Module Code: BIO00009C

Examination Candidate Number: __________
Desk Number: __________

BSc Degree Examinations 2018-9

Department:
BIOLOGY

Title of Exam:
Genetics and Evolution

Time Allowed:
1.5 hours

Marking Scheme:
Total marks available for this paper: 50
The marks available for each question are indicated on the paper

Instructions:
Answer all questions in the spaces provided on the examination paper

For marker use only:  
Office use only:

<table>
<thead>
<tr>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>Total as %</th>
</tr>
</thead>
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</tbody>
</table>

DO NOT WRITE ON THIS BOOKLET BEFORE THE EXAM BEGINS
DO NOT TURN OVER THIS PAGE UNTIL INSTRUCTED TO DO SO BY AN INVIGILATOR
1. Wild-type flowers from *Antirrhinum majus* are red. Seven white flowered mutants were identified by mutagenesis. The mutants were crossed to each other and to a red flowered wild-type strain (WT). The flower colour of the progeny was recorded and presented in the table below.

<table>
<thead>
<tr>
<th></th>
<th>mutant a</th>
<th>mutant b</th>
<th>mutant c</th>
<th>mutant d</th>
<th>mutant e</th>
<th>mutant f</th>
<th>mutant g</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
</tr>
<tr>
<td>mutant a</td>
<td>white</td>
<td>white</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
</tr>
<tr>
<td>mutant b</td>
<td>white</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
</tr>
<tr>
<td>mutant c</td>
<td>white</td>
<td>red</td>
<td>white</td>
<td>white</td>
<td>white</td>
<td>red</td>
<td></td>
</tr>
<tr>
<td>mutant d</td>
<td>white</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td></td>
</tr>
<tr>
<td>mutant e</td>
<td>white</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td>red</td>
<td></td>
<td></td>
</tr>
<tr>
<td>mutant f</td>
<td></td>
<td>white</td>
<td>red</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>mutant g</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>white</td>
</tr>
</tbody>
</table>

a) Why were all the mutant lines crossed to the wild type line? (1 mark)

To test whether or not the mutations were recessive

b) Write down the complementation groups you have identified. (4 marks)

(f e c)
(b a)
(g)
(d)

c) How many genes have been identified with roles in production of red flowers? (1 mark)

four

In the exam there was an error in the table above, which created some ambiguity about the complementation groups that could be derived. A marking scheme was applied that awarded credit for possible complementation groups taking into account the ambiguity due to the error. Where students lost marks it was mostly likely because they forgot to include g and d as complementation groups. The average mark for this question was 4.8 out of 6, which was a very good performance.
Complementation were introduced in lecture 2, and practiced in each of the three workshops I ran.

The learning outcome that was tested in the this question was “Carry out a complementation test and interpret the findings”.

2. *Mimulus cardinalis* produced red flowers. Several flower colour mutants were identified in a mutagenesis screen. One recessive mutant produced yellow flowers and another produced orange flowers. The F1 progeny from a cross between these lines produced red flowers. The F1 progeny were then self-pollinated. The F2 generation produced red, yellow and orange flowered plants in a ratio of 9:4:3, respectively.

a) Provide an explanation for the 9:4:3 ratio in the F2 generation.

(1 mark)

This is a modified 9:3:3:1 ratio. Both single mutants and the double mutant produce yellow flowers.

b) Outline a possible biosynthetic pathway that leads to the production of wild-type red pigment. Provide an explanation for your answer.

(4 marks)

There are several possible explanations. This is one possible answer. The two genes identified in the mutagenesis screen are likely to act in the biosynthetic pathway that produces the wild-type red pigment (1 mark). One gene encodes an enzyme that performs a modification to a yellow pigment to an orange pigment (1 mark). The second gene encodes an enzyme that converts the orange pigment into the wild-type red pigment (1 mark). Hence the double mutant has a yellow phenotype and the yellow gene acts upstream of the orange gene. (1 mark)

\[
\text{yellow} \rightarrow \text{orange} \rightarrow \text{red}
\]

This question was answered very well with an average mark of 3.2 out of 5. 25% of students got full marks on this question, and another 30% achieved 4 out of 5. Students who lost one mark often failed to give a complete answer to part a although they did very well on part b. Other students lost marks because they didn't demonstrate much knowledge or understanding of the question even though we practiced this question in all three of the workshops I
3. In *Petunia*, the chalcone synthase (CHS) enzyme is required for the biosynthesis of a purple pigment seen in flowers. After a mutagenesis screen it was found that plants homozygous for a mutation in the *CHS-1* gene showed reduced CHS enzyme activity, but produced purple flowers. A modifier mutagenesis screen was carried out, and second gene, *CHS-2*, was identified. Plants homozygous for *chs-2* also had reduced enzyme activity and produced purple flowers. Double mutants, homozygous for *chs-1* and *chs-2* produced white flowers despite residual levels of the CHS enzyme.

1) What type of genetic modifier is *chs-2*? \(1\) mark

An enhancer

2) Provide an explanation for your answer. \(1\) mark

The phenotype of the double mutant is more extreme (produces white flowers) than either of the two single mutants (which produce purple flowers)

3) What does this suggest about the levels of the CHS enzyme in wild-type plants? \(1\) mark

That the level of enzyme activity is well above the level required for a wild-type phenotype (purple flowers). The level in either single mutant is still above a threshold where a mutant phenotype (white flowers) might be detected.
4) Provide an explanation for the residual enzyme levels in *chs-1; chs-2* double mutants. *(2 mark)*

This may indicate that there is a third gene that also encodes the CHS enzyme (e.g. CHS-3)

Question 3 was harder than Q1 and Q2. It was another problem question similar to those we practised in all of the three workshops I ran. The average mark for this question was 2.6 out of 5. 20% of student achieved full marks, but other students found this question harder. About 30% of students managed a mark of 3 or 4 out of 5. The most common mistake was that students didn’t not know what meant by a genetic modifier, or chose the wrong modifier for this example.

Genetic modifiers were introduced in lecture 2 and we practised modifier questions in each of the three workshops I ran.

Learning outcome tested in this question: “Explain how a modifier mutagenesis screen can be used to identify functionally related genes”

4. a) Draw a diagram to explain how the ABC genes determine floral organ identity in the flower. *(2 marks)*

![Diagram of ABC gene functions]

b) Describe the floral phenotype of a ‘c class’ homeotic mutant. *(1 mark)*

‘c class’ mutants have flowers that lack stamens and carpels – these organs are replaced by petals and sepals respectively (1 mark). ‘c class’ mutants have sepals, petals, petals and sepals (1 mark).

c) What evidence demonstrates that the activities of ‘a’ and ‘c’ function genes are mutually antagonistic? *(2 marks)*

The ABC model for flower development shows that there are three regulators
for organ identity. These functions overlap to generate distinct combinations in each whorl. The phenotype of a and c function mutants shows that the ‘a’ and ‘c’ activities must be mutually antagonistic (1 mark). When ‘a’ is missing, the domain of ‘c’ expands and vice versa (1 mark).

The average mark for this question was 2.6 out of 5. 30% of students achieved 3 out 5. Full marks appeared difficult to achieve with only about 10% of students getting 5 out of 5. Typically students could explain the ABC model and answer part a and b, but the most common mistakes were in part c where students did not provide a complete answer.

The ABC model was introduced and explained in lecture 1. Learning outcome being tested: “Describe the ABC model and explain how mutant phenotypes reveal the genes and proteins that regulate flower development”.

5. Briefly describe the genetic evidence that modern humans encountered their recent evolutionary ancestors. (5 marks)

Humans encountered Neanderthals and Denisovans and interbred (1 mark). Genome sequences from humans, neanderthals and denisovans have been completed (1 mark).
Every non-african has some DNA derived from Neanderthals (1 mark). Melanesians also have DNA derived from Denisovans (1 mark). Sequences and genes from our archaic ancestors have been introgressed into the human genome (1 mark).

This question appears to have been the hardest question I set. The average mark for this question was 2.3 out of 5. This was disappointing given the similarity between the learning outcome and the question (see learning outcome below), and the explanation in these lectures about the learning outcomes would be assessed.

The topic for this question was discussed in lecture 12. The learning outcome tested was: “ Describe and explain evidence for the encounters humans had with recent evolutionary ancestors (Neanderthals and Denisovans)”

6. In a population of 1000 rats, 50 have grey fur, 260 have white fur and 690 have black fur. These phenotypes are caused by 2 alleles: a and A. AA genotypes
result in a white fur phenotype, and aa genotypes result in a black fur phenotype.

a) What are the genotype frequencies in this population? (1 mark)

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>260/1000  = 0.26</td>
</tr>
<tr>
<td>Aa</td>
<td>50/1000    = 0.05</td>
</tr>
<tr>
<td>aa</td>
<td>690/1000   = 0.69</td>
</tr>
</tbody>
</table>

b) What are the allele frequencies in this population? (1 mark)

\[
A: \frac{2 \times 0.26 + 0.05}{2} = 0.285 \\
a: \frac{2 \times 0.69 + 0.05}{2} = 0.715 \\
\]

c) Is this population in Hardy-Weinberg equilibrium? (2 marks)

\[
p = 0.285 \\
q = 0.715 \\
2pq = 0.41 \neq 0.05 \\
\text{The population is not in H-W equilibrium}
\]

7. A population of rabbits have pointed ears or floppy ears. This trait is controlled by 2 alleles A and a. AA and Aa genotypes result in pointed ear phenotype and aa genotypes result in floppy ear phenotype.

a) What can we say about the dominance relationship between alleles A and a? (1 mark)

A is dominant to a as Aa genotypes exhibit the same phenotype as AA genotypes. (1 mark)

b) The rabbit population consists of 1500 individuals. The frequency of pointed ear rabbits is 0.8. Assuming this population is in Hardy-Weinberg equilibrium, how many rabbits are homozygous for A? (2 marks)

\[
q^2 = 1-0.8 = 0.2 \\
q = 0.447 \\
p = 1-q = 0.553 \\
\]
p^2 = 0.306 (1 mark)
number of AA individuals:
1500*p^2 = 459 rabbits (1 mark)

c) How many rabbits are heterozygotes? (1 mark)

number of Aa individuals:
1500*2*p*q = 742 rabbits (1 mark)

8. What is a bottleneck event and how does it affect allele frequencies? (2 marks)

A bottleneck event is the sharp reduction in the size of a population. This can cause loss of rare alleles, reducing the overall variation in the gene pool of a population. (2 marks)

9.

a) Suggest two ways how life on Earth might have risen. (1 mark)

At submarine Deep-Sea Vents AND Was brought here from space (Panspermia) (1 mark) or other sensible suggestions

b) What process might ‘Snowball Earth’ have triggered? (1 mark)

Mass extinction or adaptive radiation (1 mark)

c) What term is used to describe the evolution of complex cells with mitochondria and/or chloroplasts? (1 mark)

Endosymbiosis (1 mark)

d) List two major challenges plants had to overcome when colonizing land. (2 marks)

For example, (each 1 mark):
- Desiccation resistance
- Support (lignin)
- Resistance to UV radiation
- Resistance to oxidation
- Reproduction in non-aquatic environment

Feedback: These questions were answered well in general. With b), ‘Snowball Earth’ question, some people described this process instead of the process it is thought to have triggered (mass extinction followed by adaptive radiation). Moreover, with d), ‘Adaptation to land’ question some people suggested predation, which was an important force of selection but appeared only after the land had been colonised.

10. List three major transitions in evolution and suggest what benefits they might have offered? (6 marks)

For example, (each transition and related benefit 1 mark each)

1) From replicating molecules to populations of molecules (1 mark); ‘Independent evolutionary unit, i.e., protocell’ (1 mark)
2) From independent replicators to chromosomes (1 mark); ‘Genome with multiple functions’ (1 mark)
3) From RNA to DNA (1 mark); ‘From single molecule to specialized molecules’ (1 mark)
4) From Prokaryotes to Eukaryotes (1 mark); ‘More efficient metabolism’ (1 mark)
5) From asexual reproduction to sexual reproduction (1 mark); ‘Faster evolution via recombination’ (1 mark)
6) From protists to multicellular animals, plants, fungi (1 mark); ‘Specialization to different niches’ (1 mark)
7) From solitary individuals to colonies (eusociality) (1 mark); ‘Division of labour’ (1 mark)
8) From primate societies to human societies (1 mark); ‘Sociocultural, non-genetic storage & transfer of information’ (1 mark)

Feedback: This question was answered very well and most of the people were able to describe three major transitions and their potential benefits in sufficient detail. Occasionally ‘Evolutionary transitions’ were mistaken for some sort of ‘mobility’ in terms of colonization of land or evolution of movement and migration.

11. By using one real-life example, describe how contemporary evolution can change species rapidly? (3 marks)
For example:

Evolution of antibiotic resistance (3 marks)

Bacteria can evolve fast due to inherently large population sizes and high \textit{de novo} mutation frequency (1 mark). This leads to high genetic variation within bacterial populations (1 mark). Antibiotics create strong selection that favours rare mutants that are resistant to antibiotics and when the antibiotic selection is continued, resistant mutants can increase in proportion in the population that becomes dominated by these resistant genotypes (1 mark).

OR

Co-evolutionary arms race (3 marks)

Co-evolutionary arms race is a struggle between competing sets of co-evolving genes, traits, or species (1 mark), that develop adaptations and counter-adaptations against each other, resembling an arms race (1 mark). Co-evolutionary arms race can lead to escalation of traits in terms of ever-increasing host resistance and parasite infectivity (1 mark).

OR

Evolution of Influenza (3 marks)

Viruses can evolve either via antigenic shift (0.5 marks) or antigenic drift (0.5 marks). Antigenic shift is the process by which two or more different strains of viruses, combine to form a new subtype having a mixture of the surface antigens of the two or more original strains (1 mark). Antigenic drift is a mechanism for variation that leads to accumulation of mutations within the genes that code for antibody-binding sites. This results in a new strain of virus particles which cannot be inhibited as effectively by the antibodies that were originally targeted against previous strains (1 mark).

Feedback: Most commonly described example was the evolution of antibiotic resistance using the MEGA plate example followed by Influenza evolution and host-parasite coevolution examples. Marks were also given for other rapid evolution examples such as speciation in Darwin finches and industrial melanism in Lepidoptera when explained in sufficient detail. While most of the
people were able to explain the process of selection as a change in allele frequencies, people often failed to describe how the genetic variation is born in the first place (mutations and/or recombination). Most of the answers scored at least one mark or higher.

Learning outcome addressed:

- Describe and explain the main processes that lead to evolutionary change, and employ simple population genetics and phylogenetic methods to illustrate them
- Recall major events and processes that have shaped the diversity of living organisms and the evidence for them