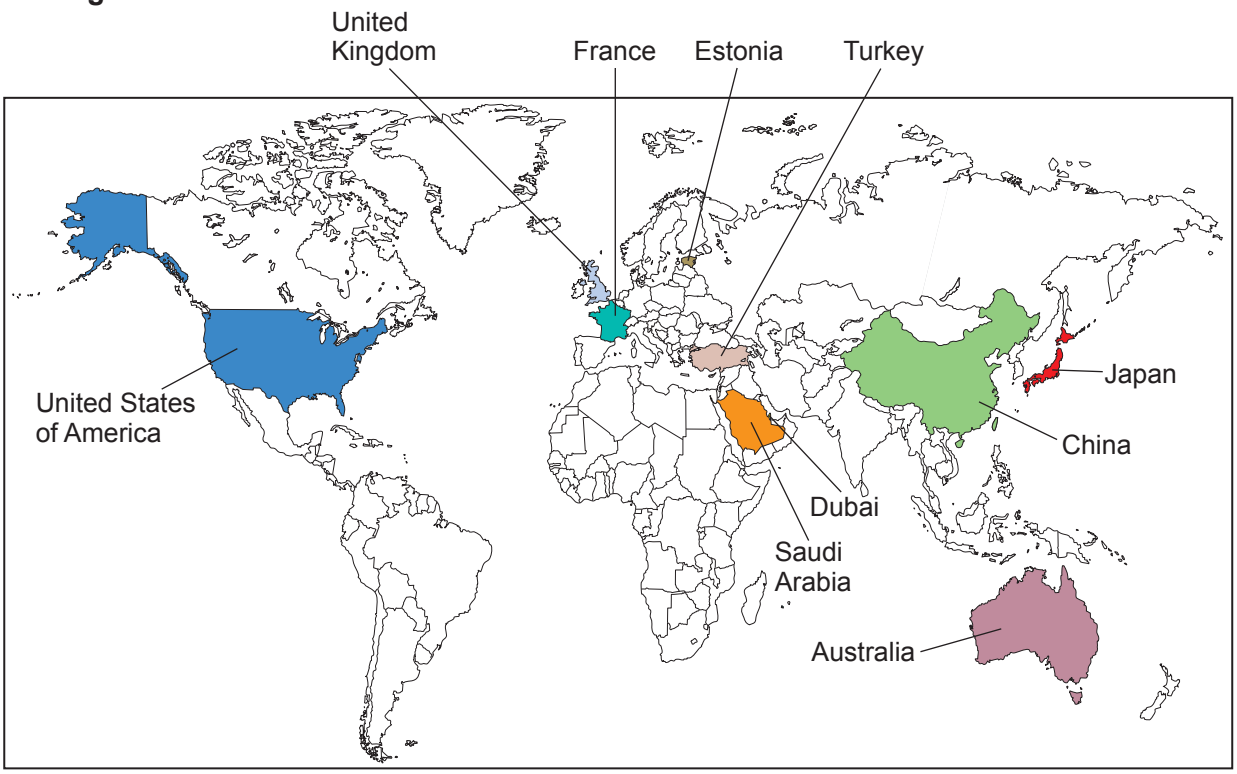
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8. Read the passage below and then answer the questions that follow.

The purpose of the original Human Genome Project was to improve our knowledge and understanding of genetic disorders. The original study was based on the analysis of DNA from a small number of anonymous donors from Europe.

Since then, 100 K projects have been set up in 10 areas around the world, as shown in **image 8.1**. These projects aim to sequence the genomes of 100 000 people with rare genetic disease or cancers.

Image 8.1



Projects have also been set up to sequence the genomes of the mosquito, *Anopheles gambiae* and the *Plasmodium* parasite that it transmits. Malaria is responsible for over a million deaths each year.

Describe how the findings of the Human Genome Project could improve the treatment of human disease and suggest why the findings of the original project may be of limited use.

Explain why the 100 K projects will eventually provide more valuable information and suggest why more projects need to be set up to improve treatment of humans on a worldwide basis.

Suggest why some countries may have invested more money into sequencing the genomes of both the malaria parasite and its vector rather than funding 100 K projects. [9 QER]

The Human Genome Project sequenced human DNA, so genes can be linked to genetic disorders. This allows the genetic cause of a disease to be identified,

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giving earlier and more accurate diagnosis and screening. Knowing a person's alleles also allows better prediction of the effect of drugs on that person, improved design of drugs that target a faulty protein, and the development of new and improved treatments such as gene therapy.

However, the findings of the original project may be of limited use. The sample size was too small to show the variation in human genomes, and all the donors were of European origin, so it does not represent different ethnicities, whose alleles differ. The donors were anonymous, so details of their health were unknown and the findings cannot be related to genetic disorders or cancer.

The 100 K projects will eventually provide more valuable information because the people sampled are selected because of their rare genetic disorders or cancer status, so mutations can be linked directly to disease. The samples are large, so variation and rare alleles can be identified, and they include more ethnicities, not just Europeans, as well as males and females of different ages.

However, the 100 K projects do not include, for example, Africa, South America or the Indian sub-continent, so they are still not wholly representative of the whole human population. More projects need to be set up in these regions so that diagnosis and treatments work for people of all ethnic groups on a worldwide basis.

Some countries may have invested more money in sequencing the genomes of Plasmodium and Anopheles because malaria is still killing over 1 000 000 people per year, so more people die from malaria than from rare genetic conditions in these countries. Plasmodium and Anopheles have a high mutation rate, so they become resistant to antimalarial drugs and insecticides. Sequencing their genomes identifies target genes and proteins, so improved drugs, vaccines and insecticides can be developed to control malaria more effectively, which would save more lives

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than a 100 K project.

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9

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