This exam consists of two parts. Answer 5 of the 6 Short Answer questions in Part One, clearly indicating which questions you want me to grade by circling their numbers. If no questions are marked for grading, I will grade the first 5. Each short answer question is worth 15 points. The second part of the exam must be completed by all students. During the test today, you will complete the individual portion of this question. On Wednesday, you will get into your groups to complete the group portion. The second part of the exam is worth 25 points.

Name___________________________________

<table>
<thead>
<tr>
<th>CROSS</th>
<th>PROGENY</th>
<th>PROGENY GENOTYPES</th>
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<tbody>
<tr>
<td>RED X RED</td>
<td>ALL RED</td>
<td></td>
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<tr>
<td>WHITE X WHITE</td>
<td>ALL WHITE</td>
<td></td>
</tr>
<tr>
<td>ROAN X ROAN</td>
<td>105 RED</td>
<td>215 ROAN 95 WHITE</td>
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a) Propose a genetic hypothesis to account for these results, writing the genotypes of all progeny in the spaces provided in the table above.

b) Using Chi-Square analysis, determine if the results of the third cross (roan x roan) support your genetic hypothesis. $\chi^2 = \sum \frac{(O-E)^2}{E}$
2) In flowers, blue petal color is determined in part by the presence or absence of the enzyme flavonoid 3',5'-hydroxylase (F3'5'H), which converts dihydroquercetin, the precursor for red-colored anthocyanins to dihydromyricetin, the precursor for violet/blue anthocyanins, as shown in the figure below. Roses are seldom blue, because they generally do not make a functional F3'5'H enzyme.

![Chemical Reaction Diagram]

a) Assuming that the amount of F3'5'H produced by one allele is capable of converting all available dihydroquercetin to dihydromyricetin, would you expect a blue allele (F\(^1\)) introduced into roses by genetic engineering to be dominant or recessive to the wild-type red allele (F\(^2\))? Justify your answer.

b) In roses, the presence of thorns (T) is dominant to their absence (t) and double flowers (D) is dominant to single flowers (d).
   i. If you cross a F\(^1\)/F\(^2\); T/t; D/d rose with a F\(^1\)/F\(^1\); t/t; D/d rose, what proportion of the progeny will phenotypically resemble the first parent?
   
   ii. What proportion of the progeny are expected to have an F\(^1\)/F\(^2\); t/t; d/d genotype?
   
   iii. What proportion of the progeny are expected to genotypically resemble either parent?
3) Hypercholesterolemia is a rare disorder in humans that causes high cholesterol due to lowered numbers of low density lipoprotein (LDL) receptors. Base your answers to the following questions on the pedigree below, which shows the presence of Hypercholesterolemia in a family from central Pennsylvania.

![Pedigree Diagram]

a) What is the most likely mode of inheritance for this trait? Justify your answer.

b) Write the genotypes for all individuals in generation III under their corresponding numbers on the pedigree.

c) If II-2 and III-8 have children, what proportion would be expected to be affected?
4) During your fluorescence microscopy laboratories, you all got some really great pictures of mitotic nuclei using the Texas Red (TRITC), DAPI and FITC fluorochromes. I have produced an overlay picture of a typical mitotic spread from your lab, and it is shown below.

![Fluorescent Microscopy Image]

a) Which nuclear structure did the blue fluorochrome bind to? Was the stain a direct, indirect or immunofluorescent stain?

b) Which nuclear structure did the red fluorochrome bind to? Was the stain a direct, indirect or immunofluorescent stain?

c) What is happening to the chromosomes in this picture? Make sure you use the terms sister chromatids and/or homologous chromosomes in your answer, as appropriate.

d) The cells you used were from *Potorous tridactylis*, the rat kangaroo. In this species, females have 5 pairs of autosomes and 1 pair of X chromosomes, while males have 5 pairs of autosomes, 1 X chromosome, and 2 Y chromosomes (so females have 2n=12, and males have 2n=13!). Without going into any details about how this all works, answer the following questions:

i. If the cell above is female, and if female PtK cells have 3 billion base pairs of DNA in a haploid genome (n), how many base pairs are present in the cell depicted above?

ii. If the cell above is female, how many chromosomes will be present in each daughter nucleus at the end of mitosis?
5) “Pointed” cats have temperature-sensitive mutations in their tyrosinase gene, which is needed for the production of melanin. The mutant alleles all produce enzymes that are not functional at high temperatures, but that work just fine at lower ones. Thus, all of the cold parts of pointed cats are pigmented (ears, nose, legs and tails), while the warmer parts are paler. And yes, that does mean that if a Siamese cat moves from Texas to Alaska it will get darker. The picture below shows 3 types of pointed cats: Burmese, Siamese and Tonkinese, displaying the typical ‘sepia’, ‘mink’ and ‘point’ phenotypes characteristic of each breed.

Basing your answers on the data below, construct a concise genetic hypothesis to explain the inheritance of the sepia, mink and point coat color patterns in cats. Make sure you define all gene symbols that you use, that you show the dominance relationships between all of the alleles, and that you show the genotypes of all of the individuals (parents and offspring) in each cross.

<table>
<thead>
<tr>
<th>Parental Phenotypes</th>
<th>Offspring Genotypes</th>
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<tbody>
<tr>
<td>sepia x sepia</td>
<td>3/4 sepia, 1/4 mink</td>
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<tr>
<td>sepia x mink</td>
<td>1/2 sepia, 1/4 mink, 1/4 point</td>
</tr>
<tr>
<td>mink x mink</td>
<td>3/4 mink, 1/4 point</td>
</tr>
<tr>
<td>sepia x sepia</td>
<td>3/4 sepia, 1/4 point</td>
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6) The Lovebird is an extremely popular pet due to its incredible color variety. One type of color, called Lutino, has a mutation that prevents the production of dark melanin, leaving behind the yellow and red carotenoids as primary color pigments. Typical Lutino Lovebirds are shown below.

![Lovebird Pair](image)

The Lutino color is due to a sex-linked recessive allele, \( Z^{l} \), while normal color is due to the dominant \( Z^{L} \) allele. Based on this knowledge, and on your knowledge of the inheritance of sex-linked traits in birds in general (Lovebirds are just like chickens in this regard), predict the phenotypic and genotypic ratios that you would see from the following crosses:

1) A purebred Lutino male x a purebred normal female

2) A cross between the male and female \( F_1 \) offspring from cross (1).

PART TWO. Answer this question completely. It will form the basis for your team question on Wednesday.
7) The Agouti color in mice is due to an alternating pattern of yellow and black bands in the hair shaft. Yellow mice lack the black pigment, and black mice lack the yellow pigment. You are in charge of mouse breeding in a large genetics research lab, and have just discovered a new yellow variety that never breeds true. In an attempt to determine just how this trait is inherited, you embark upon a series of traditional genetic crosses between 8 different mice (labeled A–H below). You also perform RFLP analysis on each of these individuals. The data are shown below:

Cross 1: Yellow (A) x Yellow (B) 48 Yellow: 25 Black
Cross 2: Black (C) x Black (D) All Black
Cross 3: Yellow (E) x Agouti (F) 48 Yellow: 22 Black: 24 Agouti
Cross 4: Agouti (G) x Agouti (H) All Agouti

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
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Figure 1: RFLP analysis of the coat color gene in mice. DNA from individuals A–H in the crosses above are depicted in wells A–H, respectively. The relative migration of DNA size standard fragments is shown to the right of the figure.

Based on the information above, provide a genetic hypothesis to account for all of the data. Make sure to define all alleles present in the population, write down the phenotype associated with each genotype, and give the size, in base pairs, for the RFLP associated with each coat color allele.

a) List alleles present in the population, using correct nomenclature:

b) List all possible genotypes in the population (not just those in the crosses), and their associated phenotypes:

c) List all alleles, and then give the size, in base pairs, of the RFLP associated with each one.
8) Your research advisor is thrilled with you! On Monday, you successfully determined that coat color in your mice was determined by three alleles of a single gene, with the following dominance relationships:

\[ Y \text{ (yellow allele)} > y^1 \text{ (agouti allele)} > y^2 \text{ (black allele)} \]

Furthermore, your RFLP analyses determined that the 400 bp fragment was associated with the Y allele, the 200 bp fragment was associated with the \( y^1 \) allele, and the 500 bp fragment was associated with the \( y^2 \) allele, as depicted on the gel below:

As a reminder, your original crosses were:

Cross 1: Yellow (A) x Yellow (B) 48 Yellow: 25 Black
Cross 2: Black (C) x Black (D) All Black
Cross 3: Yellow (E) x Agouti (F) 48 Yellow: 22 Black: 24 Agouti
Cross 4: Agouti (G) x Agouti (H) All Agouti

Using the information from these crosses, as well as from the gel above, you correctly deduced that mice A, B and E had \( Yy^2 \) genotypes, mice C and D had \( y^2y^2 \) genotypes, mice F and G had \( y^1y^2 \) genotypes, and mouse H had the \( y^1y^1 \) genotype. YY genotypes never showed up because they were lethal.

As you were basking in your glory, and preparing for a weekend of well-deserved celebration, your research advisor squinted at a couple of your mice and said, “Hey! What’s That?” Looking closely, you discovered that several of the yellow mice were actually pale yellow, and several of the black mice were pale blue-ish black. Feeling your relaxing weekend fading rapidly into oblivion, you grinned and said, “I’ll have an answer to you by Monday!”

Thus began another series of crosses and RFLP analyses. The results can be seen on the next page. As you analyze these results, remember that NOTHING HAS CHANGED for the original information you have about the Y gene and its three alleles. The system is simply more complex than you originally thought.
When you cross the original mouse A (Yellow, full color) with original mouse C (Black, full color), and perform an RFLP analysis that can analyze both the Y gene alleles AND the new color variations, the progeny are 3/8 Yellow, full color (1/8 have RFLP profile I, and 2/8 have profile J); 1/8 Yellow, Pale (with the RFLP profile seen in Lane K; 3/8 are Black, Full color (1/8 with profile L, and 2/8 with profile M); and 1/8 are pale, blue-ish black with the RFLP profile seen in lane N.

![Genetic Diagram]

a) Propose a genetic hypothesis that accounts for this new data, clearly defining all gene symbols and determining which of the new RFLP fragments is associated with each of your new alleles.

b) If individuals K and L are crossed, what phenotypic ratios do you expect in their offspring?

c) You added EZ Vision Dye to each of your samples immediately prior to loading them into the gel. Tell me two things that this dye does to make your experimental analysis possible.