



KENYATTA UNIVERSITY

UNIVERSITY EXAMINATIONS 2011/2012

SECOND SEMESTER EXAMINATION FOR THE DEGREE OF MASTER
OF SCIENCE IN BIOTECHNOLOGY
SBC 548 : MOLECULAR BREEDING

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DATE: WEDNESDAY 4TH APRIL 2012 TIME: 9.00 A.M. – 12.00 P.M.

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INSTRUCTIONS

SECTION A – ANSWER ALL QUESTIONS (5 MKS EACH)

1. Genetic analysis has shown that the recessive genes *an* ('Anther ear'), *br* ('brachytic') and *f* ('fine stripe') are all found on chromosome # 1 of maize. When a plant that is heterozygous for each of these markers is test-crossed with a homozygous recessive plant, the following results are obtained.

Test cross progeny	Numbers
wild type	98
Fine	26
brachytic	2
brachytic fine	379
anther	385
anther fine	3
anther brachytic	20
anther brachytic fine	87
Total offspring	1000

Analyze this data in two steps:

- Calculate recombination frequencies between each of these three pairs of genes.
- Draw a genetic map for the location of these 3 genes on chromosome number 1 of maize. Show the map distances between the loci.

2. You are investigating 4 recessive alleles in corn. They are whimpy ears (*w*), striped leaves (*s*), shriveled kernels (*k*), and red tassels (*r*). Their dominant counterparts are generally just represented by the "+" symbol. A plant that is homozygous recessive for all 4 genes (*ww ss kk rr*) is crossed with a plant that is homozygous dominant for all 4 genes. As expected, the F1 offspring of the cross display the dominant phenotypes of all 4 genes. These F1 plants are then crossed with a plant that is homozygous recessive for all 4 genes. A total of 1,000 F2 offspring are produced. These F2 offspring display the following phenotypes:

<i>w s k r</i>	198
<i>+ + + +</i>	202
<i>w s k +</i>	201
<i>+ + + r</i>	199
<i>w + k +</i>	49
<i>+ s + r</i>	51
<i>w + k r</i>	48
<i>+ s + +</i>	52

- First, calculate recombination frequencies between each of the 4 genes.
 - Next, Draw a genetic map for the location of these 4 genes.
3. Describe two types of mapping populations and how they are developed
4. (a) What is the purpose of gene expression microarrays? (b) What do the probes represent on a gene expression microarray? (c) What type of molecules are bound / detected by the probes? (d) When measuring differential gene expression between yeast populations grown aerobically vs. anaerobically, what labeling method allows us to distinguish the expression levels of genes between the two different populations of yeast?
5. A breeder in your research station does a cross but the embryo fails to develop due to degeneration of embryonic tissues. Describe how you would recover plants from this failed embryo