



FACULTY OF SCIENCE

DEPARTMENT OF ZOOLOGY

MODULE ZOO0037

CAMPUS APK

SUPPLEMENTARY EXAMINATION

DATE: 9 January 2017

SESSION: 11:30

ASSESSOR(S):

Prof H Van der Bank

INTERNAL MODERATOR:

Prof B Jansen Van Vuuren

EXTERNAL MODERATOR:

Prof P King

DURATION: 2 Hours

MARKS: 50

NUMBER OF PAGES: 2

INSTRUCTIONS: Answer all the questions. You may use a calculator. Show all calculations and formulae used.

YOU MAY CHOOSE TO ANSWER EITHER QUESTION 1 OR QUESTION 2.

QUESTION 1

- a) Calculate genic fitness and selection coefficient values, predict the effects on successive generations, and draw and motivate the graph (figure) you could reconstruct using the data set below.

(8)

Generation:	Genotypes:	AA	AB	BB
1		40	50	10
2		80	90	10

- b) Name four fitness components (often called viability aspects) that can influence selection for a particular genotype.

(4)

OR:

QUESTION 2

Discuss inbreeding depression in human populations and compare the effects in children (e.g.) due to marriages between first cousins) compared to those of children from unrelated parents using examples from different countries. Also speculate why such variations occur.

(12)

QUESTION 3

Describe: a) how the analysis of animal stock structure can be achieved and b) the four major factors that can influence the amount of genetic differentiation among subpopulations.

(8)

QUESTION 4

One of the guidelines to interpret genetic information at a locus is that if the alleles at the same locus for the same individual is expressed in different tissue types, then the variant phenotypes should be parallel among tissues. Explain what this implies and use examples in your answer.

(5)

QUESTION 5

Discuss: a) heterozygote advantage (*heterosis*) briefly and also

- b) a realistic example of it in human populations where malaria infections regularly occur.

(5)

QUESTION 6

The founder effect, genetic bottlenecks and supergenes can all influence speciation and evolution. Discuss each and give realistic examples.

(10)

QUESTION 7

Calculate the genetic distance between species X and Y from 13 mutually shared monomorphic loci, 301 and 701 individuals respectively, and with the following polymorphic locus: 0.3 A alleles, 0.7 B alleles for species X and 0.7 A alleles, 0.3 B alleles for species Y respectively.

(10)

Total (50)