BIOLB242: EVOLUTIONARY AND ECOLOGICAL GENETICS 2006

Answer **ONE** question from section A**, TWO** questions from section B, and **ALL** of section C (overleaf). Each section carries 1/3 of the marks of the whole paper**.**

SECTION A (carries 1/3 of the marks).
Essay. Answer **ONE** of questions 1-3.

1. Perhaps the greatest challenge in modern evolutionary biology is to understand the genetic mechanisms underlying phenotypic variation within natural populations. Evaluate, using examples, the value of quantitative trait locus (QTL) mapping in this context.

2. Write an essay on reinforcement and its relationship to sympatric speciation.

3. Describe fully the conceptual tools used to analyse how quantitative traits are expressed differently in different environments. Distinguish between phenotypic plasticity, reaction norms and genotype-by-environment (G x E) interactions.

SECTION B (carries 1/3 of the marks).
Short answers. Answer **TWO** of questions 4-8.

4. What are the key differences in assumptions and outcomes between the “blending” and “Mendelian” mechanisms of heredity?

5. What is the importance of linkage disequilibrium and its importance in modern methods of finding genes that affect phenotypic traits

6. Give details of a suitable case study to explain why “balancer” chromosomes in fruitflies are especially useful when estimating the rate of occurrence and fitness consequences of deleterious mutations.

7. "Selection is unimportant for most polymorphisms." Discuss the evidence and theory behind this assertion.

8. Compare and contrast taxonomic methods using distance-based and parsimony-based approaches. Summarise the key steps involved in each case.

TURN OVER

SECTION C. (carries 1/3 of the marks). Attempt **ALL** parts.

9. Butlin scored the following genotypes from the alcohol dehydrogenase locus in adult seaweed flies (*Coelopa frigida*) from St Mary's Island in 1980:

BB	*BC*	*BD*	*CC*	*CD*	*DD*
150	104	424	18	129	198

a) Determine the frequencies of the three alleles, B, C and D.

b) What is the expected genotypic frequency for the *BD* genotype assuming Hardy-Weinberg equilibrium? (HINT: expected genotype frequencies are calculated in exactly the same way for three allele frequencies (*p*, *q* and *r*), as for two).

c) Test for conformity to Hardy-Weinberg (over all genotypes) for the *A* translocation polymorphism using a chi-square test, helped by the table:

Table of χ^2	P values						
	0.99	0.9	0.5	0.1	0.05	0.01	0.001
Degrees of freedom							
1	0	0.02	0.46	2.71	3.84	6.63	10.83
2	0.02	0.21	1.39	4.61	5.99	9.21	13.82
3	0.12	0.35	2.37	6.25	7.81	11.34	16.27

d) In (c), you should have 3 degrees of freedom – why?

e) If deviation from Hardy-Weinberg is caused by selection on the BD heterozygote, what is the fitness of the BD genotype relative to the Hardy-Weinberg expectation?

f) Standardizing by the BD fitnesses will allow you to set the BD relative fitness to 1.0. What are the recalculated fitnesses of the other genotypes relative to BD?

g) It was later discovered that the *Adh* gene is embedded within a chromosomal inversion. Briefly, what hypotheses are most likely to explain deviations from Hardy-Weinberg at *Adh*, and why? How would you test the hypotheses?

h) Give at least one other example of inversion polymorphisms, and discuss, in population genetic terms, what factors might affect evolution of inversions.

END OF PAPER