Module Code: BIO00012H

Examination Candidate Number: __________

Desk Number: __________

BSc Degree Examinations 2018-9

Department:
BIOLOGY

Title of Exam:
Ecological genetics

Time Allowed:
2 hours

Marking Scheme:
Total marks available for this paper: 100
Section A: Short Answer / Problem / Experimental Design questions (50 marks)
Section B: Essay question (marked out of 100, weighted 50 marks)

Instructions:
Section A: Answer all questions in the spaces provided on the examination paper
Section B: Answer either question A or B. Write your answer on the separate paper provided and attach it to the back of the question paper using the cable tie provided.
SECTION A: Short Answer / Problem / Experimental Design questions

Answer all questions in the spaces provided

Mark total for this section: 50

Question 1

The Alpine Rock-Cress *Arabis alpina* is a short-lived alpine perennial that is found at altitudes between 800 m and 3,100 m in the French Alps, which is an unusually wide altitudinal range. Within this altitudinal range many genetically differentiated populations exist. The plants reproduce mostly by selfing.

a) Explain which two processes might allow *A. alpina* to persist across such a wide range of environmental conditions. (3 marks)

At different locations the plants have to cope with different and potentially extreme environmental conditions. One possible process might be phenotypic plasticity, i.e. the ability of a genotype to express different phenotypes depending on environmental conditions (1 mark). This would allow the plant to survive and reproduce under wide range of conditions (1 mark). Alternatively, local selection may lead to local genotypes being adapted to particular environments (local adaptation) (1 mark). [These genotypes will then have poor performance at other locations.]

Comments on limited gene flow facilitating local adaptation will also be given credit (max. 1 mark).

This question was generally answered well and many students got full marks.

The figure below shows the results of an experiment where seeds from six different populations (denoted by different colours) were sown in two experimental gardens (Vercors and Lautaret). The original populations were located at different altitudes, and are arranged from origins at low altitude (dark red) to high altitude (dark blue) in the figure legend. Increasing altitude correlates with lower average temperatures and shorter growing seasons.

The following parameters were measured:

**Morphotype**: ranging from 0 = not compact, to 2 = compact; **Total Fruit Length** (TFL): the combined length of all fruit on a plant (mm); **Reproductive Height** (H. repro.) in mm.

The Vercors experimental garden is at lower altitude and has a higher average temperature than the Lautaret garden.
b) Describe the main results of the experiment, focusing on a comparison of the populations at the two experimental locations. (6 marks)

The three traits show different responses to the two experimental gardens (1 mark). All populations have higher TFL and reproductive height at Vercors compared to Lautaret (1 mark), and for TFL the difference is more extreme for populations that come from the lower altitude populations than for populations from higher altitudes (1 mark). In Lautaret, there is little variation between the populations for these two traits, whereas it is more variable at Vercors (1 mark).

The pattern is more complex for morphotype. The populations from higher altitudes have on average more compact morphotypes than the lower altitude populations (1 mark), and lower altitude populations tend to have even less compact morphotypes at Vercors, whereas the opposite is found for the high altitude populations (1 mark).

Many students answered this question well and with a good level of detail. A significant number of students did not describe the data but started to interpret the patterns (e.g. whether there is evidence for local adaptation). This usually meant that the results were not described in sufficient detail, and hence marks were lost. Interpretations relevant to part (c) were given marks there.

c) Considering the experimental result, discuss how the two processes that you identified in (a) contribute to the persistence of *A. alpina* at different altitudes. (5 marks)

Reproductive height and TFL predominantly show phenotypic plasticity (1 mark), although GAL and PIC appear to have lost much of this plasticity (1 mark) possibly as a result of local adaptation (1 mark). There appears to be significant local adaptation in terms of morphotype (1 mark) with some adaptive phenotypic plasticity (low altitude populations become more compact at the higher altitude...
d) How might the predicted rise in average temperatures affect the two high elevation populations GAL and PIC? (2 marks)

The GAL and PIC population appear to have lost some phenotypic plasticity which might make it more difficult to cope with higher temperatures (1 mark). However, they have higher reproductive height and TFL at the lower altitude garden, which suggests that these are still more favourable conditions for these two populations than the conditions they are faced with at their native site (1 mark).

A lot of students did not consider the data here, but described what they think should happen (populations might shift further upwards, which is not supported by the evidence). Only answers that referred to the data were given credit, and if these were combined with range shifts in a sensible way, then this received some marks.

LOs addressed:
LO2. interpret and assess data presented in phylogenies, phylogeographic analysis, genetic clustering analysis and other forms of data presented in ecological genetics scientific papers
LO4. assess, using examples, the importance of genetic drift and selection in causing population divergence and adaptation

Question 2

a) Explain how the genetic diversity of a host population that is coevolving with a parasite is likely to change compared to a host population that is evolving resistance to a genetically uniform parasite. (3 marks)

Coevolution with a parasite is likely to increase genetic diversity in the population (1 mark) because the parasite population will also be genetically diverse with a range of virulence mechanisms (1 mark), whereas a genetically uniform parasite population will select for the most efficient form of resistance and not diversity (1 mark).

This question was generally answered well and many students got full marks.

b) Discuss whether you would expect to see any differences in mating behaviour between the populations in (a) after fifteen generations of selection, and if so describe what kind of mating behaviour might evolve. (4 marks)

Even though mating behaviour is not directly selected for, it is likely that differences will evolve because genetic diversity is beneficial in the coevolved populations (1 mark). Individuals should be selected for and evolve mating strategies that will produce genetically diverse offspring (1 mark). In the coevolved populations we would thus expect individuals to mate with a higher number of mates.
than in the other populations (1 mark) and choose mates that are genetically dissimilar from the individual (1 mark).

The vast majority of students misinterpreted this question, and explained whether sexual or asexual reproduction should evolve in these two situations. This was given a maximum of 2 marks (one for the pattern, one for the explanation. Very few students made any predictions on mating behaviour.

LOs addressed:
LO2. interpret and assess data presented in phylogenies, phylogeographic analysis, genetic clustering analysis and other forms of data presented in ecological genetics scientific papers
LO4. assess, using examples, the importance of genetic drift and selection in causing population divergence and adaptation
Question 3

In 2014, the population structure of black bear populations along the lower Mississippi valley was examined by genotyping 265 bears from seven populations (LARB, UARB, TRC, TRB, MISS WRB and MINN) using 23 microsatellite loci. The map below shows the locations of these seven populations. On the map, purple populations were present prior to 2000, and red populations were established after 2000. During the 1960s, black bears were translocated from the MINN population to the UARB and TRB populations.
The figure above shows the results of analysing the microsatellite genotypes of the sampled black bears using the program STRUCTURE in which individuals were assigned to genetic clusters (K). The analysis was carried out using a range of values of K, of which K=5 was found to be the most probable.

a) What source populations have contributed to the two newly established populations? Discuss this in the context of the locations of these populations. (5 marks)

TRC appears to be a mix of the TRB and UARB populations (1 mark), this makes sense as TRB and UARB are the closest populations to TRC and on the same side of the river (1 mark). MISS is a mix of TRB and WRB populations (1 mark). TRB is much closer to MISS than WRB, and therefore might be expected to have contributed more to MISS, but this does not appear to be the case (1 mark). MISS is on the other side of the river compared to both TRB and WRB suggesting that the river is not much of a barrier to gene flow (1 mark).

Generally answered well, although some students did not get all or some of the marks allocated for discussing result in the context of the relative locations of the source populations.

b) Evaluate what impact the translocations from MINN have had on the population genetic structure in the other six populations. (5 marks)

Expecting to find traces of MINN in both UARB and TRB (1 mark). Using K=5, MINN, UARB and TRB each belong to different clusters, suggesting that the translocations have not left a genetic trace (1 mark). Comparing K-5 with K=4, it is clear that MINN and UARB as actually relatively closely related (1 mark). MINN is a bit distinct from UARB perhaps due to interbreeding between MINN and existing UARB bears (1 mark). By contrast, the TRB population lacks any MINN genetic signature suggesting that bears translocated to from MINN to TRB failed to breed (1 mark).

Several students did not answer the question being asked with respecting to “Evaluate”. Marks were not awarded for trying to explain why there there was relatively little contribution from MINN. Many students only looked at the STRUCTURE results for K=5, and hence did not get marks allocated for explaining that UARB did show evidence of MINN contribution at lower levels of K.

LOs addressed:
LO2. interpret and assess data presented in phylogenies, phylogeographic analysis, genetic clustering analysis and other forms of data presented in ecological genetics scientific papers
LO3: Describe, using examples, the different outcomes that can occur when two populations meet.
Question 4

Fifty two thinhorn sheep (*Ovis dalli*) from North America were genotyped at 10,000 genome-wide SNPs.

Figure A) Phylogenetic tree of the 52 thinhorn sheep. * indicate nodes with 100% bootstrap support. Red/yellow/green branches colours correspond to colours of sampling locations on the map.

Figure B) Map of northwest North America showing the sampling locations of the sheep. The grey shaded area represents the extent of ice cover during the last ice age, and the white shading represents ice-free areas.

Figure C) Results of analysing the genotypes of the sampled sheep using the program STRUCTURE in which individuals were assigned to genetic clusters (*K* = 2).
Using the genetic data and ice cover information, what can you infer about the number and locations of possible ice-free refugia for thinhorn sheep, and postglacial colonisation routes out of these refugia.  

The phylogeny appears to indicate three clades, of which the Southern Clade is basal (1 mark). This could indicate that there was a single southern refugium which founded the Northeast clade which in turn founded the northwest clade (1 mark). However, the STRUCTURE plot indicates that there are in fact two clusters, corresponding to the southern and northwest clades (1 mark), and that the northeast clade is in fact a genetic mixture of the other two clades (1 mark). This is consistent with the central position of the northeast clade within the phylogeny (1 mark). This suggests that there were actually two ice-free refugia, one in the north and another in the south (1 mark). After the ice sheets retreated, the populations expanded out of these refugia, and the northeast clade, which is found in the centre, was formed from migrants from both these refugia (1 mark). This scenario is consistent with the ice cover information which shows a ice-free area across much of Alaska. A cryptic southern refugia may have existed in the southern part of the map, or was located further south (1 mark).

Most students said that the genetic data indicated the existence of two clusters, although not so many suggested a southern refugia. Some marks were awarded for suggesting two northern refuges, although this is not a likely scenario. Only a few students used both the phylogeny and the STRUCTURE results to inform their suggestions. Some students suggestions were not always linked back to the information in the figures.

LOs addressed:
LO2. interpret and assess data presented in phylogenies, phylogeographic analysis, genetic clustering analysis and other forms of data presented in ecological genetics scientific papers
LO3: Describe, using examples, the different outcomes that can occur when two populations meet.
LO4: assess, using examples, the importance of genetic drift and selection in causing population divergence and adaptation
Question 5

As plants are stationary, migration or gene flow happens via seed dispersal (nuclear and organelle genes) and pollination (nuclear genes). Discuss how different types of seed dispersal (small mammals, birds and wind) and types of pollination (self, insect and wind) might be expected to affect patterns of isolation by distance detected using nuclear and chloroplast markers. (9 marks)

Isolation by distance (IBD) is the pattern of population structure where populations close to one another are genetically more similar to one another compared to populations that are further apart (1 mark). This pattern arises due to the limited migration ability of individuals in a population (1 mark). Chloroplast population structure measures migration via seed only, so type of pollination will not affect it (1 mark). Seed dispersal distances are likely to be small mammal < wind < bird (1 mark; could be small mammal < bird < wind). IBD measured with chloroplast markers should reflect this; greatest IBD in plant species with small mammals as seed dispersers, and weakest IBD in plant species with bird seed dispersers (1 mark). Nuclear population structure measures the combined effect of migration via seed and pollen (1 mark). Pollination distances are likely to be self < insect < wind (1 mark). Nuclear IBD is expected to be highest in species with self pollination and small mammal seed dispersers, and weakest in species with wind pollination and bird seed dispersers (1 mark). Other combinations of pollination and seed dispersal should have intermediate nuclear IBD (1 mark).

Most students did not explain what isolation by distance was, or why it arises. Most students also did not address why differences in patterns might arise between chloroplast and nuclear markers. Most students did mention that self-pollinating species are likely to show high isolation by distance. Very few students explained that seed and pollen dispersal would both affect patterns of nuclear isolation by distance.

LOs addressed:
LO1: Discuss the strengths and weaknesses of different molecular markers and evaluate their suitability for a variety of ecological genetics analyses.
LO4: assess, using examples, the importance of genetic drift and selection in causing population divergence and adaptation
A) Discuss problems that might arise when conservation decisions are taken at the species level without taking lower levels of population structure into account.

A definition of what a species is.
One problem with using species as a unit is that there might be taxonomic uncertainty about the status of a taxon. This might ignore cryptic species which may then not be adequately protected. The most useful taxonomic level to consider will depend on the conservation aim, e.g. the conservation of biodiversity in general (which could be higher taxonomic groups, different species, subspecies or genetic diversity within a species), the conservation of ecosystem services, or the conservation of “evolutionary potential”.
The main problem with using species as a unit is that species do not consist of uniform individuals but that there is variation within and between populations. This within-species variation is important because there may be adaptive differences between the populations. For example, populations might be locally adapted to certain conditions. If these differences were not taken into account, much genetic diversity might be lost. This could reduce the future evolutionary potential of the population and its ability to adapt to a changing environment. If the populations were all treated as equivalent and individuals mixed between them this might lead to introgression of locally adapted alleles into the “wrong” population. There is also a risk of outbreeding depression.
One related issue is that it is important to understand patterns of migration and gene flow between the populations as these could be important for both population persistence and its genetic composition.
This question was answered by a relatively small number of students. A lot of students focussed on translocations as a conservation method and did not consider other methods (e.g. preserving habitats and how to choose those). This often led to discussions of how introduced individuals would interact with a population that is already there, and in many cases there was too much emphasis on these issues. Local adaptation was generally also discussed, but again often only in the context of translocations. Other processes were generally omitted or very briefly touched upon. Most essays provided quite good explanations, but were lacking specific examples.

LOs addressed:
LO4: Assess, using examples, the importance of genetic drift and selection in causing population divergence and adaptation.
LO5: Explain what is a species, discuss the importance of reproductive barriers to maintain species integrity, and be able to assess the main drivers of speciation.
LO6: Justify, using examples, whether or not genetic principles can be used to help conservation efforts.
B) Discuss whether or not hybridisation between species is an issue of conservation importance.

Why might interspecific hybridisation be a problem? If two species meet and hybridise, there is the possibility of genes introgressing between them. Such introgression could result in species no longer being "pure". Species could lose adaptations or even their identity if they get swamped by introgressing genes (e.g. cichlids in eutrophic lakes).

Interspecific hybridisation is relatively common; ~10% of animal and ~25% of plant species known to hybridise with one or more other species. But not so important if only F1 hybrids are formed. However, if the proportion of F1s formed is high, this could reduce the population growth of the pure species. If F1s backcross to the parental species then only will genes from one species flow into the other species. Hybridization between species may in most cases not be an issue as it occurs at a low frequency.

Species that have evolved in sympatry/parapatry will have prezygotic barriers that prevent or minimise hybridization. However, species that have evolved in allopatry may not have such barriers.

Human translocation of species between continents and islands (i.e. across geographic barriers) is now resulting in many species that have evolved in allopatry coming together. Native species may be at higher risk of genetic "contamination" from closely-related exotic species. Climate change is causing range shifts, and may result in the same problem.

Hybridization between species may in some cases be beneficial if it allows adaptive genes to move between species. With climate change, adaptation via new mutations may not be quick enough, but species could gain “warm” adapted genes from other species via hybridization. Examples of polar bears and brown bears, humans and Neandertals.

Hybrid speciation could even increase species diversity, but is uncommon in animals, but may be relatively common in plants.

Conservation legislation and policies are often based on species. Depending on the species definition used, interspecific hybridisation may affect whether or not taxa are considered separate species.

Most students discussed hybrid speciation, maintaining species “purity”, and adaptive introgression. Quite a few students were confusing the relatively common phenomenon of hybridization (different species mating and producing F1 offspring) with the much rarer phenomenon of hybrid speciation (two species hybridizing to form a third species). Only a few students discussed hybridization and associated conservation concerns are likely to increase with climate change induced range shifts and human translocations as these would bring together species that evolved in allopatry and between which reproductive barriers would be weaker.

LOs addressed:
LO3: Describe, using examples, the different outcomes that can occur when two populations meet.
LO5: Explain what is a species, discuss the importance of reproductive barriers to maintain species integrity, and be able to assess the main drivers of speciation.
LO6: Justify, using examples, whether or not genetic principles can be used to help conservation efforts.