Name: _____

7.03 Exam Three -- 2005

Name: _____

Exam starts at 11:05 am and ends at 11:55 am.

There are 8 pages including this cover page.

Please write your name on each page.

Only writing on the **FRONT** of every page will be graded.
(You may use the backs, but only as scratch paper.)

Question 1	**17 pts_____**
Question 2	**45 pts_____**
Question 3	**20 pts_____**
Question 4	**18 pts_____**
TOTAL	**out of 100_____**

Name: _____

1. (17 pts) You are studying the expression of the yeast gene ProA that is necessary for the synthesis of the amino acid proline. ProA is normally expressed only when the cell is lacking supplemental proline in the growth medium. You isolate two haploid yeast strains (ProB$^-$ and ProC$^-$) that misregulate ProA expression.

You mate a ProB$^-$ haploid strain to a wild-type haploid strain. The resulting diploid expresses ProA properly.

You mate a ProB$^-$ haploid strain to a ProA$^-$ haploid strain. The resulting diploid expresses ProA properly.

You mate a ProA$^-$ ProC$^-$ haploid strain to a ProC$^-$ haploid strain. The resulting diploid expresses ProA when proline is present in the growth medium.

You mate a ProC$^-$ haploid strain to a ProA$^-$ haploid strain. The resulting diploid expresses ProA properly.

You mate a ProB$^-$ ProC$^-$ haploid strain to a wild-type haploid strain. The resulting diploid expresses ProA properly. You induce sporulation of this diploid, and examine 40 tetrads. 30 (of those 40) each contain: two spores that do not express ProA when proline is absent from the growth medium, one spore that expresses ProA when proline is present in the growth medium, and one spore that expresses ProA properly.

(a, 6pts) Classify the ProB$^-$ mutation by its genetic properties (cis vs. trans, constitutive vs. uninducible, dominant vs. recessive).

(b, 6pts) Classify the ProC$^-$ mutation by its genetic properties (cis vs. trans, constitutive vs. uninducible, dominant vs. recessive).

(c, 5pts) If you a drew a linear pathway showing the regulation of ProA, which function would you place closer to ProA: ProB or ProC?

Name: _____

2. (45 pts) You are studying the transcriptional regulation of a mouse gene called *Stringy*. This gene is normally only expressed in tail cells due to the presence of a tail-specific inducer molecule in these cells. You have isolated two true-breeding mutant strains of mice that do not spatially regulate the expression of the *Stringy* gene properly. The strains of mice that you have, and their corresponding phenotypes, are listed in the table below.

Genotype of mouse	Phenotype of mouse
Wild-type	*Stringy* expressed only in tail
A^{-} / A^{-}	*Stringy* not expressed anywhere
B^{-} / B^{-}	*Stringy* expressed in all cells in the body

When you cross mice that are B^{-} / B^{-} to mice that are deficient in *Stringy*, the resulting mice only have *Stringy* expressed in the tail.
When you cross mice that are B^{-} / B^{-} to mice that are A^{-} / A^{-}, and then cross the resulting F1 mice to each other, you get a genotypic ratio in the F_2 that indicates that the A and B loci segregate independently of each other.

You inject a piece of DNA containing the A^{-} allele of the A gene into a fertilized egg produced by the mating of two true-breeding B^{-} mice. You then transfer this injected fertilized egg into a pseudopregnant mouse. The mouse that is born does not express *Stringy* in any cells in its body.

(a, 6pts) Classify the A^{-} mutation by its genetic properties (cis vs. trans, constitutive vs. uninducible, dominant vs. recessive).

(b, 6pts) Classify the B^{-} mutation by its genetic properties (cis vs. trans, constitutive vs. uninducible, dominant vs. recessive).

(c, 12pts) Draw TWO different linear genetic pathways that are consistent with your answers to parts **(a)** and **(b)**. Be sure to indicate the wild-type A, B, and *Stringy* genes in your model, and also include the tail-specific inducer molecule.

(d, 6pts) Clearly state which one piece of information you would need to know in order to determine which of the models you drew in part **(c)** was correct.

(e, 15pts) You want to distinguish between the two models listed in part **(c)**. You could do this by creating a genetically engineered mouse. **For the mouse you make**, please state:

i) whether you are using pronuclear injection **or** gene targeting

ii) what **DNA** you would introduce into the mouse cells (also draw the DNA)

iii) what is the **genotype** of the fertilized egg or the ES cells you would start with

iv) which **additional breeding** steps you would do to make the mouse you wanted

v) **two possible** phenotypic results you could get from the newly made mice, **and** the corresponding conclusion you would make for each result

Describe a way to create a genetically modified mouse that would allow you to gain the piece of information you stated in part **(d)** (and thereby distinguish between your models).

i)

ii)

iii)

iv)

v)

Name: _____

3. (20 pts) For each situation below, predict whether the frequency of the ALLELE ("q") associated with the trait/disorder in consideration will **stay the same**, **rise**, or **fall**. If you cannot conclude, choose "***inconclusive***."

For parts **(a)**, **(b)** and **(c)**, assume that the mutation rate is zero.

(a, 5pts) There is a population in which a rare autosomal recessive trait (with S = 0, h = 0) exists. This population always mates randomly. All of a sudden, heterozygotes obtain a selective advantage.

The allele frequency "q" will: stay the same rise
(CIRCLE ONE OF THE FOUR)
inconclusive fall

(b, 5pts) There is a population in which a rare autosomal recessive disorder (with **S = 1**, h = 0) exists. All of a sudden, this population goes from mating randomly to participating in some amount of inbreeding.

The allele frequency "q" will: stay the same rise
(CIRCLE ONE OF THE FOUR)
inconclusive fall

(c, 5pts) There is a population in which a rare autosomal **dominant** trait (with S = 0, h = 0) exists. All of a sudden, this population goes from mating randomly to participating in some amount of inbreeding.

The allele frequency "q" will: stay the same rise
(CIRCLE ONE OF THE FOUR)
inconclusive fall

(d, 5pts) There is a population in which a rare autosomal recessive disorder (with **S = 1**, h = 0) exists. All of a sudden, this population goes from mating randomly to participating in some amount of inbreeding. Simultaneously, the mutation rate rises from being negligible to a rate that would now affect allele frequency.

The allele frequency "q" will: stay the same rise
(CIRCLE ONE OF THE FOUR)
inconclusive fall

Name: _____

4. (18 pts) Consider a gene in which mutations occur at a rate of 10^{-6}. Mutations in this gene will cause an autosomal recessive disease. Homozygotes for the allele associated with the disease have a fitness which is 10% that of those not carrying that allele. SHOW ALL OF YOUR WORK, indicate all equations you use, and use clear labels.

Note: If you need the quadratic formula, it is: **[** $-b +/- \sqrt{(b^2 - 4ac)}$ **]** / 2a

(a, 6pts) Assume that, for many generations, this population has been at steady state because of a balance between mutation, selection for heterozygotes, and selection against affected individuals. Assume heterozygotes have a fitness which is 103% that of those not carrying the allele associated with the trait. Assume random mating. Calculate the steady-state value of q.

(b, 5pts) Now assume that, for many generations, this population has been at steady state because of a balance between mutation, inbreeding, and selection against affected individuals (i.e. there is NO heterozygote advantage in this population). For a very long time, 15% of all children have been products of uncle-niece matings (and the remaining 85% have been products of random matings).
What is F equal to for an uncle-niece mating?

(c, 7pts) Calculate the steady-state value of q for the situation described in part **(b)**.