Candidate Name	Centre Number	Candidate Number
StemUp Model Solution		

A LEVEL BIOLOGY

COMPONENT 2

Continuity of Life

SPECIMEN PAPER

2 hours

For Examiner's use only		
Question	**Maximum Mark**	**Mark Awarded**
1.	**10**	
2.	**12**	
3.	**12**	
4.	**18**	
5.	**13**	
6.	**12**	
7.	**14**	
8.	**9**	
Total	**100**	

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.

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.

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*Answer **all** questions.*

1. Species richness is one measure of biodiversity providing information on the number of species found in a particular area.

Simpson's Diversity Index is a different measure of biodiversity. It is calculated as shown below:

Simpson's Diversity Index = $1-D$

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

N = the total number of organisms of all species
n = the total number of organisms of a particular species

(a) (i) Which measure provides better information regarding biodiversity? Explain your answer. [1]

..Simpson's..Index,..as..it..uses..the..number..of..species..and..the..number..of.....

..individuals..of..each..species;..richness..only..counts..species.....

(ii) There are 288 known species of mammal on the island of Borneo. Explain how you could obtain the data required to calculate a Simpson's Diversity Index for the biodiversity of mammals on this island. [2]

..Use..the..capture-mark-recapture..technique..(Lincoln..Index)..for..each.....

..species..of..mammal.....

..Trap..a..sample..of..each..species,..mark..and..release..them;..trap..a..second.....

..sample,..count..the..marked..animals..and..calculate..the..population..(n).....

..from..the..proportion..of..marked..animals..Add..these..to..give..N.....

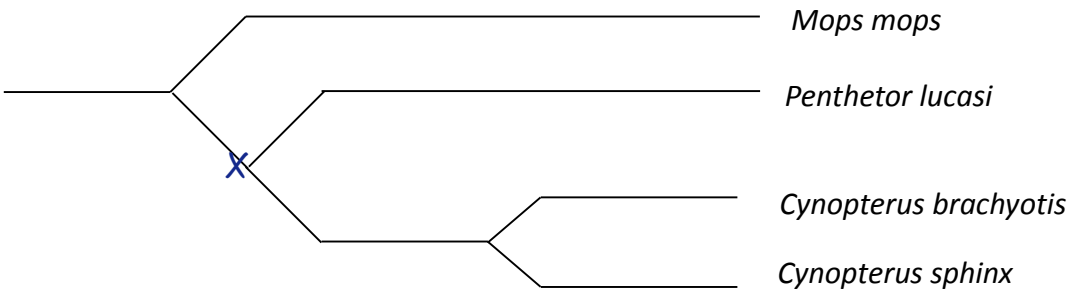
(iii) Suggest one problem associated with this method. Explain how it could affect the validity of any conclusions based on the calculated diversity index. [2]

..Marked..animals..may..be..seen..more..by..predators,..so..fewer..are.....

..re-caught;..numbers..are..overestimated,..so..the..index..is..not..valid.....

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(b) Of the 288 species of mammals in Borneo, 102 are bats. The following diagram is a phylogenic tree showing the evolutionary relationship between some of the bats.



Amino acid sequences of cytochrome oxidase from blood samples from each species were prepared. The sequences for the other three bats were compared with the sequence for *Cynopterus brachyotis.* The number of positions at which there was a different amino acid is recorded in the table below.

Bat	**A**	**B**	**C**
Number of amino acids different to *Cynopterus brachyotis*	**19**	**7**	**13**

(i) Mark clearly on the phylogenic tree, with the letter **X**, the position of an ancestor common to *Penthetor lucas*i and *Cynopterus sphinx* but not common to *Mops mops*. [1]

(ii) Use the information in the table and the phylogenic tree to identify the bats. [1]

A ..*Mops mops*.....

B ..*Cynopterus sphinx*.....

C ..*Penthetor lucasi*.....

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(c) *Mops mops* is a fruit-eating bat while *Cynopterus sphinx* feeds on insects. The table below shows the approximate nutritional composition of the food of these species.

	% composition	
	fruit	**insects**
carbohydrate	**23.4**	**2.5**
fat	**0.7**	**16.0**
protein	**2.2**	**18.0**

With reference to respiratory pathways, explain why *Cynopterus sphinx* eats a lower mass of food than *Mops mops* but is able to synthesise more ATP. [3]

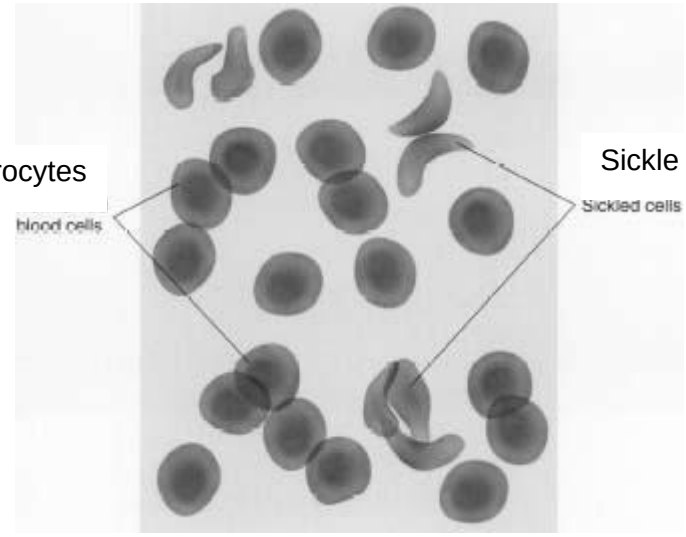
Insects have more fat than fruit and fat releases nearly twice the energy per g of carbohydrate in respiration, so less needs to be eaten. Fatty acids and glycerol contain more H atoms than glucose, so more reduced NAD / FAD is made to pass H atoms to the electron transport chain, making more ATP.

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2. Sickle cell anaemia is an inherited disease. People who have the disease inherit two genes for sickle haemoglobin—one from each parent.

Sickle haemoglobin causes red blood cells to develop a sickle shape. These block blood flow in the blood vessels causing pain and organ damage. It leads to much reduced life expectancy. The photograph below shows the shape of normal and sickle cells.



People who inherit a sickle haemoglobin allele from one parent and a normal allele from the other parent have **sickle cell trait**. They usually have few symptoms and lead normal lives.

Plasmodium falciparum is one of the organisms that cause malaria in humans. When it infects erythrocytes it uses oxygen and causes the haemoglobin of people with sickle-cell trait to change its tertiary structure and the erythrocytes to take on the classic sickle cell shape.

(a) A survey was conducted into the relationship between sickle-cell trait and the incidence of malaria. Patients were tested for the presence of the malarial parasite *P.falciparum* and if they were positive for sickle-cell trait. The results of the survey of 150 people are shown below.

percentage of people in the sample			
sickle-cell trait		**normal haemoglobin**	
infected with *P.falciparum*	**not infected with *P.falciparum***	**infected with *P.falciparum***	**not infected with *P.falciparum***
4.7	**12.4**	**58.2**	**24.6**

(i) What conclusion can be drawn from these results? [1]

People with sickle-cell trait are less likely to be infected with P. falciparum, so sickle-cell trait must provide protection against malaria.

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(ii) Suggest how the survey could be modified to improve the validity of your conclusion. [2]

Increase the sample size (well above 150 people) and account for age and sex, e.g. by using matched groups.

(b) In the United States, the sickle cell disease occurs in 1 out of every 625 African-Americans.

The Hardy-Weinberg formula states that if alleles **A** and **a** are present in a population with the frequencies of p and q, the proportion of individuals homozygous for the dominant allele (**AA**) will be p^2, the proportion of heterozygotes (**Aa**) will be $2pq$, and the proportion or homozygous recessives (**aa**) will be q^2, where $p + q = 1$.

Use the Hardy Weinberg formula to estimate the number of African Americans from a population of 1000 people that would have **sickle cell trait**. [4]

$q^2 = 1/625 = 0.0016$, so $q = \sqrt{0.0016} = 0.04$
$p + q = 1$, so $p = 1.0 - 0.04 = 0.96$
$2pq = 2 \times 0.04 \times 0.96 = 0.0768$
Number $= 0.0768 \times 1000 = 76.8 \approx 77$

Estimation of African Americans with sickle cell trait = *77 (76.8)*

(c) The Hardy-Weinberg Principle states that allele frequencies remain the same from generation to generation in the absence of natural selection.

In the nineteenth century, many sub-Saharan Africans were taken as slaves to America. In 2007 fewer than 2000 cases of malaria were reported in the USA while over 150 million were affected in sub-Saharan Africa in the same year.

Predict how the proportion of people with sickle cell trait could have changed in the USA and sub-Saharan Africa since the nineteenth century. Explain the basis for your prediction. [5]

Sickle cell trait would increase in sub-Saharan Africa but decrease in the USA.

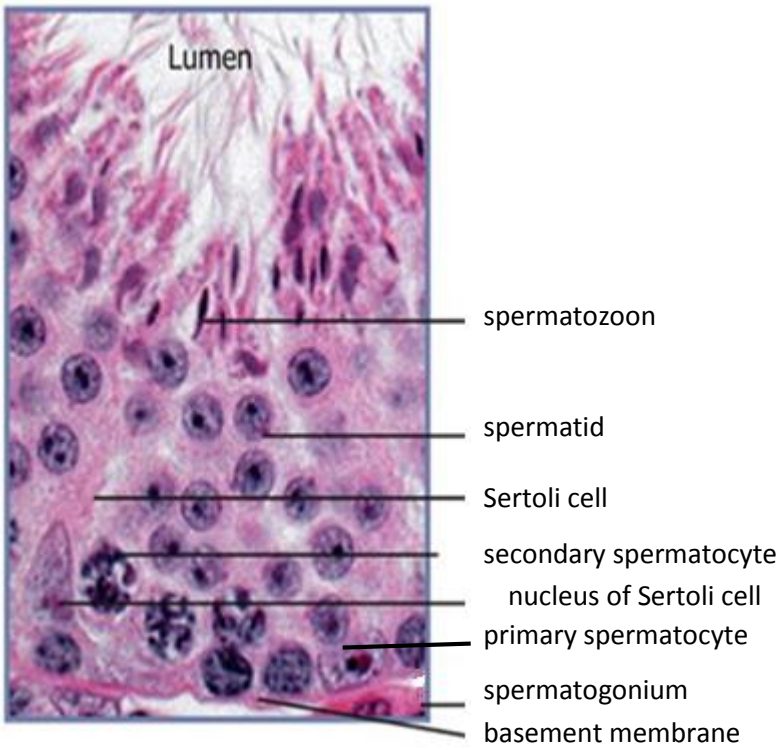
In Africa people with the trait have a selective advantage, as they are less likely to be killed by malaria, so more survive to pass the sickle allele to the next generation.

In the USA there are few cases of malaria, so no selective advantage; the trait is a disadvantage and is selected against.

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3. Spermatogenesis takes place in the seminiferous tubules of male mammals. The image below shows a transverse section of mouse seminiferous tubule.



(a) (i) Identify cells in the section that match the descriptions listed in the table below. The cells can match more than one description or none. [4]

Description	Name of cell(s)
undergoing meiosis	primary and secondary spermatocytes
will produce more cells by mitosis	spermatogonium
provides protection from the male immune system	Sertoli cell
will undergo differentiation to produce a fully functional cell	spermatid

(ii) Explain why there will be more spermatids than spermatogonia. [1]

..Spermatogonia..divide..by..mitosis..to..produce..primary..spermatocytes,..and....

..each..primary..spermatocyte..produces..4..spermatids..by..meiosis.....

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(iii) The Sertoli cell contains a prominent nucleolus and large numbers of ribosomes. It is known that these cells are involved in providing nourishment to developing sperm cells.
Suggest what nutrients the Sertoli cells provide to the developing cells? Give reasons for your answer. [2]

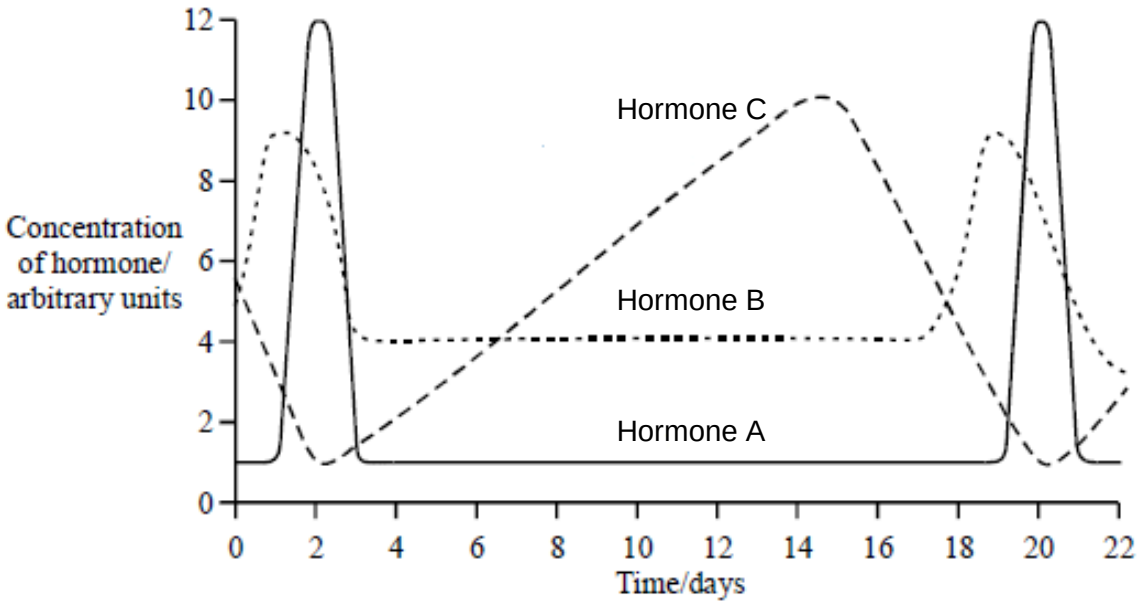
..Protein..(amino..acids),..because..the..nucleolus..produces..rRNA../.....

..ribosomes..and..ribosomes..carry..out..protein..synthesis.....

(iv) Another function of Sertoli cells is to remove debris from the lumen of the seminiferous tubule. Name the process by which Sertoli cells carry out this function. [1]

..Phagocytosis..(endocytosis).....

(b) The menstrual cycle in cows is controlled by the same hormones as women. The diagram below shows the changes in the levels of some hormones of a cow over a 22 day period.



(i) Identify hormones **A**, **B** and **C** shown in the graph above. [3]

A ..LH..(luteinising..hormone).....

B ..oestrogen.....

C ..progesterone.....

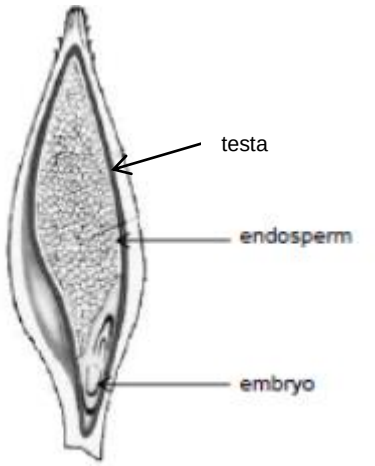
(ii) Estimate the length of the menstrual cycle shown. [1]

.....18..... days

12

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4. Barley (*Hordeum vulgare),* is an important cereal grown in the UK. It is used widely for animal fodder and as a source of maltose when brewing beer. The diagram below is a cross-section through a grain of barley, *Hordeum vulgare*.



(a) Explain why a barley grain is technically a fruit and not a seed. [2]

A seed is surrounded by the testa only, whereas a fruit develops from the ovary and has a pericarp. A barley grain is a fruit because it is surrounded by both the testa and the pericarp.

(b) The endosperm cells contain 21 chromosomes. Calculate how many chromosomes there are in the cells of the embryo. Explain how you arrived at your answer. [4]

Number of chromosomes in embryo cells = 14

Explanation: Double fertilisation. Endosperm is triploid: 1 male gamete + 2 polar nuclei, each with 7 chromosomes. Embryo cells are diploid: 1 male gamete + 1 female gamete, so 2 x 7 = 14.

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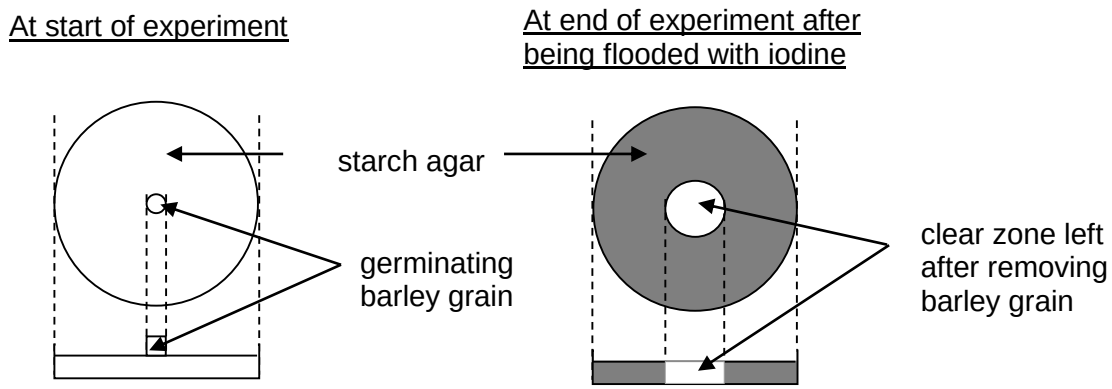
(c) The table below shows the results obtained from a study of the germination and early growth of barley grains.

Time after sowing (days)	Dry mass of endosperm (mg)	Dry mass of embryo (mg)
0	42	2
2	41	2
4	32	8
6	20	16
8	9	24
10	6	34

What can be concluded from these results? [2]

The dry mass lost from the endosperm must be used to increase the dry mass of the embryo, as food stores are mobilised. The mass of the embryo is increasing but the seedling cannot yet produce biomass by photosynthesis.

(d) The diagram below shows a view from above and from the side of an experiment demonstrating the presence of amylase in a germinating barley grain.



(i) The agar contained 1g starch per 100cm^3 of agar. The agar in each plate was 5mm deep and the clear zone left after removing the barley grain was 25mm in diameter. The volume of agar in the clear zone can be calculated as follows:

Volume = $\pi r^2 h$ (π = 3.142)

Calculate the mass of starch digested by the germinating barley grain. Show your working and give your answer in standard form. [3]

r = 25 ÷ 2 = 12.5 mm = 1.25 cm, h = 5 mm = 0.5 cm

Volume = 3.142 × 1.25^2 × 0.5 = 2.4547 cm^3

Mass of starch = 2.4547 × 1 ÷ 100 = 0.0245 g

Mass of starch digested = *2.45×10^{-2}* g

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(ii) During germination the amylase is synthesised from amino acids from protein stored in the barley grain. Name the tissue where the protein is stored and name the hormone responsible for mobilising the amino acids. [2]

Tissue: aleurone layer

Hormone: gibberellin

(iii) It is important that brewers know how the age of their barley affects the concentration of amylase produced so that they can obtain the best yield of malt.
Using the apparatus shown, design a method to investigate the effect of age of seed on the concentration of amylase produced. [5]

Use barley grains of a range of different ages (e.g. 0, 1, 2, 3 and 4 years old) and germinate them.

Place grains of the same mass on starch agar plates of the same depth for the same fixed time (e.g. 24 h) at the same temperature.

Remove the grains, flood with iodine and measure the diameter of the clear zone and calculate its area.

Repeat 3 times for each age and find a mean. Control: boiled grains (no clear zone).

18

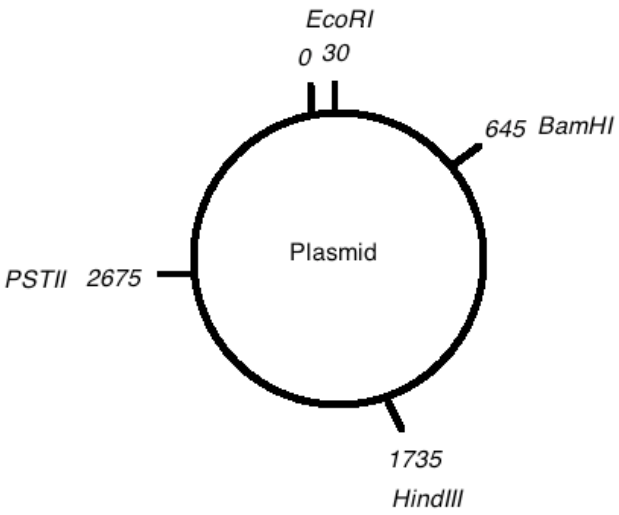
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5. Bacteria and Archaea produce restriction enzymes that cleave DNA that is foreign to their own DNA. These enzymes recognize and cut DNA molecules at or near specific sequences of nucleotides called restriction sites. One theory is that these enzymes have evolved as a defence mechanism against viruses called bacteriophages that can infect bacteria.
More than 3000 different restriction enzymes have been discovered to date and over 600 are available commercially for use in genetic engineering.

(a) Explain why these enzymes could be effective as defence mechanisms against these viruses. [1]

The enzymes would digest the viral DNA and destroy its genes, making it impossible for viral proteins to be made.

(b) The diagram below is of a bacterial plasmid 3 450 base pairs in length with the restriction sites of four different enzymes, EcoRI, BamHI, HindIII and PSTII shown.



Total length = 3450 base pairs (bp)
NOT drawn to scale

(i) If the plasmid was cut using EcoRI and PSTII **only**, what would be the size of the smallest fragment? Show your working. [2]

Smallest fragment: PSTII (2675) to EcoRI (30)
3450 − 2675 = 775
775 + 30 = 805 bp

Answer *805 bp*

(ii) A gene was present between 550 and 1 699 base pairs. Which two enzymes would be needed to cut out the gene leaving the smallest number of additional bases? [1]

EcoRI and HindIII

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(c) "D7S280" is a short tandem repeat (STR) sequence of "GATA" found on human chromosome 7. This STR was sequenced and found to lie between 126 and 177 base pairs within the 341 base pair sequence shown below (**GATA shown in bold**).

Starting base number						
1	AATTTTTGTA	TTTTTTTTAG	AGACGGGGTT	TCACCATGTT	GGTCAGGCTG	ACTATGGAGT
61	TATTTTAAGG	TTAATATATA	TAAAGGGTAT	GATAGAACAC	TTGTCATAGT	TTAGAACGAA
121	CTAAC**GATAG**	**ATAGATAGAT**	**AGATAGATAG**	**ATAGATAGAT**	**AGATAGATAG**	**ATAGATA**GAT
181	TGATAGTTTT	TTTTTATCTC	ACTAAATAGT	CTATAGTAAA	CATTTAATTA	CCAATATTTG
241	GTGCAATTCT	GTCAATGAGG	ATAAATGTGG	AATCGTTATA	ATTCTTAAGA	ATATATATTC
301	CCTCTGAGTT	TTTGATACCT	CAGATTTTAA	GGCC		

The STR was then extracted and amplified using PCR.

(i) Explain why each stage of the PCR is conducted at the following temperatures: [3]

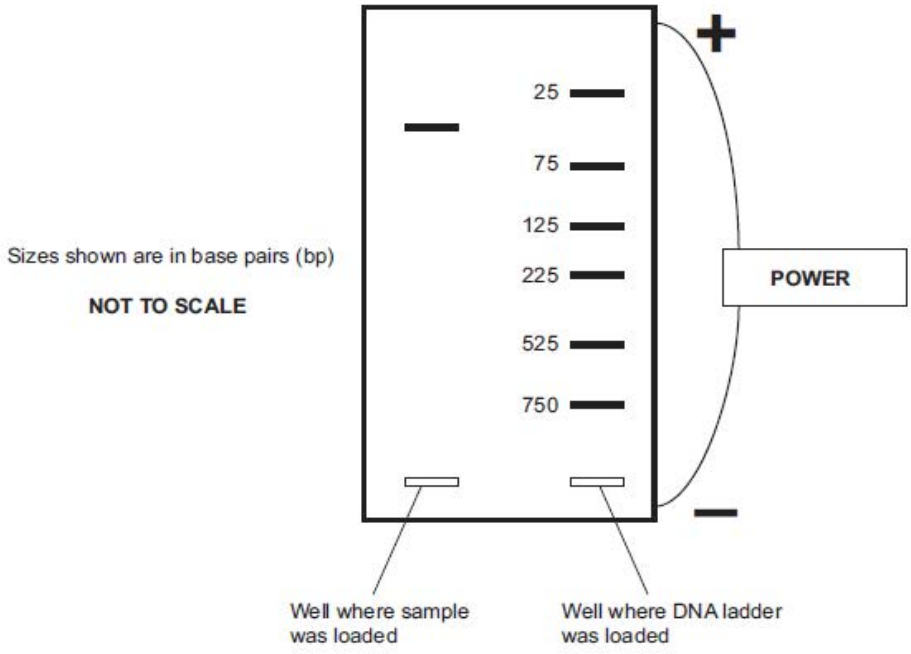
I 95°C *Breaks the hydrogen bonds between the bases, causing the two DNA strands to separate*

II 50 – 60°C *Allows the primers (short pieces of DNA) to anneal (bind) to the complementary bases at the ends of the STR*

III 70°C *Optimum for Taq DNA polymerase, which adds complementary nucleotides (extension), forming phosphodiester bonds in the sugar-phosphate backbone*

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(ii) The amplified STR was run on an agarose gel using gel electrophoresis. The result is shown below.



Describe and explain how electrophoresis produced the results seen in the gel result. [3]

DNA is attracted to the positive electrode due to the negative charge on its phosphate groups. Smaller fragments find it easier to migrate through the pores in the gel, so they travel further than larger fragments in the same time. Fragment size is estimated by running a DNA ladder of fragments of known size alongside.

(iii) Evaluate how well the results of the electrophoresis match the sequencing results. [2]

Sequencing gives 52 bp; the gel band is about 50 bp (half way between the 25 and 75 bp bands), so good agreement.

(iv) How could the gel result be made more accurate? [1]

Use a DNA ladder with more fragments of sizes between 25 and 75 bp.

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6. In peas, the allele for wrinkled seeds (R) is dominant to that for smooth (r) and the allele for yellow seed colour (Y) is dominant to green (y).

A plant breeder has developed a new variety of wrinkled, yellow peas but thinks that his new variety is a hybrid. In order to confirm this, he crossed his new variety with a plant that produced smooth, green peas.

When the F_1 generation grew, he recorded the phenotype of the seeds they produced. His results are shown below.

Number of plants	Phenotype of seeds produced
31	yellow, wrinkled coat
22	green, wrinkled coat
29	yellow, smooth coat
26	green, smooth coat

(a) Complete the genetic diagram below to show how F_1 inherited the phenotypes shown in the table. [5]

Parental genotype ....RrYy..... x .....rryy.....

Gametes ..RY, .Ry, .rY, .ry..... x .....ry.....

gametes	RY	Ry	rY	ry
ry	RrYy	Rryy	rrYy	rryy

F_1 genotypes ...RrYy.....Rryy.....rrYy.....rryy.....

F_1 phenotypes ..wrinkled, yellow....wrinkled, green.....smooth, yellow.....smooth, green

Phenotype ratio ...1...:...1...:...1...:...1.....

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(b) Based on the results of this cross he concluded that the new variety was pure-breeding.

(i) Calculate χ^2 for the results of this cross. A table is provided below for you to use. [3]

Phenotype of seeds produced	Observed O	Expected E	O − E	(O − E)²	(O − E)²/E
yellow, wrinkled coat	31	27	4	16	0.593
green, wrinkled coat	22	27	−5	25	0.926
yellow, smooth coat	29	27	2	4	0.148
green, smooth coat	26	27	−1	1	0.037
	108	108			Σ = 1.70

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$ 0.593 + 0.926 + 0.148 + 0.037

= ....1.70.....

(ii) Use your calculated value of χ^2 and the probability table to justify whether the plant grower's conclusion was valid. [4]

Degrees of freedom	Probability		
	P = 0.10	P = 0.05	P = 0.02
1	2.71	3.84	5.41
2	4.61	5.99	7.82
3	6.25	7.82	9.84
4	7.78	9.49	11.67
5	9.24	11.07	13.39

df = 3, so critical value at p = 0.05 is 7.82. χ^2 = 1.70 < 7.82, so the difference is not significant; the deviation is due to chance, so the conclusion is valid.

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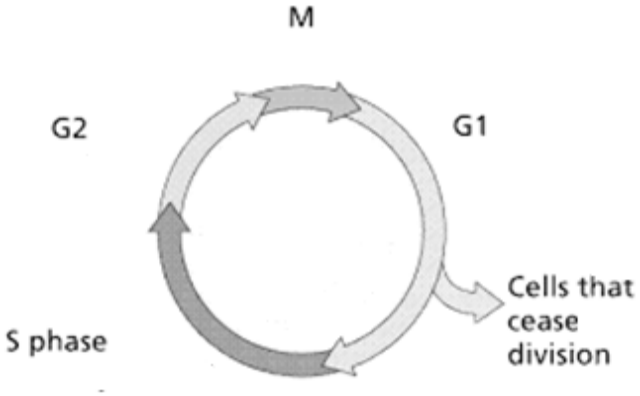
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7. In 2011, over 330,000 cases of cancer were diagnosed in the UK of which, cancer of the kidney was the eighth most common..

(a) With reference to the structures involved in the production of urine, explain how a kidney tumour could result in the presence of blood in the urine. [2]

The tumour damages the basement membrane in the glomerulus, so red blood cells can pass through into the filtrate and so into the urine

Cancer has been described as the uncontrolled, abnormal proliferation of cells and involves disruptions to the control of the normal cell cycle, as shown in the diagram below.

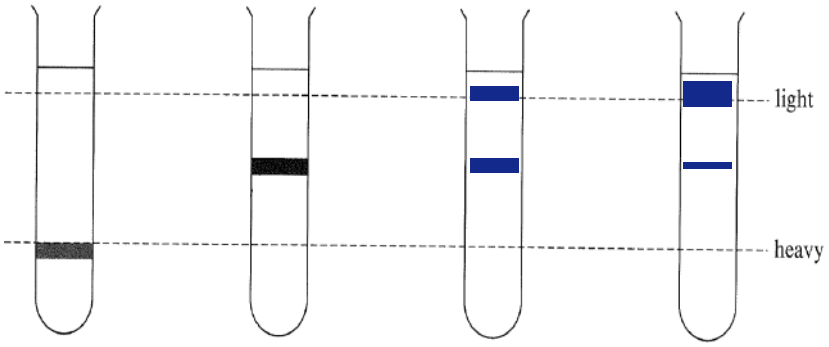


(b) During the S phase, cells that are undergoing cell division carry out DNA synthesis. In 1958, Meselson and Stahl carried out experiments to test which of three different theories did indeed describe the mechanism of DNA replication. Here is a brief description of their experimental method.

> The bacterium *Escherichia coli* (E. coli) was cultured in a nutrient broth, containing the heavy isotope as a source of nitrogen, ^{15}N, instead of the normal ^{14}N. After several generations all of the DNA in all of the bacteria contained the heavy isotope ^{15}N. They were then washed and transferred to a ^{14}N medium and allowed to replicate. After each generation, bacteria were removed and spun in a centrifuge. The position of the DNA in the medium was then determined.

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(i) The diagram shows how the position of the DNA changed after successive cell divisions.



Initial position after growing in ^{15}N culture medium	After 1 division in ^{14}N culture medium	After 2 divisions in ^{14}N culture medium	After 3 divisions in ^{14}N culture medium

Complete the diagrams to show the pattern and relative proportions of DNA you would expect after 2 and 3 divisions in ^{14}N culture medium. [2]

(ii) Name the theory of DNA replication supported by the results of this experiment. [1]

Semi-conservative

(iii) Explain how their results before and after the first division in ^{14}N culture medium support this theory and not the other theories proposed. [2]

Before, all DNA was heavy; after 1 division in ^{14}N all DNA formed one intermediate band, a mixture of heavy and light DNA, not separate heavy and light bands. So each molecule has 1 original (heavy) and 1 new (light) strand

(c) p27 is a protein that is involved in the control of the cell cycle. High levels of this protein block the initiation of the S phase. This results in cells remaining in the G_1 phase for longer. In cells taken from breast cancers, it has been found that the levels of p27 are abnormally low.

(i) Suggest why it would be an advantage for normal cells to have: [2]

I high levels of p27 *Cells stay longer in the period of normal cell activity, so they can continue to perform their particular function*

II low levels of p27. *Decreases the time before cell division, increasing the rate of growth or repair, e.g. after injury*

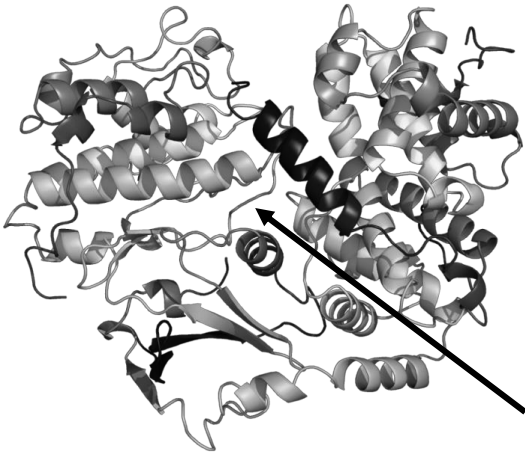
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(ii) Suggest why abnormally low levels of p27 could result in the development of a tumour. [2]

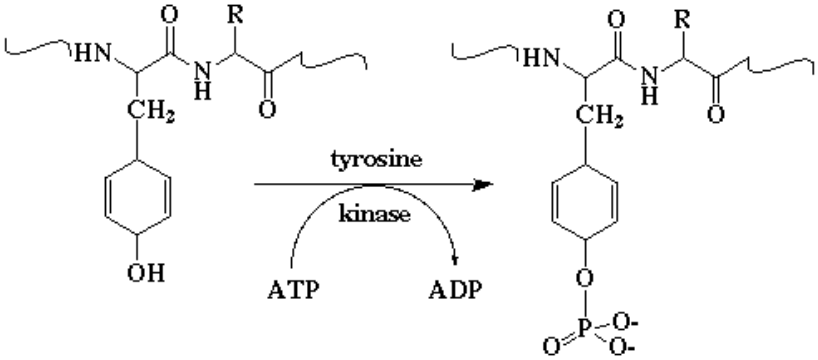
Low p27 does not block initiation of S phase, so cells enter S phase too quickly and keep dividing.

The rate of growth is speeded up above the normal rate with no control on cell division, so a mass of cells (tumour) forms.

(d) The structure of the p27 protein is shown in the diagram below.



Research has shown that p27 acts as a competitive inhibitor of one of the enzymes responsible for the initiation of DNA replication.
The enzyme tyrosine kinase can phosphorylate a tyrosine molecule at position 88 in the p27 polypeptide chain as shown in the diagram below.



Explain how this could reduce p27s ability to inhibit its target enzyme. [3]

The phosphate group has a strong negative charge, which could change the tertiary structure of p27, so p27 would not bind to the active site of the target enzyme and cannot inhibit it.

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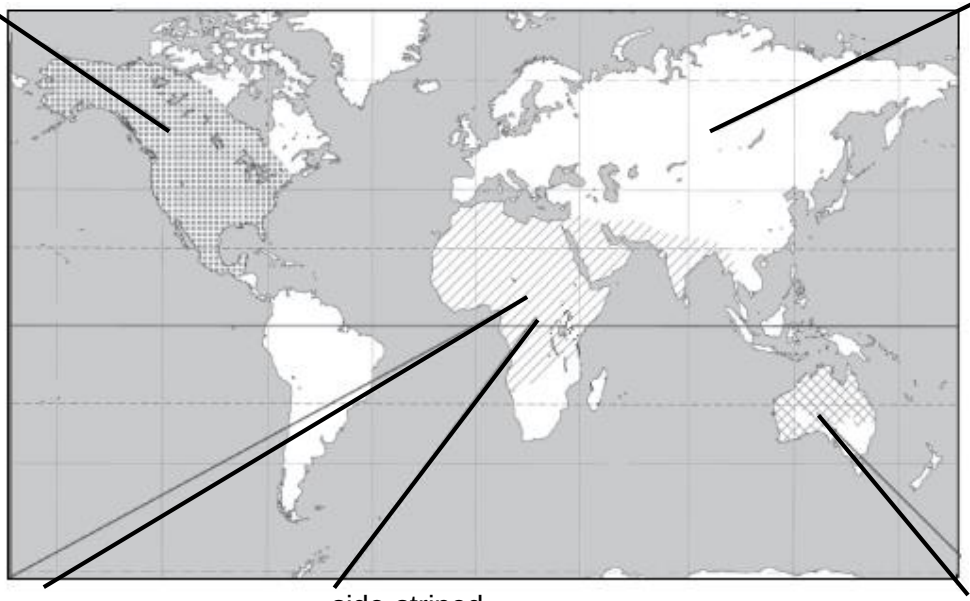
8. It is believed that the canine (dog) family evolved from a common ancestor about seven million years ago. The map below shows the world distribution of some members of the canine family.

coyote



wolf





black-backed jackal



side-striped jackal



dingo



In order to determine whether all the examples shown on the map were the same species, mating experiments were carried out. The results are shown in the table below.

	Coyote	Wolf	Dingo	Black backed Jackal	Side striped jackal
Coyote	✓	✓	✓	×	×
Wolf	✓	✓	✓	×	×
Dingo	✓	✓	✓	×	×
Black backed jackal	×	×	×	✓	×
Side striped jackal	×	×	×	×	✓

Using the information given, determine how many different species are shown on the map. Explain how you arrived at your conclusion and suggest how the different species could have arisen.
(The quality of your extended response will be assessed in this question.) [9QER]

There are three species shown on the map. A species is a group of organisms that

can interbreed to produce fertile offspring.

The coyote, wolf and dingo can all interbreed to produce fertile offspring, so they

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are one species. The black-backed jackal and the side-striped jackal cannot interbreed successfully with any other canine shown, or with each other, so each is a separate species, giving three species in total.

Following evolution from a common ancestor about seven million years ago, the canines migrated to different parts of the world. Here they met different selection pressures in different habitats, such as differences in climate, predators and food availability.

There is variation within each population, caused by mutation. Individuals with variations that give a selective advantage under the local selection pressures are more likely to survive and reproduce, passing on their advantageous alleles to their offspring (survival of the fittest). Over many generations natural selection changes allele frequencies, resulting in morphological differences between the canines.

Allopatric speciation has occurred between the canines that can produce fertile offspring and the two jackals, due to geographical isolation by barriers such as oceans and deserts. With no gene flow between the separated populations, different mutations and selection pressures caused them to diverge until they were reproductively isolated.

The wolf, dingo and coyote appear to have diverged relatively recently, as even though they are geographically separated they can still interbreed: reproductive isolation has not yet developed. The black-backed and side-striped jackals appear to have diverged less recently, allowing more time for speciation to occur.

Sympatric speciation has produced the black-backed and side-striped jackals, as they occupy the same habitat in Africa but cannot produce fertile offspring. Reproductive isolation arose without geographical separation.

This could be caused by isolation mechanisms such as different reproductive cycles, differences in reproductive or courtship behaviour, changes in chromosome number (plaidy), different activity times or mechanical isolation. These prevent gene flow, so each population evolves independently into a separate species.

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