






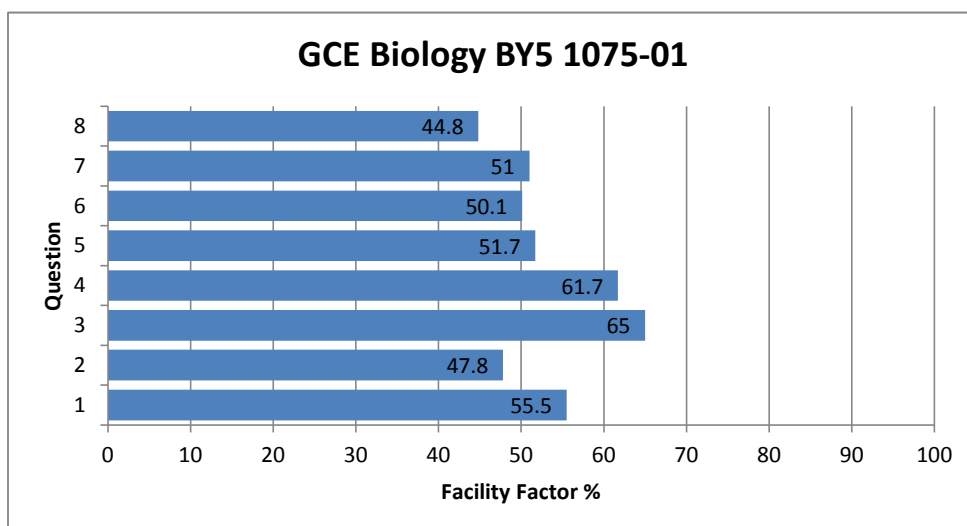


GCE Biology BY5 1075-01

All Candidates' performance across questions

						
Question Title	N	Mean	SD	Max Mark	FF	Attempt %
1	5207	4.4	1.9	8	55.5	99.9
2	5207	2.9	1.5	6	47.8	99.9
3	5211	5.2	1.6	8	65	100
4	5210	6.8	2.5	11	61.7	99.9
5	5192	6.2	3.1	12	51.7	99.6
6	5207	6	2	12	50.1	99.9
7	5202	6.6	2.8	13	51	99.8
8	5194	4.5	2.1	10	44.8	99.6



5. The techniques of recombinant DNA technology and micro-propagation are used to produce Genetically Modified Crops. The following summary is adapted from an account given on the Food Standards Agency's web site [www.food.gov.uk]

1. A plant with the desired characteristic is identified – e.g. resistance to the herbicide 'Roundup'.
2. The specific gene that produces this characteristic is found in the plant's DNA and cut out.
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5. The 'gene package' is put in a bacterium, which multiplies, to create many copies of the 'gene package'.
6. A copy of the 'gene package' is dried onto a gold or tungsten particle – and fired into a piece of tissue from the plant being modified. The particle carries the 'gene package' into the plant's cells.
7. The plant tissue is put into a selective growth medium so that only modified tissue develops into plants.

- (a) Explain how different types of enzymes are used in stages 2 and 3 to produce the 'gene package'. [4]

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- (b) Describe the steps involved in the culture of a large number of genetically identical plants from the plant tissue produced in stage 7. [3]

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- (c) (i) Explain the advantage to farmers of having crops resistant to 'Roundup'. [3]

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- (b) Describe the steps involved in the culture of a large number of genetically identical plants from the plant tissue produced in stage 7. [3]

Micropropagation, ~~meristem~~ a sterile loop takes meristems, at the tip of the plant. Meristems ~~are grown on a~~ ^{are} grown on a ~~medium containing required nutrients~~ ^{medium} and DNA is inserted into ~~plants~~ ^{meristem}. This makes an explant, goes into a callus where many plantlets grow in tubes.

- (c) (i) Explain the advantage to farmers of having crops resistant to 'Roundup'. [3]

~~Crops need to be sprayed~~ herbicide doesn't kill crops, crops can grow so farmers can apply herbicide making a higher yield as doesn't effect crop.

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More farmers spray pesticides therefore contaminating near by rivers / lakes, ~~when~~ washed down. This deoxygenates water, therefore contaminates fish and birds that feed from rivers causing death.

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(a) Explain how different types of enzymes are used in stages 2 and 3 to produce the 'gene package'. [4]

Restriction endonuclease enzymes are used to cut out the DNA fragment holding the required resistant gene of the donor plant. Restriction endonuclease will cut between specific base pairs, leaving 'sticky ends', which are now on the edge of the DNA fragment with unpaired base. The same restriction endonuclease cuts the plasmid, which will produce complementary sticky ends to the DNA fragment's. The DNA fragment's sticky ends aligns with the plasmid's sticky ends and DNA ligase annals the 2 sticky ends together, producing recombinant DNA. ~~Alternately~~

- (b) Describe the steps involved in the culture of a large number of genetically identical plants from the plant tissue produced in stage 7. [3]

Micropropagation ~~set~~ is completed. So meristems from the tip of the shoot / plant tissue is removed from the plant tissue produced with a sterile scalpel. The explant is then subdivided into many pieces and each piece is placed on a sterile, aerated nutrient medium such as agar jelly. A callus will grow, which is a mass of undifferentiated cells. The callus is subdivided and each piece placed on a growth medium, ~~which~~ ^{and} will grow into a plantlet.

- (c) (i) Explain the advantage to farmers of having crops resistant to 'Roundup'. [3]

Farmers can spray 'roundup' onto their crops, so killing off any weeds, while the crops will remain alive. This is economically beneficial to the farmers as they will produce a larger crop yield due to more crops surviving due to the decreased interspecific competition for food and space that would have been present if the weeds were still present.

- (ii) Explain why environmentalists might have legitimate objections to using GM crops resistant to 'Roundup'. [2]

The resistant gene to roundup may pass onto closely related species of plants or weeds. This may mean that 'superweeds' are produced which will be herbicide resistant.

The GM crops may have an effect on the ~~number of~~ organic farm as the crops may become undifferentiable.

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Small cuttings of totipotent cells are placed in a sterile nutrient medium. They are called explants. These explants then divide to form a large mass of undifferentiated cells called a callus. This callus is split up and grown with ~~some~~ certain growth factors which cause the cells to differentiate into plantlets. Once of a sufficient size, these are placed in sterile soil and are allowed to grow. (continued)

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The pollen from the plant ^{with the resistant gene} may be transferred and cross-pollinate with undesirable weed species, causing them to be resistant to the herbicide ^{increasing inter specific competition} to ~~it~~.

Also, it is unknown whether this foreign DNA could be toxic or dangerous to the consumer, and if the plants are used near organic farms, the organic status of the farm may be compromised by cross-pollination between the two groups/batches of crops.



5. (d) A selective growth medium is used, which only allows those plant cells that have taken up the recombinant plasmid to divide. This medium could contain the herbicide Round-up as then only the plant cells with the newly resistant gene would survive.

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6. A species of mouse *Peromyscus polionotus* found in Florida, USA, has a number of different coat colours. Coat colour in mice is controlled by several genes. Dark fur is produced when the hair producing cells secrete a pigment called eumelanin. A high level of eumelanin is produced when a transmembrane protein called MC1R is stimulated by a hormone.

- (a) The diagram below shows part of the amino acid sequence of MC1R, part of the sequence of nucleotides in the gene for MC1R and how it might change to produce light fur:

Original

Amino acid sequence

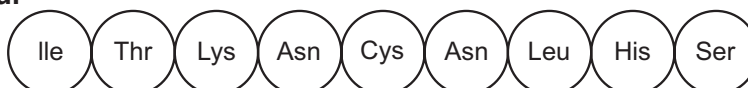


Nucleotide sequence
(allele R)

ATCACCAAAAACCGCAACCTGCACTCG

Changed to produce light fur

Amino acid sequence



Nucleotide sequence
(allele C)

ATCACCAAAAACCTGCAACCTGCACTCG

- (i) Describe the change in the gene and the subsequent change in the MC1R molecule. [2]

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- (ii) Using the information provided, explain how this change results in mice with light fur. [2]

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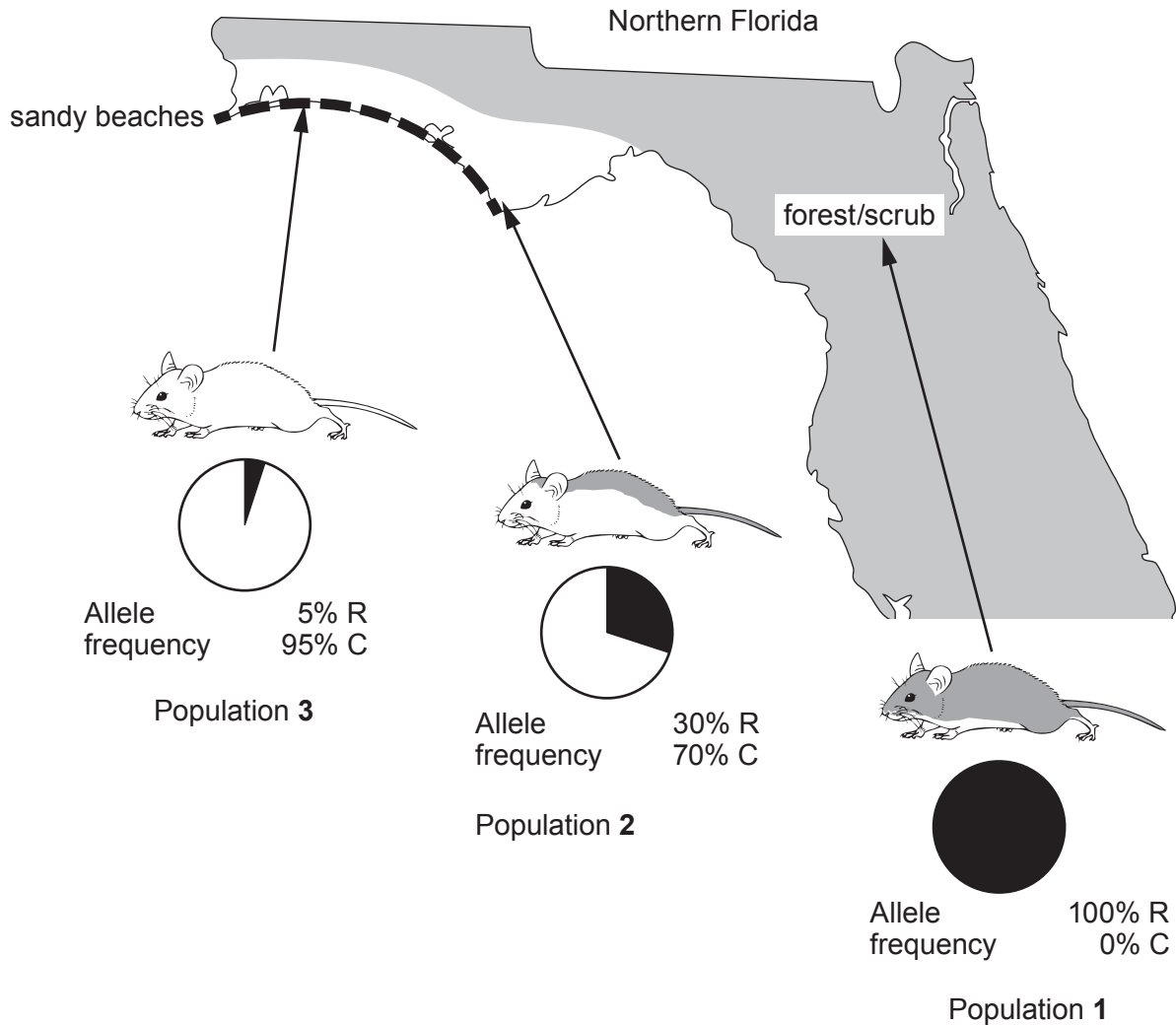
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- (b) This change in the MC1R gene means that there are two alleles, R and C. The map below shows the distribution of the different coloured mice and the relative frequencies of the alleles R and C in each population.



- (i) Use the diagram to suggest how fur colour is related to environmental conditions. [2]

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- (ii) Under what circumstance could the difference between the allele frequencies in populations 2 and 3 be explained by **genetic drift**, despite both living on beaches? [1]

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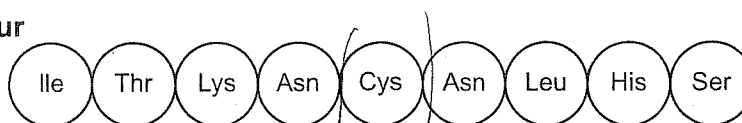


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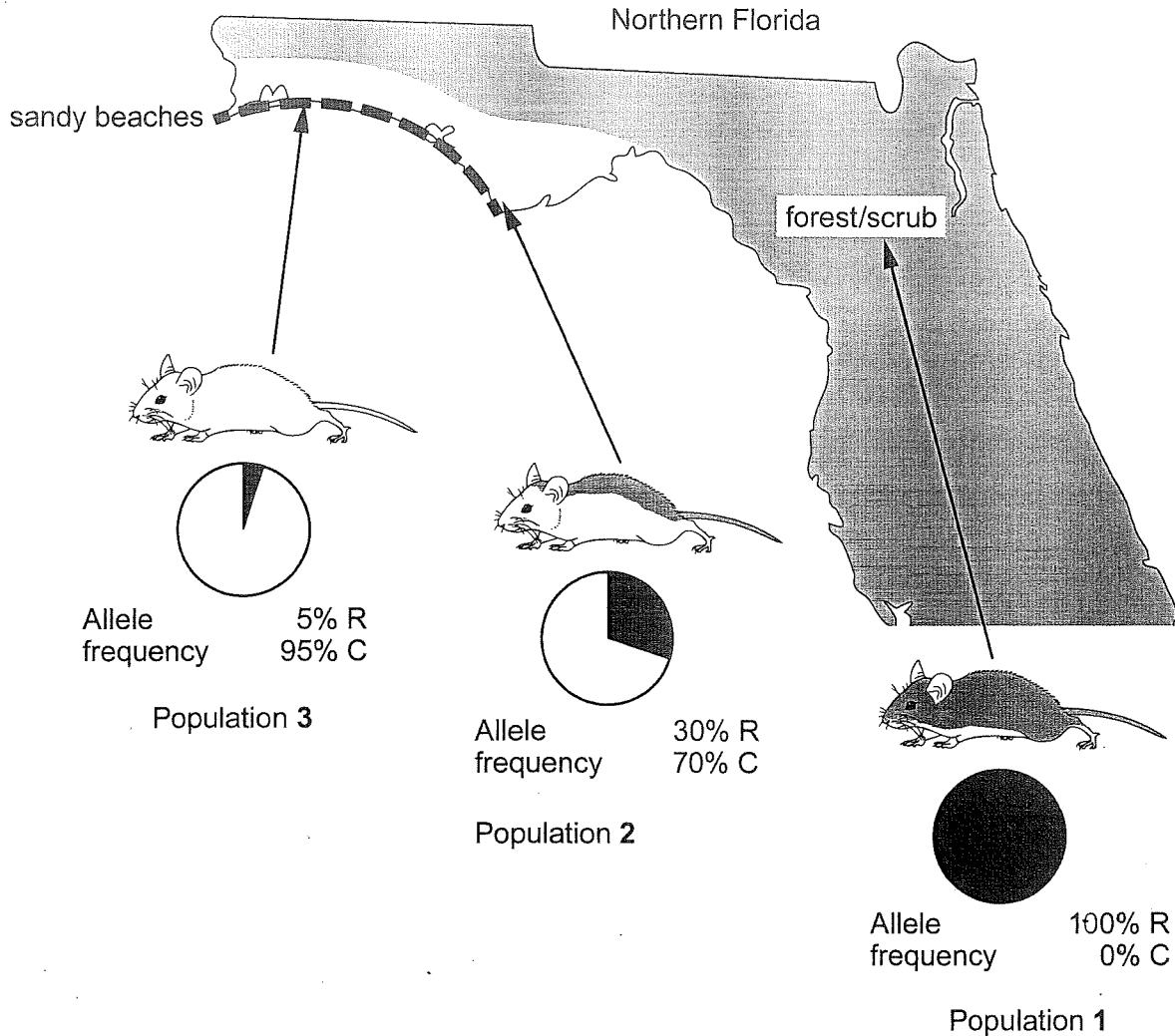
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Cytosine in original nucleotide sequence changes to thymine. ~~to~~ There this changes the code making a different amino acid. Therefore amino acid sequence will make a different protein.

- (ii) Using the information provided, explain how this change results in mice with light fur. [2]

~~with~~ The new/changed protein doesn't secrete the eumelanin pigment due to the transmembrane protein, MC1R not stimulated by hormone

- (b) This change in the MC1R gene means that there are two alleles, R and C. The map below shows the distribution of the different coloured mice and the relative frequencies of the alleles R and C in each population.



- (i) Use the diagram to suggest how fur colour is related to environmental conditions.

[2]

A lighter coat colour is more likely to survive on a sandy beach than a dark coat as it is less likely to be seen. Lighter coats in forest is more obvious so are out as killed by predators.

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[1]

Population 2 could have bred with heritable variation

- (iii) Explain how **Natural Selection** could have caused the relative allele frequency shown in population 3. [4]

Dark coated mice are more likely to survive in forests as they are harder to see by predators.

Therefore increased dark coat population as they reproduce offspring, passing on R allele. any mice with C allele are spotted easily so killed. This is selection pressure.

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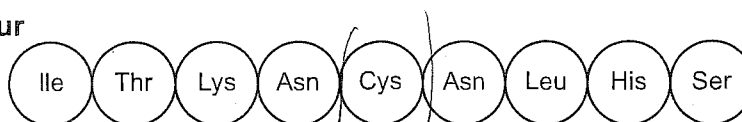


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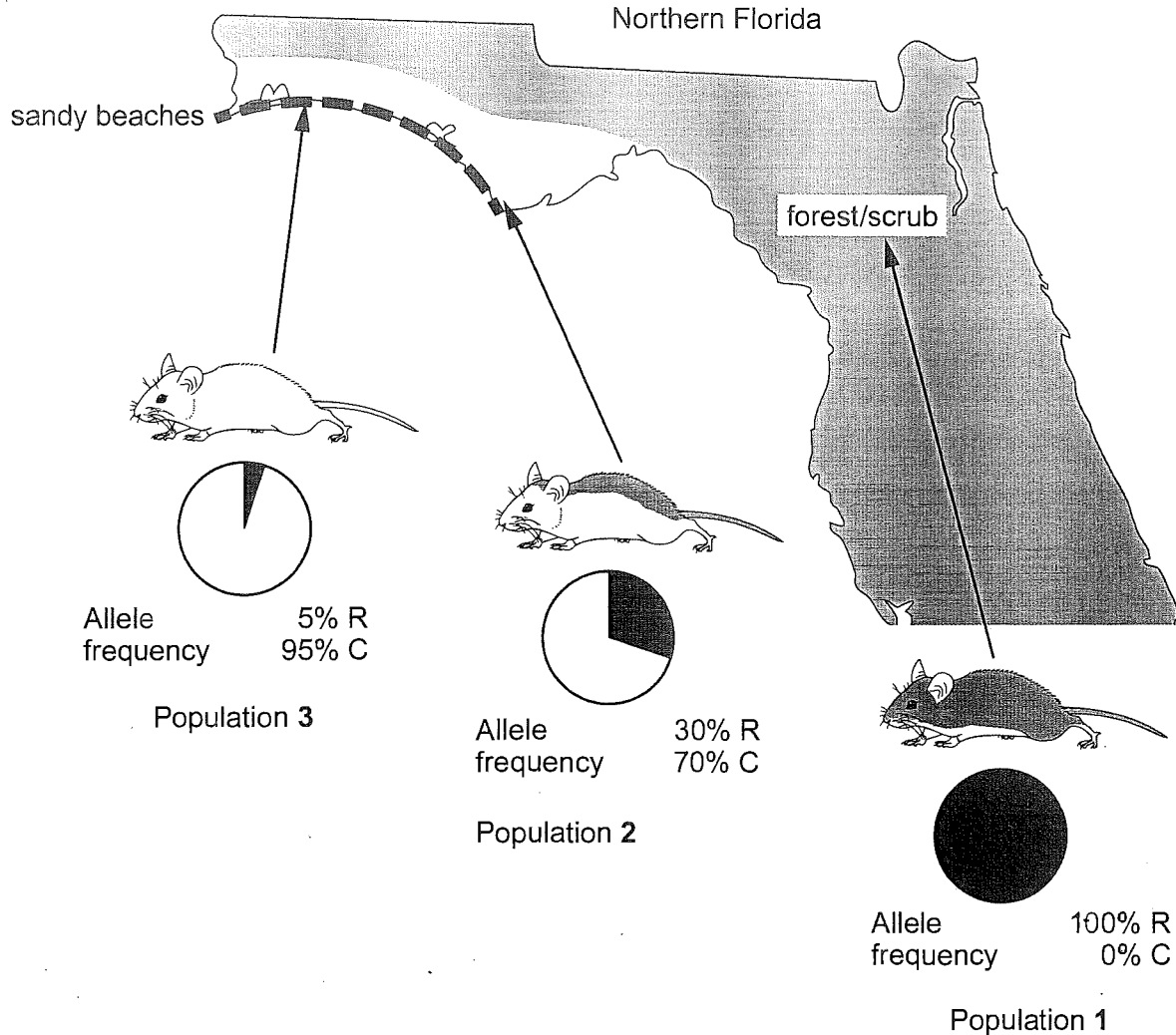
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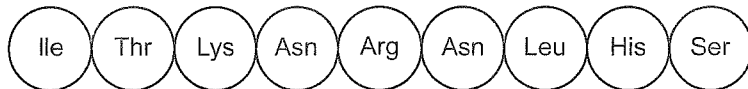
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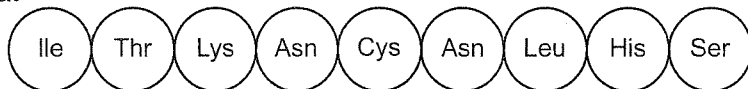


Nucleotide sequence
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ATC|ACC|AAA|AC|CGC|AA|CTG|CA|CTCG

Changed to produce light fur

Amino acid sequence



Nucleotide sequence
(allele C)

ATC|ACC|AAA|AC|TGC|AA|CTG|CA|CTCG

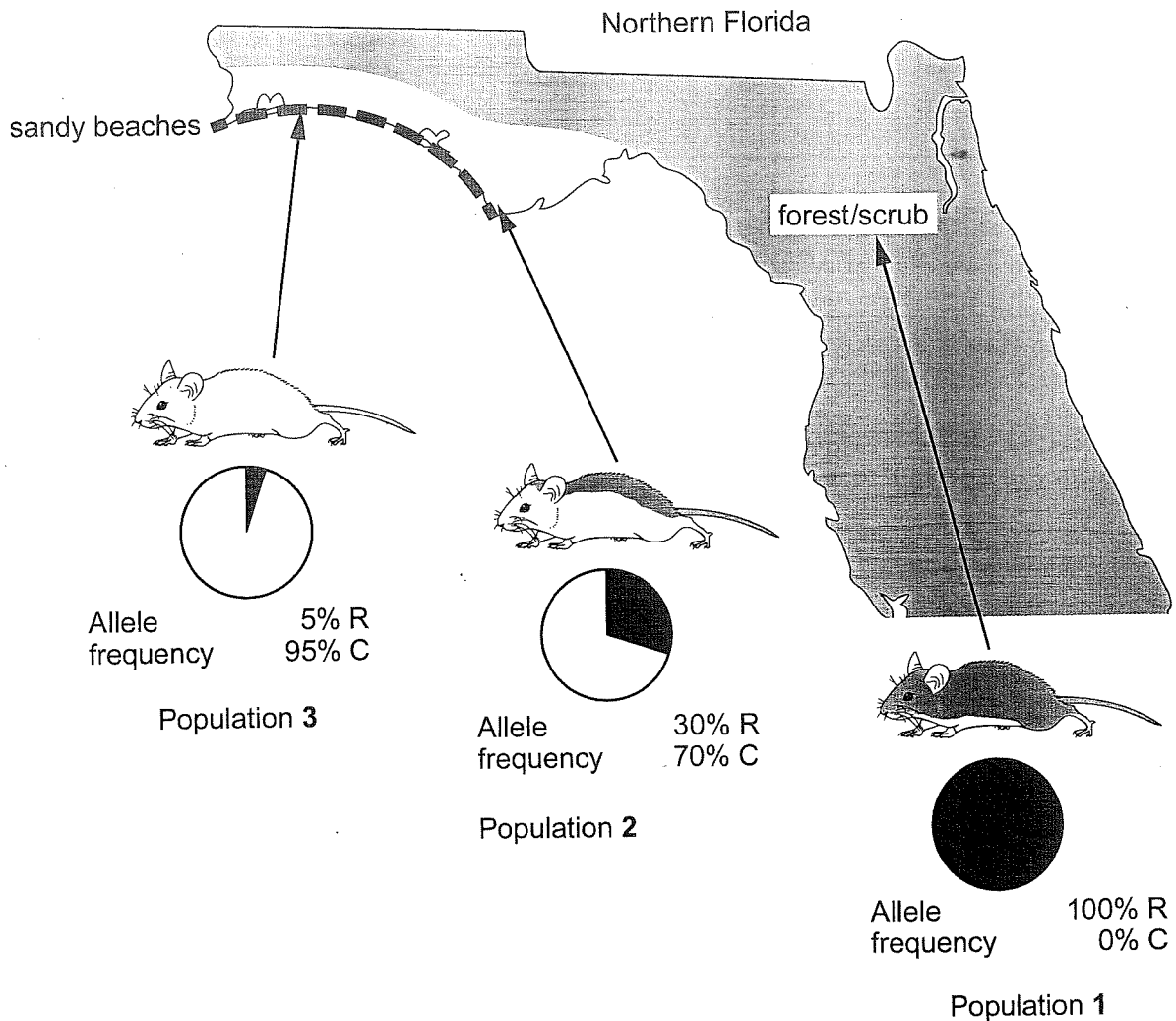
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The fifth triplet code in sequence has changed from 'CAG' to 'TGC' and so the amino acid in sequence has changed from 'Arg' to 'Cys'. This means the polypeptide chain has changed and so the MC1R molecule is a new protein. ~~molecule is no longer stimulated by a hormone so hair~~

- (ii) Using the information provided, explain how this change results in mice with light fur. [2]

The change has resulted in the function of MC1R not operating properly. The MC1R no longer is stimulated by a hormone and so a ^{low} level of eumelanin is produced, resulting in the mice having light fur.

- (b) This change in the MC1R gene means that there are two alleles, R and C. The map below shows the distribution of the different coloured mice and the relative frequencies of the alleles R and C in each population.



- (i) Use the diagram to suggest how fur colour is related to environmental conditions. [2]

Fur colour is related to the habitat they occupy. In population 3, 95% have light fur as they live in sandy beaches and in population 1, 100% have dark fur as they live in forest. This is because they have an advantage by camouflaging in with the surroundings.

(ii) Under what circumstance could the difference between the allele frequencies in populations 2 and 3 be explained by genetic drift, despite both living on beaches? [1]

Genetic drift selection pressure

- (iii) Explain how **Natural Selection** could have caused the relative allele frequency shown in population 3. [4]

in population 3, mice with light fur had a desirable characteristic as they blended in with their environment making them less likely to be eaten by predators. This meant those mice with light fur were more likely to survive and reproduce, passing on their alleles for light fur to their offspring. Over several generations, the allele for light fur increased until the frequency reached 95% in the current gene pool.

- (iv) Under what circumstances would the mouse population become a separate species? [1]

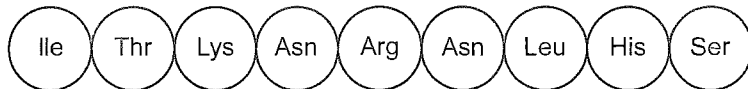
If they could no longer interbreed and produce fertile offspring.

6. A species of mouse *Peromyscus polionotus* found in Florida, USA, has a number of different coat colours. Coat colour in mice is controlled by several genes. Dark fur is produced when the hair producing cells secrete a pigment called eumelanin. A high level of eumelanin is produced when a transmembrane protein called MC1R is stimulated by a hormone.

- (a) The diagram below shows part of the amino acid sequence of MC1R, part of the sequence of nucleotides in the gene for MC1R and how it might change to produce light fur:

Original

Amino acid sequence

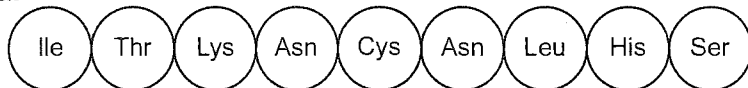


Nucleotide sequence
(allele R)

ATC|ACC|AAA|AAC|CGC|AAQ|CTG|CAQ|TCG

Changed to produce light fur

Amino acid sequence



Nucleotide sequence
(allele C)

ATC|ACC|AAA|AACT|GCA|AAC|CTG|CAQ|TCG

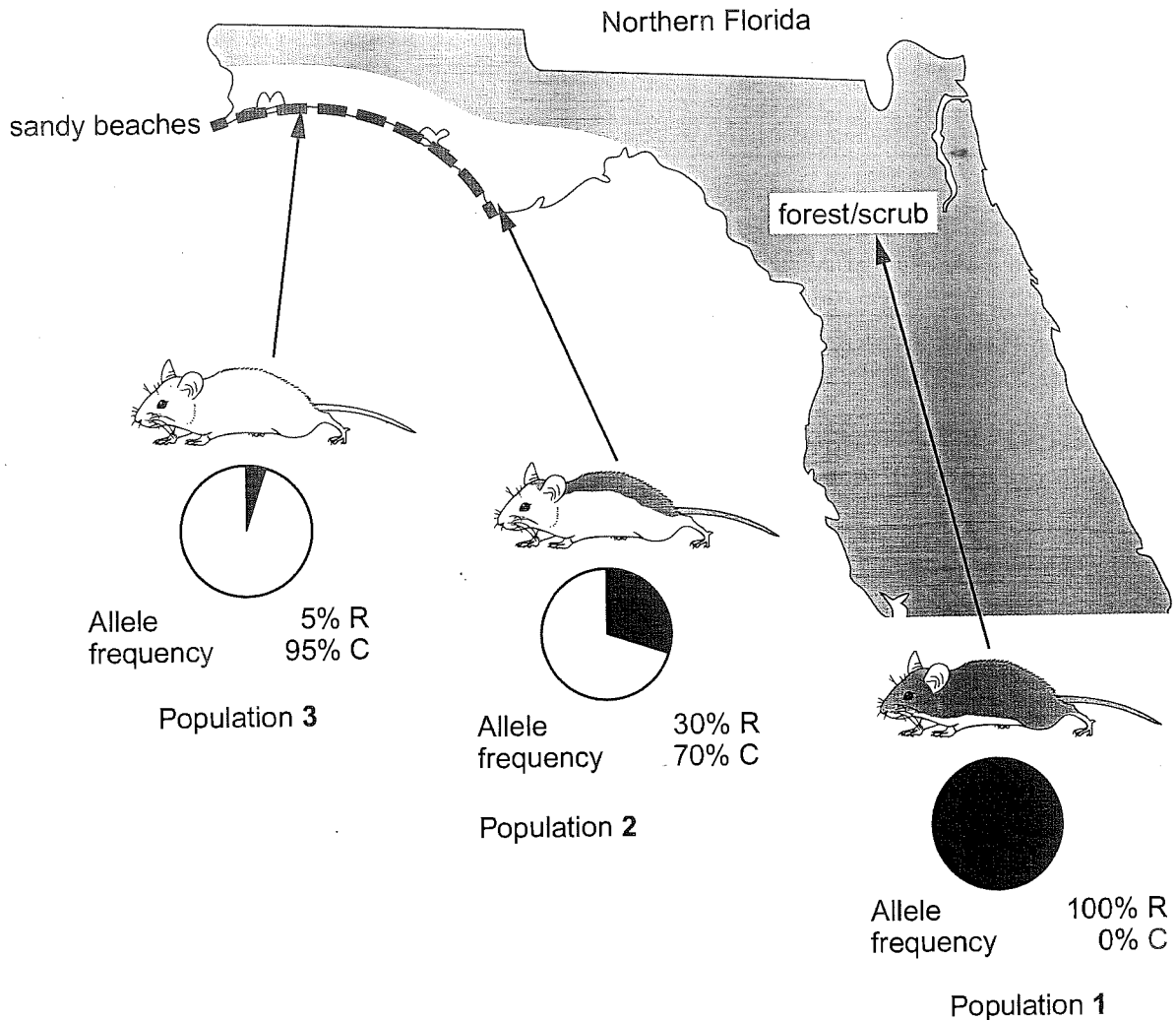
- (i) Describe the change in the gene and the subsequent change in the MC1R molecule. [2]

The fifth triplet code in sequence has changed from 'CAG' to 'TGC' and so the amino acid in sequence has changed from 'Arg' to 'Cys'. This means the polypeptide chain has changed and so the MC1R molecule is a new protein. ~~molecule is no longer stimulated by a hormone so hair~~

- (ii) Using the information provided, explain how this change results in mice with light fur. [2]

The change has resulted in the function of MC1R not operating properly. The MC1R no longer is stimulated by a hormone and so a low level of eumelanin is produced, resulting in the mice having lighter fur.

- (b) This change in the MC1R gene means that there are two alleles, R and C. The map below shows the distribution of the different coloured mice and the relative frequencies of the alleles R and C in each population.



- (i) Use the diagram to suggest how fur colour is related to environmental conditions.

[2]

Fur colour is related to the habitat they occupy.

In population 3, 95% have light fur as they live in

sandy beaches and in population 1, 100% have dark

fur as they live in forest. This is because they

have an advantage by camouflaging in with the surroundings.

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[1]

Genetic drift selection pressure

- (iii) Explain how **Natural Selection** could have caused the relative allele frequency shown in population 3. [4]

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- (iv) Under what circumstances would the mouse population become a separate species? [1]

If they could no longer interbreed and produce fertile offspring.

Examiner
only



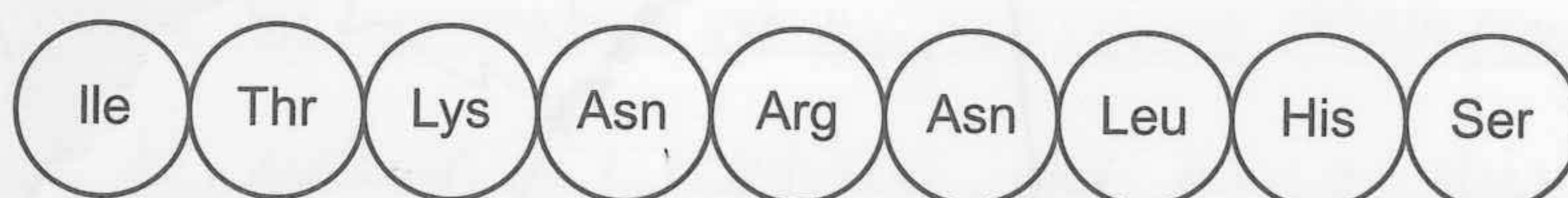
12

6. A species of mouse *Peromyscus polionotus* found in Florida, USA, has a number of different coat colours. Coat colour in mice is controlled by several genes. Dark fur is produced when the hair producing cells secrete a pigment called eumelanin. A high level of eumelanin is produced when a transmembrane protein called MC1R is stimulated by a hormone.

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Amino acid sequence

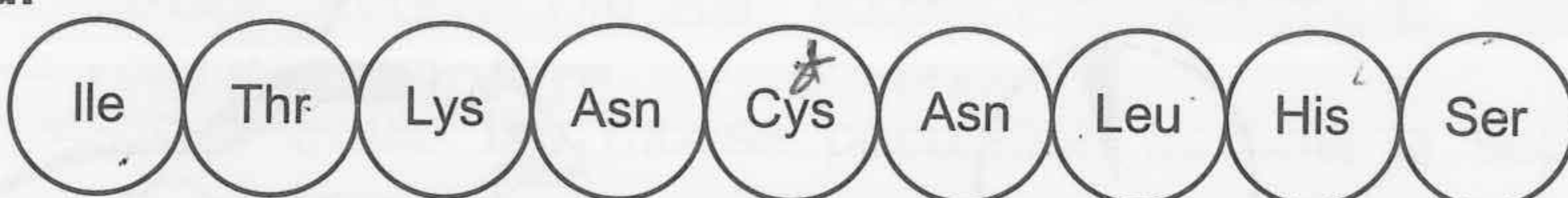


Nucleotide sequence
(allele R)

ATCACC~~AAA~~AACCGCAACCTGCACTCG

Changed to produce light fur

Amino acid sequence



Nucleotide sequence
(allele C)

ATCACC~~AAA~~ACTGCAACCTGCACTCG

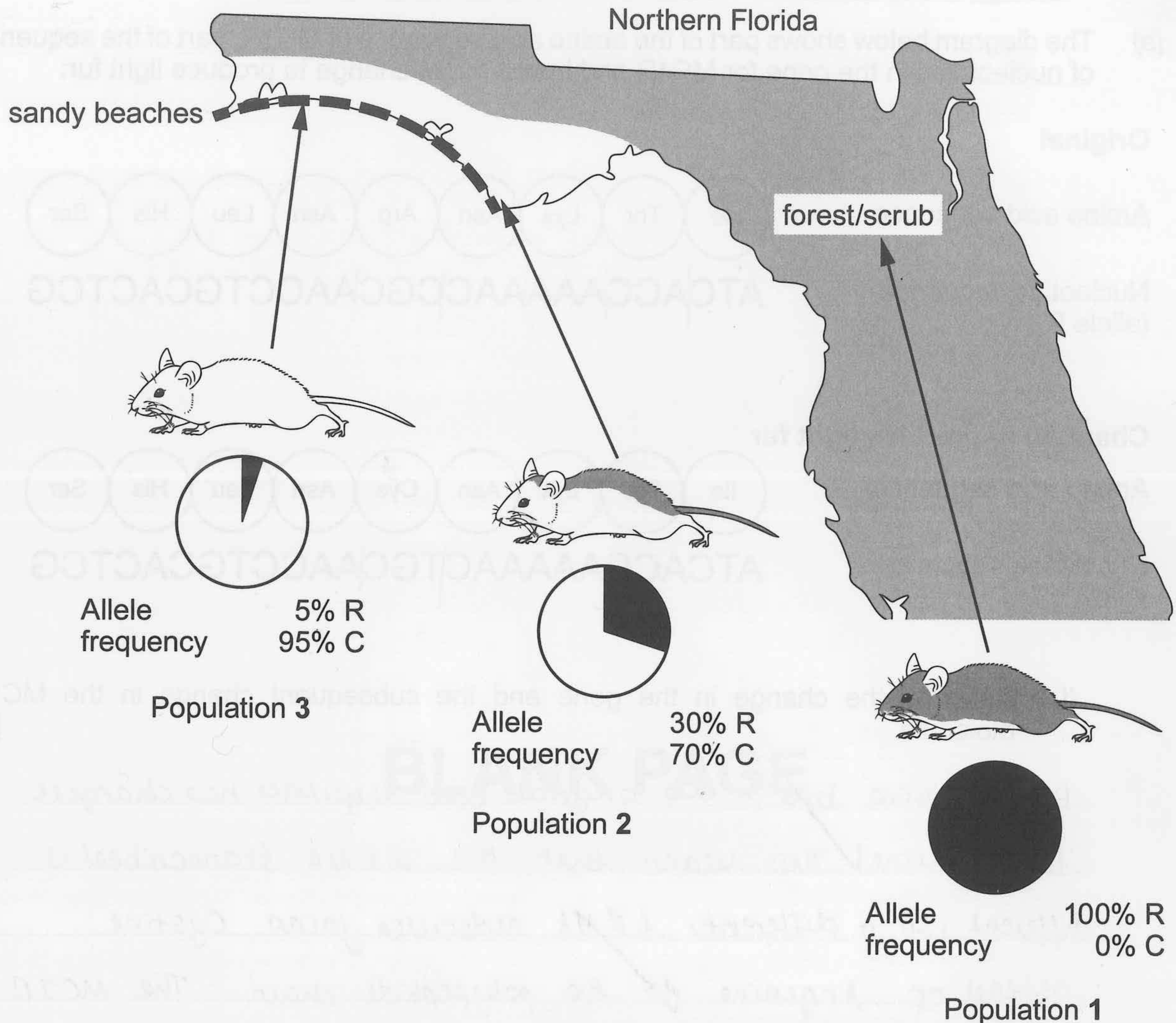
- (i) Describe the change in the gene and the subsequent change in the MC1R molecule. [2]

A Cytosine base in the original base sequence has changed to thymine. This means that the mRNA transcribed is different, so a different tRNA molecule joins Cystine instead of Arginine to the polypeptide chain. The MC1R molecule is therefore also different, as its amino acid sequence is different.

- (ii) Using the information provided, explain how this change results in mice with light fur. [2]

Since the amino acid sequence making up the polypeptide is different, the resulting polypeptide is different, so the complex 3D protein is a different shape. The transmembrane protein therefore cannot secrete high levels of eumelanin, and so the dark pigment is not expressed, leaving the mice with lighter mouse fur.

- (b) This change in the MC1R gene means that there are two alleles, R and C. The map below shows the distribution of the different coloured mice and the relative frequencies of the alleles R and C in each population.



- (i) Use the diagram to suggest how fur colour is related to environmental conditions. [2]

In sandy beaches, the lighter mice have a selective advantage as they are more camouflaged than their predators from the darker mice as they blend in with the light sand. However in forest/scrub, it is a selective advantage to have the allele for dark fur, as this is (continued)

- (ii) Under what circumstance could the difference between the allele frequencies in populations 2 and 3 be explained by **genetic drift**, despite both living on beaches? [1]

The populations are small, so by chance, the allele for dark fur could have been passed on by ten mice in population 3 then population 2.

- (iii) Explain how **Natural Selection** could have caused the relative allele frequency shown in population 3. [4]

The mice show variation, with some having alleles for light fur, and others dark fur. There is a selection pressure of predation on the mice. Those with lighter fur have a selective advantage so are less likely to be killed by predation as they are more camouflaged. They therefore survive to maturity, reproduce and pass on their favourable alleles for light fur to the next generation.

Over time, the allele frequencies change, as a greater proportion of mice with light fur alleles survive, so the allele frequency of light fur increases and that for dark fur decreases.

- (iv) Under what circumstances would the mouse population become a separate species? [1]

When the different demes became so phenotypically different, that they no longer reproduced with each other demes. This is reproductive isolation. They (continued)

6. (b) (iv) They are separate species when the offspring produced by them interbreeding are infertile. They cannot interbreed to produce fertile offspring.

6. A species of mouse *Peromyscus polionotus* found in Florida, USA, has a number of different coat colours. Coat colour in mice is controlled by several genes. Dark fur is produced when the hair producing cells secrete a pigment called eumelanin. A high level of eumelanin is produced when a transmembrane protein called MC1R is stimulated by a hormone.

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Amino acid sequence

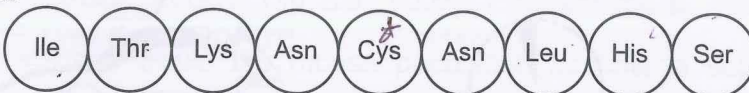


Nucleotide sequence
(allele R)

ATCACCAAAAACCGCAACCTGCACTCG

Changed to produce light fur

Amino acid sequence



Nucleotide sequence
(allele C)

ATCACCAAAAAC TGCAACCTGCACTCG

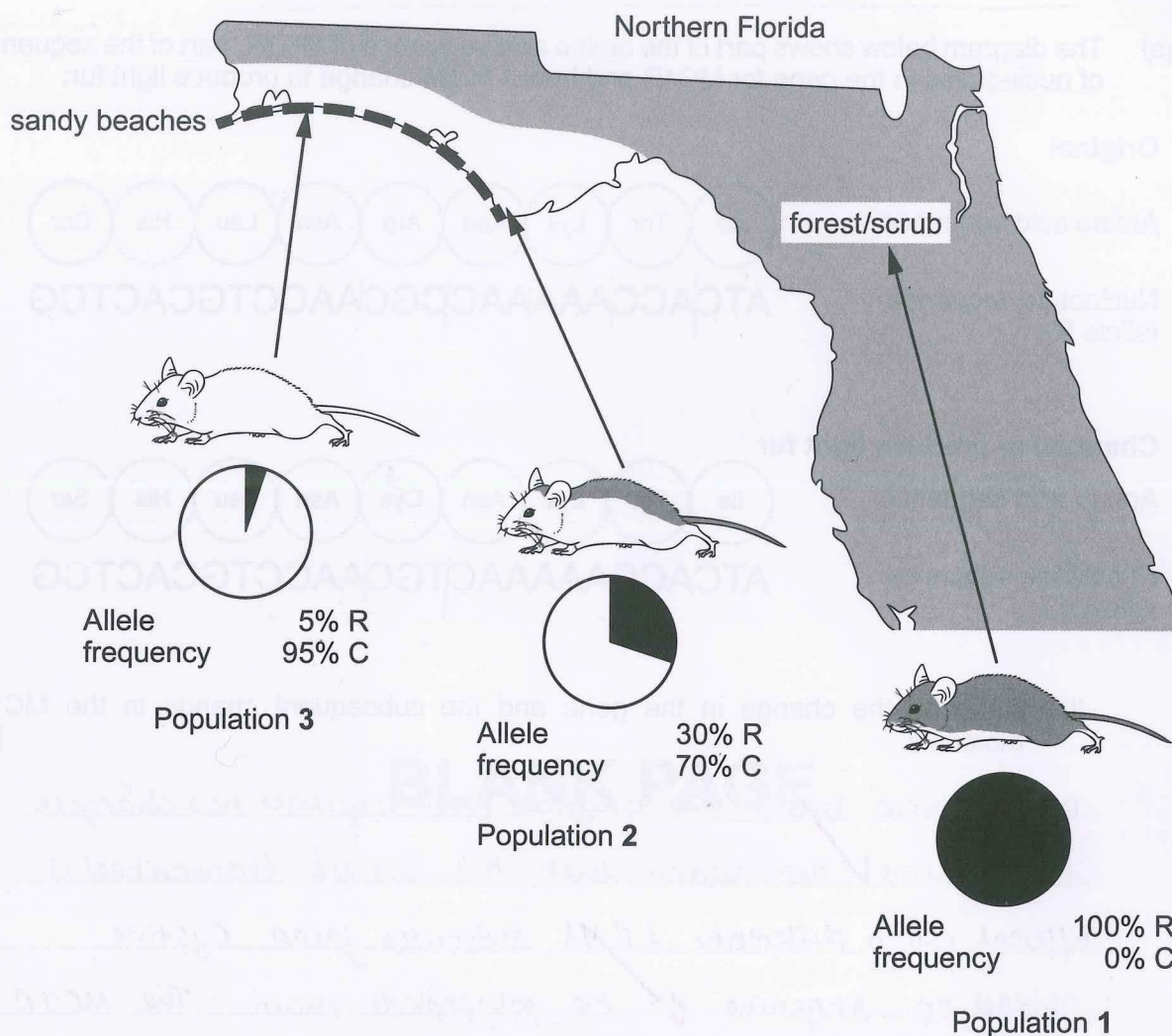
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- (ii) Using the information provided, explain how this change results in mice with light fur. [2]

Since the amino acid sequence making up the polypeptide is different, the resulting polypeptide is different, so the complex 3D protein is a different shape, the transmembrane protein therefore cannot secrete high levels of eumelanin and so the dark pigment is not expressed, leaving the mice with lighter, uncoloured fur.

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[2]

In sandy beaches, the lighter mice have a selective advantage as they are more camouflaged than their predators. However, in forest/scrub, it is a selective advantage to have the allele for dark fur, as this is. (continued)

- (ii) Under what circumstance could the difference between the allele frequencies in populations 2 and 3 be explained by **genetic drift**, despite both living on beaches?

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7. The following is a quotation from an ecological investigation.

“Lowland heaths are high-profile ecosystems for conservation action in England, but they are under threat from invasion by *Betula spp.*, *Pinus sylvestris*, and *Ulex europaeus*.”

[R.J. Mitchel et al. *Journal of Applied Ecology*, 1997, 37, 1426-1444]

- (a) Distinguish between primary succession and secondary succession.

[2]

.....

.....

.....

.....

The authors studied a number of heathland sites in Dorset including Arne, Blackhill, and Higher Hyde, where succession to one or another of the three species had taken place. The data below are based on the paper but have been simplified and modified for illustrative purposes.

The successional stages in the study were named according to the dominant invasive species; **plus B**, where *Betula spp.* was the invader, **plus PS**, where *Pinus sylvestris* was the invader and **plus U**, where *Ulex europaeus*, was the invader.

- (b) The group examined changes in soil chemistry from the original heath stage. Some of their results are summarised in the table below:

soil chemical property	value by succession stage			
	original heath	plus B	plus PS	plus U
pH				
Arne	3.63	4.01	3.60	3.63
Blackhill	3.52	3.66	3.48	3.54
Higher Hyde	3.53	5.06	3.51	3.47
mean	3.56	4.24	3.53	3.55
phosphorus μgPg^{-1}				
Arne	2.41	3.85	2.69	3.16
Blackhill	4.15	4.91	3.79	4.55
Higher Hyde	5.08	5.35	3.55	4.76
mean	3.88	4.70	3.34	4.16
nitrate/nitrite μgNg^{-1}				
Arne	0.51	0.65	0.59	1.16
Blackhill	0.84	0.88	0.97	2.31
Higher Hyde	0.69	0.98	1.17	3.64
mean	0.68	0.84	0.91	2.37

- (i) What do the pH values tell us about the soil in all stages in all sites? [1]

.....

- (ii) Use **mean** values from the table above to compare **three** changes to soil chemistry following invasion by *Betula spp.* with the changes following invasion by *Ulex europaeus*. [3]

pH

.....

phosphorus

.....

nitrate/nitrite

.....

- (c) The table below shows changes to the vegetation in the successional stages:

Species (by successional stage)	% cover of species (by site)		
	Arne	Blackhill	Higher Hyde
original heath			
<i>Calluna vulgaris</i>	62.0	66.1	88.2
<i>Erica cinerea</i>	22.4	25.7	2.6
<i>Erica tetralix</i>	9.9	2.6	9.9
<i>Cladonia portentosa</i>	8.5	0	0.5
plus B			
<i>Betula spp.</i>	18.9	11.7	16.5
<i>Agrostis curtisii</i>	0.0	53.6	0.0
<i>Pteridium aquilinum</i>	25.2	7.5	1.6
<i>Calluna vulgaris</i>	0.0	0.0	0.4
plus PS			
<i>Pinus sylvestris</i>	36.2	38.2	
<i>Pteridium aquilinum</i>	0.3	24.7	
<i>Erica cinerea</i>	0.0	0.0	
<i>Calluna vulgaris</i>	0.0	0.0	
plus U			
<i>Ulex europaeus</i>	87.0	75.3	79.0
<i>Calluna vulgaris</i>	14.7	5.8	7.2
<i>Erica cinerea</i>	1.5	11.3	4.3
<i>Erica tetralix</i>	0.1	0.3	0.3

- (i) Which invading species has least impact on the vegetation on the original heathland? [1]

.....

- (ii) With reference to the data for **plus B** in both tables suggest a mechanism by which changes to vegetation occur during succession. [2]

.....

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(d) Sixteen years later some of these successions have reached their natural conclusions.

- (i) What name is given to the group of organisms that inhabit the ecosystem at the end of successional change? [1]

.....

- (ii) What usually happens to species diversity as succession proceeds? [1]

.....

- (iii) Using **named** species from the table in part (c) explain why conservationists in Dorset are taking steps to prevent **plus B** and **plus PS** succession in heathland, but are less worried about type **plus U** succession. [2]

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[R.J. Mitchel et al. *Journal of Applied Ecology*, 1997, 37, 1426-1444]

(a) Distinguish between primary succession and secondary succession.

[2]

Primary Succession is bare rock that has no passed life. Secondary Succession is ^{re}introducing organism back after a previous forest fire or deforestation

The authors studied a number of heathland sites in Dorset including Arne, Blackhill, and Higher Hyde, where succession to one or another of the three species had taken place. The data below are based on the paper but have been simplified and modified for illustrative purposes.

The successional stages in the study were named according to the dominant invasive species; **plus B**, where *Betula spp.*, was the invader, **plus PS**, where *Pinus sylvestris* was the invader and **plus U**, where *Ulex europaeus*, was the invader.

- (b) The group examined changes in soil chemistry from the original heath stage. Some of their results are summarised in the table below:

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mean	0.68	0.84	0.91	2.37

- (i) What do the pH values tell us about the soil in all stages in all sites? [1]

it was ~~high~~ acidic

- (ii) Use **mean** values from the table above to compare **three** changes to soil chemistry following invasion by *Betula spp.* with the changes following invasion by *Ulex europaeus*. [3]

pH more acidic

phosphorus lowered phosphorus

nitrate/nitrite increased nitrate/nitrite levels.

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Species (by successional stage)	% cover of species (by site)		
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- (i) Which invading species has least impact on the vegetation on the original heathland? [1]

plus U

- (ii) With reference to the data for **plus B** in both tables suggest a mechanism by which changes to vegetation occur during succession. [2]

depletion of nutrients
and build up of excretion

(d) Sixteen years later some of these successions have reached their natural conclusions.

- (i) What name is given to the group of organisms that inhabit the ecosystem at the end of successional change? [1]

oak trees

- (ii) What usually happens to species diversity as succession proceeds? [1]

increases

- (iii) Using **named** species from the table in part (c) explain why conservationists in Dorset are taking steps to prevent **plus B** and **plus PS** succession in heathland, but are less worried about type **plus U** succession. [2]

Percentage of species drop
dramatically when plus B and
plus PS successions by plus U
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(a) Distinguish between primary succession and secondary succession.

[2]

Primary succession is the colonisation of land that has never been inhabited like a bare rock. Secondary succession is the colonisation of land which has previously been inhabited but life has been stopped ~~the~~ again. for example by a fire.

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- (i) What do the pH values tell us about the soil in all stages in all sites? [1]

tell us how much nitrogen is available in the soil.

- (ii) Use **mean** values from the table above to compare **three** changes to soil chemistry following invasion by Betula spp. with the changes following invasion by Ulex europaeus. [3]

pH the invasion of Betula spp. made the soil more alkaline from the original heath, whereas Ulex the reactivity stayed the same.

phosphorus The phosphorus concentration in the soil increased with Betula spp. and increased with Ulex. However it increased more with Betula spp.

nitrate/nitrite The nitrate concentration decreased with the invasion of plus B but increased with the invasion of plus U.

- (c) The table below shows changes to the vegetation in the successional stages:

Species (by successional stage)	% cover of species (by site)		
	Arne	Blackhill	Higher Hyde
original heath			
<i>Calluna vulgaris</i>	62.0	66.1	88.2
<i>Erica cinerea</i>	22.4	25.7	2.6
<i>Erica tetralix</i>	9.9	2.6	9.9
<i>Cladonia portentosa</i>	8.5	0	0.5
plus B			
<i>Betula spp.</i>	18.9	11.7	16.5
<i>Agrostis curtisii</i>	0.0	53.6	0.0
<i>Pteridium aquilinum</i>	25.2	7.5	1.6
<i>Calluna vulgaris</i>	0.0	0.0	0.4
plus PS			
<i>Pinus sylvestris</i>	36.2	38.2	
<i>Pteridium aquilinum</i>	0.3	24.7	
<i>Erica cinerea</i>	0.0	0.0	
<i>Calluna vulgaris</i>	0.0	0.0	
plus U			
<i>Ulex europaeus</i>	87.0	75.3	79.0
<i>Calluna vulgaris</i>	14.7	5.8	7.2
<i>Erica cinerea</i>	1.5	11.3	4.3
<i>Erica tetralix</i>	0.1	0.3	0.3

- (i) Which invading species has least impact on the vegetation on the original heathland? [1]

~~Pinus sylvestris~~ PWS PS

- (ii) With reference to the data for **plus B** in both tables suggest a mechanism by which changes to vegetation occur during succession. [2]

first the *Betula spp.* would invade the area, making the soil more alkaline. then *Pteridium aquilinum* would grow, then *Agrostis curtisii* then *Calluna vulgaris* would start to colonise the area.

(d) Sixteen years later some of these successions have reached their natural conclusions.

- (i) What name is given to the group of organisms that inhabit the ecosystem at the end of successional change? [1]

climax community

- (ii) What usually happens to species diversity as succession proceeds? [1]

species diversity increases

- (iii) Using **named** species from the table in part (c) explain why conservationists in Dorset are taking steps to prevent **plus B** and **plus PS** succession in heathland, but are less worried about type **plus U** succession. [2]

Because plus U has already colonised the area & and has had little effect on the % cover of species so far however plus B and plus PS are still in the early stages of colonisation and if their numbers grow then plus B *Calluna vulgaris* would be in direct competition with the original site *Calluna vulgaris*.

7. The following is a quotation from an ecological investigation.

"Lowland heaths are high-profile ecosystems for conservation action in England, but they are under threat from invasion by *Betula* spp., *Pinus sylvestris*, and *Ulex europaeus*."

[R.J. Mitchel et al. *Journal of Applied Ecology*, 1997, 37, 1426-1444]

(a) Distinguish between primary succession and secondary succession.

[2]

Primary succession is the colonisation of land that has never been inhabited like a bare rock. Secondary succession is the colonisation of land which has previously been inhabited by but life has been stopped ~~the~~ ~~the~~ for example by a fire.

The authors studied a number of heathland sites in Dorset including Arne, Blackhill, and Higher Hyde, where succession to one or another of the three species had taken place. The data below are based on the paper but have been simplified and modified for illustrative purposes.

The successional stages in the study were named according to the dominant invasive species; plus B, where Betula spp. was the invader, plus PS, where Pinus sylvestris was the invader and plus U, where Ulex europaeus, was the invader.

- (b) The group examined changes in soil chemistry from the original heath stage. Some of their results are summarised in the table below:

soil chemical property	value by succession stage			
	original heath	plus B	plus PS	plus U
pH				
Arne	3.63	4.01	3.60	3.63
Blackhill	3.52	3.66	3.48	3.54
Higher Hyde	3.53	5.06	3.51	3.47
mean	3.56	4.24	3.53	3.55
phosphorus μgPg^{-1}				
Arne	2.41	3.85	2.69	3.16
Blackhill	4.15	4.91	3.79	4.55
Higher Hyde	5.08	5.35	3.55	4.76
mean	3.88	4.70	3.34	4.16
nitrate/nitrite μgNg^{-1}				
Arne	0.51	0.65	0.59	1.16
Blackhill	0.84	0.88	0.97	2.31
Higher Hyde	0.69	0.98	1.17	3.64
mean	0.68	0.84	0.91	2.37

- (i) What do the pH values tell us about the soil in all stages in all sites? [1]

tell us how much nitrogen is available in the soil.

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(d) Sixteen years later some of these successions have reached their natural conclusions.

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- (iii) Using **named** species from the table in part (c) explain why conservationists in Dorset are taking steps to prevent **plus B** and **plus PS** succession in heathland, but are less worried about type **plus U** succession. [2]

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(a) Distinguish between primary succession and secondary succession.

[2]

Primary succession occurs when a habitat is initially colonised by species, starting with pioneers, and where the habitat is considered bare ground in that it has never previously supported an ecosystem. Secondary succession occurs when species re-inhabit an area after they were
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The authors studied a number of heathland sites in Dorset including Arne, Blackhill, and Higher Hyde, where succession to one or another of the three species had taken place. The data below are based on the paper but have been simplified and modified for illustrative purposes. The successional stages in the study were named according to the dominant invasive species; **plus B**, where *Betula spp.*, was the invader, **plus PS**, where *Pinus sylvestris* was the invader and **plus U**, where *Ulex europaeus*, was the invader.

- (b) The group examined changes in soil chemistry from the original heath stage. Some of their results are summarised in the table below:

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- (i) What do the pH values tell us about the soil in all stages in all sites? [1]

All soils are acidic

- (ii) Use **mean** values from the table above to compare **three** changes to soil chemistry following invasion by *Betula spp.* with the changes following invasion by *Ulex europaeus*. [3]

pH plus B is able to increase the pH of the soil, making the soil less acidic than before its invasion. more acidic than plus U, which makes the soil

phosphorus plus B is able to increase the phosphorus concentration of the soil more than plus U

nitrate/nitrite plus B increase the nitrate/nitrite concentration of the soil less so than plus U, which increases this concentration by a greater amount than plus B

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- (i) Which invading species has least impact on the vegetation on the original heathland? [1]

Ulex europaeus plus U has the least impact, as most of the original species are still present.

- (ii) With reference to the data for **plus B** in both tables suggest a mechanism by which changes to vegetation occur during succession. [2]

Plus B is able to increase both the pH levels and phosphorus concentration of the soil to such levels that the plant species *Erica cinerea*, *Erica tetralix* and *Cladonia portentosa* are able to survive, causing the death of these species and the subsequent
* see additional answer booklet

(d) Sixteen years later some of these successions have reached their natural conclusions.

- (i) What name is given to the group of organisms that inhabit the ecosystem at the end of successional change? [1]

Climax Community

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Plus U succession only removes *Cladonia portentosa* via plus U succession, maintaining *Erica cinerea* and *Erica tetralix* along with *Calluna vulgaris* in the ecosystem, whereas plus B and plus PS remove more species, including *Erica tetralix* in both, causing a greater change.

* see additional
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7.(c) Wiped out due to natural disaster or human impacts. This takes the
Continued form of seeds that survived germinating to form new plants and
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Continued acidic and more concentrated phosphorus soils, causing the vegetational
change during succession *seen*

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