**NAME** _____ **STUDENT #**_____

# SC/BIOL 2040 4.0 GENETICS

## TEST #1 Jan 28, 2010

**(TOTAL PAGES = 9)**
**(TOTAL MARKS = 24)**
**(TIME = 60 MINS)**

INSTRUCTIONS:

1) INCLUDE YOUR NAME AND STUDENT NUMBER ON THE SCANTRON (BUBBLE IT IN AS SHOWN). ENTER THE TEST VERSION NUMBER INDICATED ON THIS TEST PAPER WHICH IS PROVIDED IN QUESTION 1.
2) PLEASE KEEP YOUR TEST PAPER TO YOURSELF, SO THAT IT MAY NOT BE SEEN BY OTHERS.
**3)** ANSWER ALL QUESTIONS DIRECTLY ON THE SCANTRON SHEET. ALSO, CIRCLE THE ANSWER ON THE TEST.
**4) READ QUESTIONS CAREFULLY, AND THINK CAREFULLY BEFORE ANSWERING.PROVIDE THE BEST ANSWER IN EACH CASE**
5) YOU MAY USE A non-programable CALCULATOR.

6) BUDGET YOUR TIME APPROPRIATELY.

YOU MIGHT NEED THE INFORMATION BELOW:

| df | $\chi^2_{\alpha=0.05}$ |
|---|---|
| 1 | 3.841 |
| 2 | 5.991 |
| 3 | 7.815 |
| 4 | 9.488 |

1. For question 1 enter your test version as **A**

2. Forward genetic analysis is best described as:

a. The laws and ratios obtained by Mendel and subsequent geneticists.
b. The analysis of the total of all genes in the genome of an organism.
c. The mathematics of the process of genetic transmission.
d. An analysis beginning with a DNA sequence and the subsequent discovery of its effects on the phenotype of an organism.
e. only a & c above.
f. none of the above

**Answ. F. none of these describes forward genetic analysis.**

3. Which of the following best describes genotype-environment interaction?

a. Genes solely determine the phenotype of an organism.
b. Genes and the environment both contribute to the phenotype of an organism.
c. The phenotype causes a particular genotypic constitution.
d. Phenotypic variation is the result of microenvironmental differences.
e. all of the above.
f. none of the above.

**Answ. B. both genes and enviroment interact in some way to produce the final phenotype.**

4. Which of the following apply to model organisms:

a. They are usually microbes
b. They are usually haploid
c. They are all eukaryotes
d. They have relatively rapid generation times
e. There are no mammalian model organisms
f. only c & e
g. none of the above

**Answ. D. They have relatively rapid generation times.**

5. A haploinsufficient gene is one for which

a. a null mutation results in a heterozygote that phenotypically resembles the wildtype.
b. a null mutation is dominant
c. half of a gene sequence is sufficient for producing a functional protein
d. a genetic phenomenon restricted to haploid organisms such as *Neurospora*.
e. none of the above

**ANSW. B. the heterozyote for a haploinsufficient gene will look like the mutant homozygote so the null mutation is dominant.**

6. Which of the following does **NOT** apply to Gregor Mendel?

a. He discovered gene segregation
b. He observed the segregation of chromosomes during meiosis
c. He quantified the results of crosses, by counting the numbers of various visible phenotypes.
d. He discovered dominance versus recessiveness
e. All of the above apply to Mendel

**Answ. B. He didn't observe chromosomes**

7. Imagine that you quantify the amount of DNA in the nucleus of a sperm cell of an aardvark and find the value is c picograms. How many picograms of DNA would there be in a cell nucleus at pachytene in the aardvark?

a. 1/2 c picograms
b. c picograms
c. 2 c picograms
d. 3 c picograms
e. 4 c picograms
f. none of the above

**Answ. E. pachytene is a stage of prophase I and DNA replication had already occurred so you have the greatest amount of DNA (4pg) in the meiocyte nucleus at this stage. Since homologues and then chromatids later separated into the gametes, you can simple add the 4 gametic nuclei values together.**

8. Consider an organism with 2n=36 chromosomes. What is the total number of chromatids you would expect to find in just one of the nuclei at Metaphase II of meiosis.

a. 9
b. 18
c. 36
d. 72
e. none of the above

**Answ C. the 36 homologues separate in to two nuclei at first division with each chromosome having 2 chromatids. So at Metaphase II there are 18 chromosomes x chromatids = 36**

9. Which of the following is true of chromosomes found in eukaryotes?

a. The DNA is double-stranded, with 2 double-stranded molecules per chromatid
b. The DNA is single-stranded but with one strand in each chromatid, and packaged with a number of histone proteins.
c. There are two homologous chromosomes per somatic cell (except in gametes) in all eukaryotes and these usually look identical, and contain the same genes, usually the same gene order, but with some differences in gene sequence.
d. Eukaryotic chromosomes are solely composed of euchromatin
e. All of the above
f. None of the above

**Answ: F**. **none of these is true.** There is 1 doubled stranded DNA molecule per chromatid packaged with histones. C is wrong because Neurospora and many other fungi and algae have haploid somatic cells.

10. Hemophilia is caused by an X-linked recessive allele. In a mating between a male with hemophilia and a female carrier (heterozygote), what is the expected proportion of various offspring:

a. 1/4 Female Normal : 1/4 Female Hemophilia : 1/4 Male Normal : 1/4 Male Hemophilia
b. 1/2 Female Normal : 1/4 Male Normal : 1/4 Male Hemophilia
c. 1/2 Female Hemophilia: 1/4 Male Normal : 1/4 Male Hemophilia
d. 1/2 Female Hemophilia : 1/2 Male Hemophilia
e. because it is X-linked, females will never have the disease

**Answ A. diagram out the Punnett square to get the answer.**

11. You find two colour forms of hermaphrodite snails. One snail is orange and the other brown in colour. You generate pure breeding lines of both snails and cross a pure breeding orange snail with a pure breeding brown snail.

All the F1 snails are brown. Since the snails are hermaphrodites, you allow one of the F1 snails to self-fertilize. You raise 200 progeny and count the numbers of brown versus orange snails:

Number of brown = 110;  Number of orange 90.

Carry out a statistical test to determine whether the numbers meet with the expected ratio for a single gene trait.

a. The chi-square goodness-of-fit-test value is approximately 2.0
b. The chi-square goodness-of-fit-test value is approximately 42.7
c. The chi-square goodness-of-fit-test value is approximately 1.0
d. The chi-square goodness-of-fit-test value is approximately 21.3
e. None of these are even approximately correct

(you can work out your answer in the space below):
**ANSW. B**
Well, Brown is dominant to organge. So BB and Bb are brown. bb is orange.
F1 must be Bb.
Selfing gives an F2 with expected ratio of  0.75 Brown : 0.25 orange.

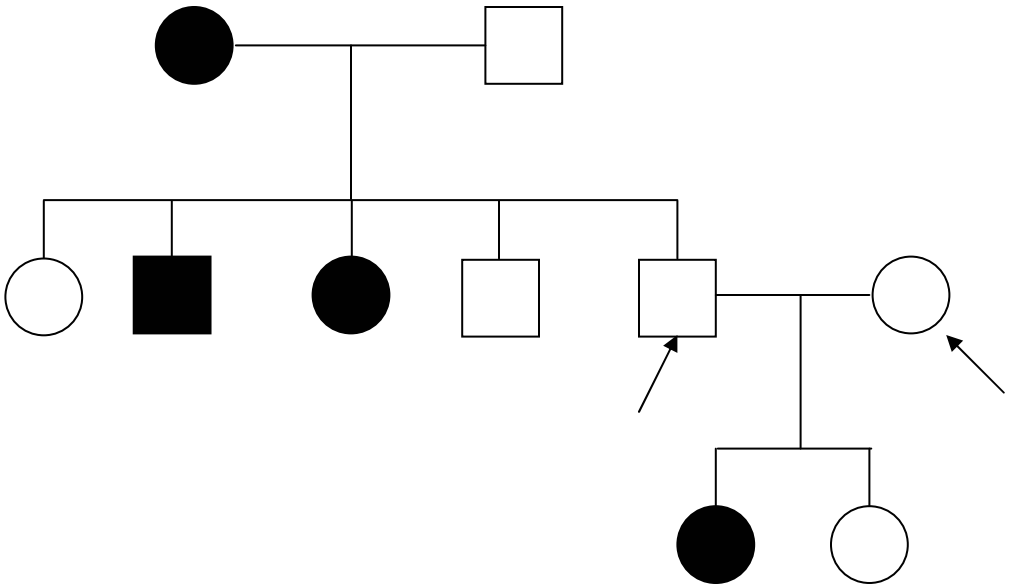
So do the goodness of fit test.

| | brown | orange | N |
|---|---|---|---|
| observed # | 110 | 90 | 200 |
| exp proportion | .75 | .25 | |
| exp number | 200x.75=150 | 200x.25 = 50 | |

$X^2 = (110-150)^2 /150 + (90-50)^2 /50 = 42.7$

with 1 degree of freedom, this vastly exceeds the critical value of 3.841 so the ratio doesn't meet the expected 3 : 1.

12. A single gene trait is shown in the pedigree below. From this pedigree we can conclude:



a. The trait must be determined by an X-linked recessive
b. The trait must be determined by an X-linked dominant
c. The trait could be determined by an X-linked or autosomal recessive
d. The trait could be determined by an X-linked or autosomal dominant
e. None of the above

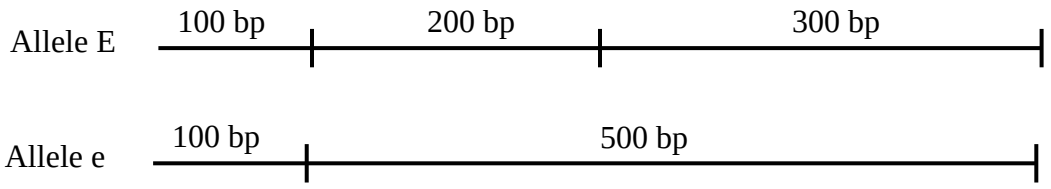
**Answ. E. The single gene trait shown cannot be X-linked. It must be an autosomal recessive. One piece of evidence showing it is not X-linked is that the male shown by the arrow would have to have the trait, if it was an X-linked recessive or if it was an X-linked dominant, the female indicated by the arrow would have to have the trait.**

13. Imagine you toss a fair coin 5 times. What is the probability of getting all 5 heads or all 5 tails?

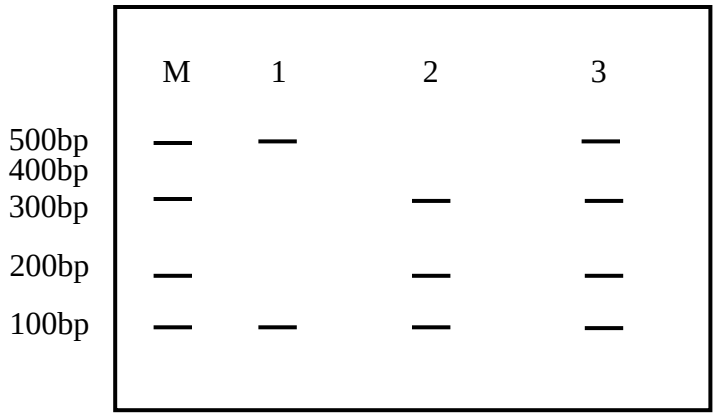
a. 1/32
b. 5/32
c. 1/16
d. 1/1024
e. none of the above

**Answer C. prob of five heads is 1/2 x /12 x 1/2 x 1/2 x 1/2 = 1/32**
**OR**
**prob of five tails is 1/2 x /12 x 1/2 x 1/2 x 1/2 = 1/32**
**so, 1/32 + 1/32 = 2/ 32 = 1/16**

14. You use a cleaved amplified polymorphism (CAPs) to study the segregation of two alleles for a particular gene of interest. The two alleles differ in the number of EcoRI restriction sites (indicated by the vertical bars) they possess as illustrated below and yield DNA fragments of the sizes indicated (in number of base pairs, bp):




You carry out gel electrophoresis and the first lane contains DNA markers (lane M) of known size. The remaining three lanes (labeled 1, 2, 3) represent the CAPs banding patterns of three individuals.



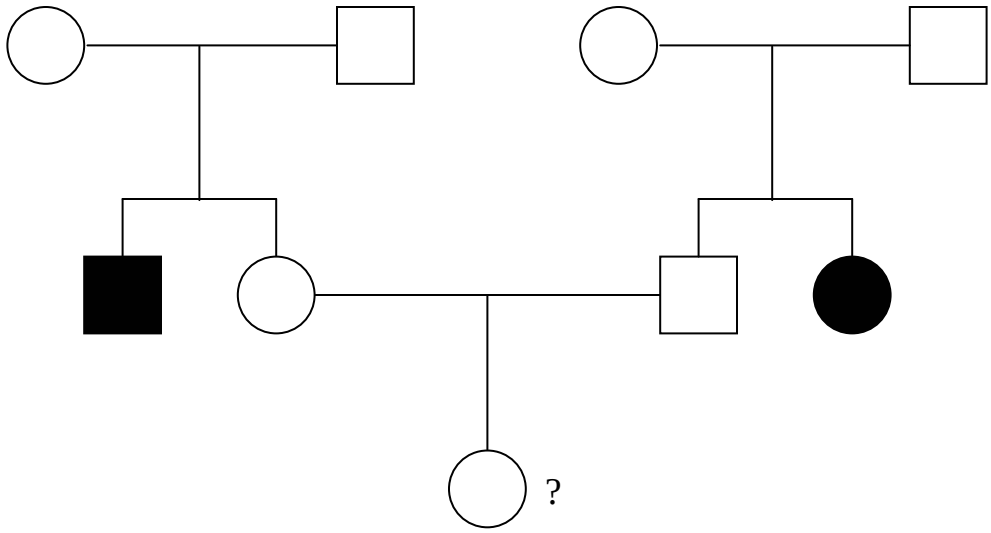

Based upon the restriction sites indicated and the gel above what are the genotypes of the individuals 1, 2, and 3, indicated on the gel.

a. 1 is EE; 2 is ee; 3 is Ee
b. 1 is e; 2 is Ee; 3 is Eee
c. 1 is ee; 2 is EE; 3 is Ee
d. 1 is ee; 2 is Ee; 3 is EE
e. none of the above

**ANSW. C the ee genotype will have two bands one of size 500bp the other 100bp.**
**EE will have three bands of sizes 300bp, 200bp, 100bp**
**Ee will have the additive pattern of bands 4 bands, 500bp, 300bp, 200bp, 100bp**

15. For the pedgree illustrated below, the single gene trait shown MUST be the result of:

a. An X-linked recessive allele
b. An autosomal recessive allele
c. An X-linked dominant allele
d. An autosomal dominant allele
e. none of the above




**ANSW. B. the single gene trait must be recessive since offspring appear both of whose parents don't exhibt the trait. The trait cannot be X-linked if it is recessive since the female with the trait gets an X chromosome from her father, but her father doesn't have show the trait so can't have the allele causing the trait.**

16. For the pedigree of question 15 illustrated above, the female child shown (with the adjacent question mark) is born and doesn't possess the trait. What is the probability that this child is heterozygous and thus carries the allele under consideration?

a. 1/9
b. 8/27
c. 6/27
d. 14/27
e. 17/27
f. 7/54

**ANSW. D.**

**You need to think about all the ways the child could end up being heterozygous given the pedigree and knowing the trait is due to an autosomal recessive. There are three possible ways the child shown could be heterozygous:**

**1.Mother Aa Father Aa Child Aa**
**prob(2/3) x prob(2/3) x prob (2/3)-since we know child isn't aa) = prob = 8/27**

**2. Mother AA Father Aa Child Aa**
**prob (1/3) x prob (2/3) x prob(1/2) = 1/9 = 3/27**

**3. Mother Aa Father AA Child Aa**
**prob (2/3) x prob (1/3) x prob(1/2) = 1/9 = 3/27**

**Prob child is heterozgyous is 8/27 + 3/27 + 3/27 = 14/27**

17. Often, there are numerous alleles of a gene in a population. For a particular gene, there are three alleles: $A_1$, $A_2$, $A_3$.

For the cross: $A_1\ A_2$ x $A_2\ A_3$, which of the following is true?

a. only 1/4 of the progeny will have a parental genotype
b. only 1/2 of the progeny will have a parental genotype
c. no progeny will have a parental genotype
d. all progeny will be heterozygous
e. none of the above

**ANSW B: do a punnett square for this cross. You should get the following**
**1/4 $A_1\ A_2$ : 1/4 $A_1\ A_3$ : 1/4 $A_2\ A_2$ : 1/4 $A_2\ A_3$**
**Two of these are the same genotypes as the parents used in the cross. $A_1\ A_2$ & $A_2\ A_3$**

18. In *Neurospora*, the wild-type allele, *lys-5*$^{+}$, causes the ascospores to be black in colour, while a mutant allele, *lys-5*, causes ascospores to be white in colour.
For the cross *lys-5*$^{+}$ x *lys-5*, how many ascospores of each colour do you expect to find in a single ascus?

a. 2 white and 2 black
b. 4 white and 4 black
c. 8 white and 8 black
d. 1 white and 3 black
e. 2 white and 6 black
f. none of the above

**ANSW B. Neurospora produces 8 ascospores in an ascus. Four will be black and four white**

19. A husband and wife are both heterozygous for a recessive allele for albinism. What is the probability that both of their offspring will have the same phenotype for skin pigmentation (assume they don't have identical twins)?

a. 9/16
b. 1/16
c. 3/4
d. 5/8
e. 1
f. none of the above

**ANSW D. The cross is Aa x Aa.**
**There are two ways children can have the same skin pigmentation.**
**Both could be normal pigmented with prob 3/4 x prob 3/4 = 9/16**
**OR**
**Both could be albino with prob 1/4 x prob 1/4 = 1/16**

**so summing gives 10/16 = 5/8**

20. You walk into the forest on the York University campus and find two plants of goldenrod growing. One is 1 meter tall, and the other is very short (only 10 cm). You cross the plants, and grow 100 progeny in a climate controlled greenhouse for 1 year and then measure the progeny. The progeny average height is 110 cm and the smallest is 90cm while the largest is 120 cm.

Which of the following statements is correct?

a. Height differences must be the result of environmental differences between the original parental plants and variation for height has no genetic basis.
b. The original 1 meter tall plant must be homozgyous for a dominant allele for "tallness" while the 10 cm parent is homozygous for an allele for small size. The progeny are quite tall on average, demonstrating the dominance.
c. There must be more than one gene involved in determining variation in the height of these plants
d. As shown by Mendel, small plants must be determined by a single recessive allele.
e. The F2 will show a ratio of 3 tall : 1 short.
f. None of the above

**ANSW F. Here you begin by collecting two plants from the field. You don't know anything about them at the outset and why the differ in height (they could be different ages, they could receive different levels of light, there could be more nutrients in the soil for one versus the other or a myriad of other environmental differences could exist. Likewise they could be genetically different at one or more genes. You have no idea at all. Furthermore, the experiment should have been first undertaken by making pure breeding lines of the two plants, or at least selfing both parental plants (as well as crossing them). This would then give further insight into whether there might be any genetic basis to the traits. Further crosses would be required to determine the numbers of genes. Basically, from the information given and the 1 cross done, you can say almost nothing about the height variation. The word "must" in the possible answers is far too strong a word to use given the lack of information you will obtain from the one cross carried out.**

21. Which of the following statements is correct about mutations in introns?

a. They are always silent
b. They never occur
c. They can result in a change in the amino acids the intron sequence encodes.
d. They can result in a null mutation
e. None of the above

**ANSW: D. As mentioned explictly in class, a mutation in an intron could result in a null mutation if, for example, the mutation causes a change at the beginning or end of the intron so that it isn't properly cut out of the mRNA transcript.**

22. A synaptonemal complex

a. is a rare genetic disorder in humans and some other primates
b. occurs at prophase of mitosis
c. was discovered by Thomas Hunt Morgan
d. is best seen at pachytene
e. none of the above

**ANSW. D. with appropriate microscopic methods you can see this structure in paired homologs at pachytene of meiosis.**

23. A polymorphism for white versus grey coat colour in squirrels occurs near the town of Exeter Ontario (a place you must visit to see them). White is known to be recessive to the dominant grey coat colour allele. You randomly capture a grey squirrel and perform a test cross. Which of the following statements is correct.

a. The result would be either all grey progeny or 1/2 grey to 1/2 white
b. The result would be 3/4 grey to 1/4 white
c. The result would be 1/4 grey to 3/4 white
d. The result would be either 3/4 grey or 1/2 grey to 1/2 white
e. none of the above are correct

**ANSW A. The white squirrel must be gg. The grey could be either GG or Gg. So work out the two possibilities. GG x gg gives all grey. Ggxgg give 1/2 grey to 1/ 2 white**

24. Mutations in an exon that encodes amino acids comprising the active site of an enzyme

a. Will always result in a null mutation.
b. Could result in a leaky mutation
c. Will never result in a null mutation
d. Will result in lethality when heterozygous
e. none of the above

**ANSW. B. These can often result in a null mutation but don't always have to. They certainly could result in a leaky mutation or even a silent mutation depending on the amino acid that the mutation changes to.**

25. For the cross Aa x Aa, you raise 10 progeny. What is the probability that all ten progeny will be heterozgyous?

a. 0
b. 1
c. 1/1024
d. 1/512
e. none of the above

**ANSW. C. Each progeny has 1/2 probability of being heterozygous.**

**So the answer is $(1/2)^{10} = 1/1024$**